

EP 1 130 094 A2

	MAMMA1001161	4.3	5.27	19.53	18.34	10.8	14.8
5	MAMMA1001162	1.98	1.77	3.16	5.25	5.13	2.25
	MAMMA1001181	2.44	2.28	4.87	5.06	4.74	3.62
	MAMMA1001186	2	2.66	4.66	5.38	5.48	3.9
	MAMMA1001189	2.23	3.68	7.17	11	11.17	9.9 *
	MAMMA1001191	2.54	2.07	5.49	4.37	3.89	2.97
10	MAMMA1001198	368.47	416.05	784.82	647.17	738.61	605.52
	MAMMA1001202	11.78	11.85	30.06	34.39	28.74	25.16
	MAMMA1001203	2.57	3.01	7.15	8.72	6.26	5.56
	MAMMA1001206	1.91	3.28	4.5	3.69	6.66	2.65
	MAMMA1001208	2.66	2.93	3.31	3.82	4.95	3.19
15	MAMMA1001215	2.9	3.08	6.55	3.49	8.09	4.74
	MAMMA1001220	2.63	3.03	7.25	7.16	7.17	6.03
	MAMMA1001222	1.25	1.18	4.18	2.18	5.85	0.53
	MAMMA1001223	2.48	3.32	6.53	4.95	6.51	4.1
	MAMMA1001232	2.82	4.27	8.08	12.22	8.82	9.57
20	MAMMA1001234	1.25	3.27	3.17	5.05	3.91	3.26
	MAMMA1001237	1.22	1.56	4.21	1.94	3.66	2.09
	MAMMA1001243	2.18	2.28	4.06	4.05	4.89	1.99
	MAMMA1001244	1.22	1.16	2.86	2.96	4.79	2.22
	MAMMA1001249	2.3	1.89	5.93	5.19	5.8	3.75
25	MAMMA1001256	3	3.09	8.29	5.89	7.83	8.01
	MAMMA1001259	4.38	3.25	7.15	7.94	9.24	6.63
	MAMMA1001260	1.76	2.71	5.42	6.51	5.33	7.33
	MAMMA1001262	2.1	4.11	5.28	7.86	8.04	6.25 *
	MAMMA1001268	2	2.16	4.59	2.56	4.23	2.48
30	MAMMA1001271	4.84	5.78	17.37	18.29	14.24	15.67
	MAMMA1001274	2.88	3.06	6.17	6.22	8.55	7.93
	MAMMA1001280	2.09	1.48	4.36	1.84	3.78	1.73
	MAMMA1001283	1.63	1.71	6.34	6.88	5.63	4.83
	MAMMA1001284	2.27	2	8.67	5.08	9.09	9.51
35	MAMMA1001286	13.83	9.72	17.39	12.15	11.83	14.63
	MAMMA1001289	17.63	13.49	23.32	21.02	26.39	36.8
	MAMMA1001292	3	3.01	5.94	7.26	6.31	6.85 *
	MAMMA1001296	3.55	3.76	12.61	14.11	12.37	12.8
	MAMMA1001298	1.26	1.7	6.26	4.25	6.78	4.07
40	MAMMA1001305	0.86	1.59	4.43	2.49	4.07	2.63
	MAMMA1001309	0.61	0.9	2.7	1.84	3	1.49
	MAMMA1001310	1.72	2.17	3.64	4.81	7.38	4.42
	MAMMA1001322	0.99	1.54	1.83	2.83	1.77	2.13
	MAMMA1001324	1.3	1.12	3.16	2.03	2.83	1.94
45	MAMMA1001330	3.35	2.65	9.53	7.93	9.75	5.36
	MAMMA1001333	3.1	3.74	10.23	9.88	11.4	9.07
	MAMMA1001334	5.53	4.17	4.83	10.97	8.23	10.16 **
	MAMMA1001337	2.49	3.54	6.6	6.99	9.16	8.05 *
	MAMMA1001341	1.21	1.14	3.48	1.54	5.66	1.41
50	MAMMA1001343	2.37	1.89	8.07	8.17	9.75	10.95
	MAMMA1001344	9.59	9.07	11.75	13.63	11.67	15.98
	MAMMA1001346	1.34	1.25	3.9	2.05	3.9	2.94
	MAMMA1001383	3.07	3.61	8.52	8.3	9.02	9.38
	MAMMA1001388	1.62	1.93	5.34	3.38	6.11	4.58
55	MAMMA1001396	4.2	2.12	8.12	11.39	10.42	8.68

EP 1 130 094 A2

	MAMMA1001397	2.59	2.27	5.79	8.33	8.96	7.78	*	+
5	MAMMA1001401	26.87	16.48	32.72	43.47	57.55	45.66	*	+
	MAMMA1001408	1.06	1.06	2.57	0.65	4.22	1.19		
	MAMMA1001411	1.65	1.26	3.84	4.38	3.33	3.51		
	MAMMA1001414	3.12	3.85	5.74	12.58	10.67	15.28	**	+
	MAMMA1001415	2.45	3.16	11.93	14.57	20.15	13.69	*	+
10	MAMMA1001418	0.66	2.2	5.36	3.57	6.04	4.46		
	MAMMA1001419	0.8	2.43	4.93	6.03	7.01	3.92		
	MAMMA1001420	0.96	3.09	4.5	3.23	4.11	3.41		
	MAMMA1001426	20.24	32.21	42.42	44.31	39.63	38.75		
	MAMMA1001428	1.94	2.83	6.35	3.8	6.93	4.33		
15	MAMMA1001432	1.19	2.33	8.19	5.62	6.19	6.68		
	MAMMA1001435	1.43	0.78	3.32	3.48	3.67	2.64		
	MAMMA1001442	1.96	3.94	7.41	8.18	8.6	6.63		
	MAMMA1001446	2.17	2.57	6.71	6.9	7.34	7.97		
	MAMMA1001450	1.22	2.05	3.58	2.81	4.18	2.39		
20	MAMMA1001452	1.99	1.78	5.92	8.38	6.19	4.83		
	MAMMA1001465	3.93	3.25	13.61	16.65	14.6	13.82		
	MAMMA1001476	1.63	1.09	4.25	5.87	5.95	4.64	*	+
	MAMMA1001478	2.28	2.12	5.98	3.55	6.27	4.19		
	MAMMA1001479	3.11	4.71	8.32	5.58	6.74	6.21		
25	MAMMA1001487	1.1	1.14	3.84	4.73	3.26	2.08		
	MAMMA1001498	1.93	3.41	7.78	6.17	7.45	5.64		
	MAMMA1001501	0.88	1.97	4.49	2.8	4.77	2.36		
	MAMMA1001502	1.82	1.91	6.48	3.29	6.29	6.26		
	MAMMA1001510	0.48	0.78	2.92	0.54	3.04	1.19		
30	MAMMA1001522	1.03	1.29	3.94	5.05	4.9	3.39		
	MAMMA1001529	0.72	2.06	3.22	3.74	4.07	2.57		
	MAMMA1001532	1.74	1.86	4.27	3.79	5.71	3.12		
	MAMMA1001533	0.61	1.31	2.9	1.52	3.06	1.64		
35	MAMMA1001534	0.44	2.59	2.4	1.48	3.64	1.14		
	MAMMA1001535	1.38	1.91	3.99	2.12	3.98	2.38		
	MAMMA1001547	2.8	2.89	7.77	9.23	8.22	6.22		
	MAMMA1001551	1.1	1.48	4.46	2.23	2.88	2.99		
	MAMMA1001569	1.27	1.68	3.41	2.03	3.41	1.94		
40	MAMMA1001575	1.48	2.41	3.42	4.01	4.43	2.81		
	MAMMA1001576	4.79	8.23	9.65	14.75	9.39	17.03		
	MAMMA1001584	0.89	2.48	3.33	3.11	4	3.09		
	MAMMA1001586	1.43	2.41	3.34	3.78	3.31	1.84		
	MAMMA1001590	2.96	2.53	5.55	5.44	6.47	6.04		
45	MAMMA1001599	4.64	7.15	16.79	15.8	15.18	15.06		
	MAMMA1001600	1.45	2.22	4.73	2.98	4.68	2.11		
	MAMMA1001604	1.03	1.76	3.62	2.35	4.01	1.64		
	MAMMA1001606	1.64	2.04	5.15	3.58	5.45	4.27		
	MAMMA1001609	1.31	2.37	4.36	3.05	5.43	1.59		
50	MAMMA1001614	2.91	3.57	6.15	5.94	6.11	4.14		
	MAMMA1001615	3.98	2.61	10.12	8.87	8.29	8.41		
	MAMMA1001619	7.73	7.8	14.29	16.33	12.93	14.61		
	MAMMA1001620	2.53	2.41	7.98	5.77	7.13	4.54		
	MAMMA1001623	4.11	4.58	9.3	7.34	9.28	6.75		
55	MAMMA1001626	0.83	1.98	2.52	3.24	3.93	1.93		
	MAMMA1001627	1.11	1.98	3.57	2.63	3.68	1.63		

EP 1130 094 A2

	MAMMA1001630	2.02	3.08	7.83	7.49	7.53	4.29		
5	MAMMA1001633	2.64	3.12	8.8	12.09	9.59	6.16		
	MAMMA1001634	2.83	2.7	6.11	8.69	8.27	6.9	*	+
	MAMMA1001635	5.65	2.39	9.52	7.92	8.3	8.37		
10	MAMMA1001649	1.61	1.63	4.71	2.95	4.62	2.53		
	MAMMA1001654	8.14	9.45	39	43.4	55	46.79		
	MAMMA1001660	19.61	17.92	37.43	40.94	27.03	34		
	MAMMA1001663	1.9	4.73	9.42	9.59	9.56	6.58		
	MAMMA1001670	1.12	2.66	3.97	3.65	4.09	2.62		
	MAMMA1001671	1.08	1.42	3.56	1.37	4.64	1.77		
	MAMMA1001679	6.85	6.37	13.89	11.48	17.04	13.91		
15	MAMMA1001683	2.15	3.29	9.6	6.58	6.53	6.96		
	MAMMA1001686	1.25	1.34	3.77	1.39	2.97	3.06		
	MAMMA1001688	113.39	113.61	245.56	392.2	458.41	413	**	+
	MAMMA1001689	1.01	3.76	4.1	5.04	3.79	4.44		
	MAMMA1001692	1.97	2.59	5.37	3.66	5.3	3.88		
20	MAMMA1001711	1.99	3.64	8.65	4.35	5.51	6.1		
	MAMMA1001715	1.31	1.64	3.95	4.64	4.87	4.13		
	MAMMA1001730	2.01	2.15	2.5	2.8	4.42	2.83		
	MAMMA1001735	44.73	48.32	102.35	94.99	156.23	119.88		
	MAMMA1001740	0.64	1.6	4.59	2.06	3.91	1.95		
25	MAMMA1001743	9.84	11.15	33.16	41.97	51.62	49.6	*	+
	MAMMA1001744	0.63	0.72	0.86	1.1	1.72	1.71	*	+
	MAMMA1001745	1.41	2.15	6.15	3.27	4.46	3.93		
	MAMMA1001751	1.38	2.41	3.24	2.85	4.51	4.32		
	MAMMA1001752	4.7	4.78	9.75	6.12	9.61	8.4		
30	MAMMA1001754	7.25	7.89	7.34	11.04	9.63	9.39	*	+
	MAMMA1001757	1.21	1.1	2.32	2.21	3.25	2.43		
	MAMMA1001760	3.87	4.52	20.01	22.91	24.2	27.59	*	+
	MAMMA1001764	2.62	2.36	5.97	7.13	10.17	6.51		
	MAMMA1001767	1.22	1.55	2.13	1.61	2.96	1.55		
35	MAMMA1001768	0.57	1.18	4.25	4.74	4.72	4.37		
	MAMMA1001769	2.48	2.83	9.22	9.3	9.81	8.94		
	MAMMA1001771	2.66	1.58	3.74	2.86	5.85	6.77		
	MAMMA1001773	2.7	3.53	3.87	4	6.29	7.61		
	MAMMA1001778	0.88	1.92	3.14	3.13	4.21	3.61		
	MAMMA1001783	2.01	2.1	11.25	11.63	18.46	13.04		
40	MAMMA1001785	3	3.52	8.85	10.56	13.38	11	*	+
	MAMMA1001788	0.49	0.86	1.21	0.72	1.72	1.11		
	MAMMA1001790	1.68	1.67	5.1	2.37	3.73	3.93		
	MAMMA1001800	0.83	0.99	1.47	1.5	2.24	3.25		
45	MAMMA1001804	1.02	1.41	3.18	2.37	4.16	2.4		
	MAMMA1001806	2.13	2.78	6.4	3.15	5.5	4.72		
	MAMMA1001812	1.46	1.33	5.52	4.21	5.86	5.05		
	MAMMA1001815	0.33	1.76	3.07	1.22	3.67	1.24		
	MAMMA1001817	3.19	3.38	9.5	6.78	10.89	13.3		
50	MAMMA1001818	1.68	2.08	3.41	3.94	8.52	3.41		
	MAMMA1001819	2.57	4.12	5.82	8.7	10.29	7.87	*	+
	MAMMA1001820	2.68	4.51	8.27	7.51	10.98	6.07		
	MAMMA1001824	1.66	2.83	8.36	7.55	9.8	7.11		
	MAMMA1001832	6.72	7.99	11.85	20.17	21.28	17.21	**	+
55	MAMMA1001836	1.74	1.66	5.08	4.79	8.19	4.88		

EP 1 130 094 A2

	MAMMA1001837	2.61	2	5.84	7.1	9.19	5.37
5	MAMMA1001848	1.02	1.61	3.3	2.81	5.33	3.18
	MAMMA1001850	3.79	4.51	9.31	9.98	9.93	14.19
	MAMMA1001851	1.49	2.33	4.98	4.97	4.12	4.02
	MAMMA1001852	2.98	4	9.68	6.4	7.56	6.8
10	MAMMA1001854	2.56	3.11	9.16	10.59	10.64	9.98
	MAMMA1001858	3.11	2.22	5.28	9.93	7.91	8.87 ** +
	MAMMA1001864	1.69	1.91	4.09	8.91	6.18	4.37
	MAMMA1001868	0.71	0.92	2.64	1.68	2.58	0.91
	MAMMA1001874	1.2	0.87	2.52	1.06	3.48	1.17
	MAMMA1001878	3.1	3.46	10.86	7.7	13.37	6.77
15	MAMMA1001880	2.67	2.99	7.24	5.58	7.17	8.12
	MAMMA1001885	1.14	1.93	6.19	4.7	5.54	4.58
	MAMMA1001890	3.54	3.95	12.93	13.59	13.29	12.2
	MAMMA1001893	3.74	3.42	6.25	6.59	5.49	5.58
	MAMMA1001901	1.13	1.5	5.4	4.53	5.72	2.67
20	MAMMA1001907	2.57	1.62	6.43	4.15	7.36	6.34
	MAMMA1001908	3.2	3.36	8.35	11.83	12.96	12.46 * +
	MAMMA1001919	0.23	0.97	3.3	2.24	3.9	2.07
	MAMMA1001931	0.76	1.65	4.04	3.36	5.89	3.25
	MAMMA1001937	2.27	3.15	5.5	6.44	5.06	3.78
25	MAMMA1001951	1.74	2.57	6.47	6.48	6.15	4.83
	MAMMA1001956	3.02	3.48	9.72	8.52	7.66	6.76
	MAMMA1001957	3.39	3.51	9.15	7.88	9.47	7.66
	MAMMA1001960	3.1	3.34	7.24	12.06	9.14	6.1
	MAMMA1001963	0.57	0.78	2.14	1.3	2.36	1.06
30	MAMMA1001969	1.7	3.43	10.86	8.54	11.14	8.74
	MAMMA1001970	2.86	3.04	8.48	13.11	6.59	6.64
	MAMMA1001978	0.57	1.85	1.76	2.42	3.87	1.53
	MAMMA1001992	2.07	2.04	5.65	6.79	6.75	5.09
	MAMMA1001994	7.97	3.65	11	18.83	13.23	17.17 * +
35	MAMMA1002008	3.28	3.77	6.42	3.43	4.06	1.24
	MAMMA1002009	1.46	2.94	5.17	5.73	7.57	4.06
	MAMMA1002011	1.77	1.71	4.26	6.5	6.45	3.37
	MAMMA1002022	1.51	2.1	5.92	6.64	7.42	5.2
40	MAMMA1002024	9.79	9.67	19.03	17.61	16.96	22.43
	MAMMA1002032	2.78	2.41	7.25	5.29	6.16	8.07
	MAMMA1002033	3.23	3.95	7.73	11.24	7.23	6.62
	MAMMA1002041	2.87	2.25	3.18	4.74	5.39	1.71
	MAMMA1002042	2.54	2.34	5.66	5.65	5.78	3.76
45	MAMMA1002045	2.33	3.51	7.28	8.39	5.05	4.44
	MAMMA1002047	2.58	2.98	8.83	8.7	8.9	6.89
	MAMMA1002056	2.01	5.78	11.14	11.35	10.64	9.14
	MAMMA1002058	1.67	2.61	8.19	4.84	4.66	4.27
	MAMMA1002060	1.08	2.08	1.41	2.5	4.09	1.2
50	MAMMA1002065	1.81	2.75	6.04	7.19	5.19	3.26
	MAMMA1002068	2.43	1.84	5.29	4.98	5.6	4.47
	MAMMA1002070	4.5	2.92	4.15	2.58	5.23	2.81
	MAMMA1002078	1.32	1.43	2.94	1.12	4.4	1.07
	MAMMA1002080	7.98	9.71	13.38	14.92	20.84	14.26
55	MAMMA1002082	2.54	4.96	13.04	9.67	8.15	7.78
	MAMMA1002084	1.78	3.47	3.38	4.68	4.48	3.6

EP 1 130 094 A2

	MAMMA1002087	1.12	2.15	5.37	3.6	4.67	2.36		
5	MAMMA1002091	3.79	3.22	4.32	7.18	6.76	6.41	**	+
	MAMMA1002093	0.72	1.4	4.31	2.74	4.39	2.33		
	MAMMA1002095	2.4	3.22	7.5	4.73	7.52	4.54		
10	MAMMA1002108	1.84	1.02	2.63	1.87	3.24	1.31		
	MAMMA1002112	2.94	3.4	7.03	12.79	16.02	11.28	**	+
	MAMMA1002118	1.02	1.61	2.24	1.41	3.18	2.01		
15	MAMMA1002119	0.76	2.15	3.61	1.51	3.12	2.54		
	MAMMA1002125	1.79	2.61	6.95	4.52	4.19	4.11		
	MAMMA1002126	3.72	4.25	9.79	10.08	9.02	11.03		
	MAMMA1002128	0.9	2.36	3.07	2.7	3.49	2.88		
20	MAMMA1002132	3.78	3.24	11.42	6.18	9.05	6.81		
	MAMMA1002140	1.46	1.87	3.68	2.18	3.24	2.33		
25	MAMMA1002142	3.13	3.43	7.06	5.18	7.62	5.46		
	MAMMA1002143	5.42	2.27	7.96	7.98	9.87	13.23		
	MAMMA1002145	1.47	1.34	3.3	2.9	4.02	2.64		
	MAMMA1002147	0.81	1.59	2.9	2.71	4.4	3		
30	MAMMA1002153	0.99	1.92	5.55	3.52	6.41	4.75		
	MAMMA1002155	2.11	1.93	6.76	4.4	6.46	4.46		
	MAMMA1002156	0.81	0.8	1.94	0.67	2.63	0.78		
	MAMMA1002158	1.38	1.83	5.12	4.09	7.73	5.2		
35	MAMMA1002164	2.01	2.09	5.86	3.17	3.18	4.04		
	MAMMA1002165	4.04	4.29	7.25	8.65	8.1	6.81		
	MAMMA1002170	1.01	1.48	154.53	2.65	3.24	4.11		
	MAMMA1002174	1.66	2.9	5.88	4.55	7.78	8.58		
	MAMMA1002175	3.27	3.3	7.02	6.95	6.64	7.22		
40	MAMMA1002180	8.59	6.53	35.97	55.49	48.49	51.08	*	+
	MAMMA1002198	3.11	2.3	9.33	7.6	11.22	7.13		
	MAMMA1002205	2.93	1.66	6.15	6.3	8.04	7.54		
	MAMMA1002206	4.6	3.59	8.14	12.4	13.97	11.74	**	+
45	MAMMA1002209	1.7	1.93	4.03	4.43	4.23	4.57		
	MAMMA1002215	4.17	2.72	15.2	11.05	12.43	17.14		
	MAMMA1002219	1.57	1.96	4.99	4.84	6.34	5.96		
	MAMMA1002224	3.18	2.9	8.18	5.49	7.25	5.86		
50	MAMMA1002229	3.74	2.21	8.83	8.48	9.26	6.82		
	MAMMA1002230	2.02	2.21	6.63	5.31	8.91	6.58		
	MAMMA1002233	3.01	1.6	6.03	4.21	7.91	6.14		
55	MAMMA1002234	3.05	3.06	6.7	8.6	10.45	10.76	*	+
	MAMMA1002236	4.13	3.68	14.08	26.56	20.38	24.71	*	+
	MAMMA1002243	0.97	2.48	3.48	3.28	3.43	2.96		
	MAMMA1002250	1.06	2.09	5.2	3.95	6.82	6.01		
	MAMMA1002253	2.77	2.39	3.45	4.84	6.18	3.37		
	MAMMA1002267	17.17	19.95	51.7	130.02	108.53	115.75	**	+
	MAMMA1002268	1.72	2.28	5.82	6.92	11.3	6.52		
	MAMMA1002269	0.89	0.73	2.25	2.32	2.58	1.67		
	MAMMA1002282	0.86	1.09	4.95	5.87	5.31	6.81		
	MAMMA1002292	2.71	2.25	7.77	10.57	10.52	11.53	*	+
	MAMMA1002293	3.71	3.31	12.81	8.54	10.47	12.05		
	MAMMA1002294	0.9	1.71	4.61	3.68	6.03	4.2		
	MAMMA1002297	1.53	3.25	7.45	5.77	7.8	6.91		
	MAMMA1002298	1.48	1.4	3.98	3.85	3.11	2.46		
55	MAMMA1002299	1.5	1.69	3.16	3.91	2.97	2.2		

EP 1 130 094 A2

	MAMMA1002308	1.39	1.35	6.55	4.5	3.11	2.54		
5	MAMMA1002310	3.56	3.84	12.73	9.92	12.66	11.48		
	MAMMA1002311	2.52	2.13	6.82	9.61	9.66	6.9 *	+	
	MAMMA1002312	1.63	2.22	5.19	3.51	8.45	2.55		
10	MAMMA1002317	2.08	2.55	4.89	4.08	3.85	4.09		
	MAMMA1002319	0.8	2.78	3.51	2.68	3.97	2.85		
	MAMMA1002322	2.48	3.23	7.84	12.21	10.02	8.55	*	+
15	MAMMA1002329	1.64	1.67	2.93	2.9	3.3	2.76		
	MAMMA1002332	2.17	2.38	4.58	5.98	4.14	3.05		
	MAMMA1002333	1.7	1.74	4.19	5.35	5.07	3.54		
20	MAMMA1002335	1.75	2.72	8.53	6.93	11.32	4.23		
	MAMMA1002339	2.09	2.42	7.34	5.21	7.5	5.14		
25	MAMMA1002347	1.7	2.3	6.39	5.5	5.32	4.64		
	MAMMA1002351	2.08	2.68	5.74	3.03	4.48	4.84		
	MAMMA1002352	1.27	2.28	3.66	3.53	4.63	2.8		
	MAMMA1002353	4.46	2.5	5.84	5.95	4.19	4		
30	MAMMA1002355	3.97	3.38	8.37	7.98	7.31	8.57		
	MAMMA1002356	2.18	1.49	4.36	5.43	4.13	3.75		
	MAMMA1002359	3.95	3.35	16.09	23.81	24.53	19 *	+	
	MAMMA1002360	0.93	1.73	3.77	2.48	3.2	1.67		
	MAMMA1002361	2.01	2.64	4.53	4.17	4.95	4.03		
35	MAMMA1002362	2.33	2.33	3.36	5.31	5.51	3.99	*	+
	MAMMA1002367	2.97	3.64	14.63	18.34	21.06	21.56	*	+
	MAMMA1002371	2.28	3.75	8.3	6.15	6.74	5.88		
	MAMMA1002380	1.81	2.26	4.9	4.71	5.76	3.55		
	MAMMA1002384	2.14	1.53	4.73	4.48	5.36	4.05		
40	MAMMA1002385	1.19	2.05	5.63	3.34	4.8	2.47		
	MAMMA1002390	1.41	2.04	3.75	5.48	5.4	3.43		
	MAMMA1002392	1.94	3.1	6.1	4.06	5.95	3.32		
	MAMMA1002396	4.87	3.49	12.87	10.79	12.9	8.08		
	MAMMA1002399	4.42	5.13	10.69	10.95	8.66	4.57		
45	MAMMA1002400	3	2.22	4.69	3.11	4.36	3.53		
	MAMMA1002409	51.57	55.16	63.3	77.54	80.62	77.88	**	+
	MAMMA1002411	1.08	1.88	4.13	3.43	5.49	1.92		
	MAMMA1002413	2.02	3.01	9.19	5.93	7.17	6.75		
	MAMMA1002417	1.83	2.24	4.87	3.45	4.25	2.63		
50	MAMMA1002427	1.5	2.38	4.54	4.78	5.56	3.41		
	MAMMA1002428	2.47	2.26	5.38	4.46	5.11	4.28		
	MAMMA1002433	1.74	2.18	6.84	6.72	6.96	6.22		
	MAMMA1002434	2.94	2.4	7.38	5.34	4.65	5.03		
	MAMMA1002446	1.39	2.34	5.62	3.98	5.84	5.96		
55	MAMMA1002447	2.51	1.38	6.4	5.11	6.26	5.45		
	MAMMA1002454	7.77	9.16	18.07	21.71	17.12	18.35		
	MAMMA1002461	2.06	4.11	7.7	4.92	5.41	6.47		
	MAMMA1002463	3.28	3.32	8.09	6.98	7.82	5.39		
	MAMMA1002464	16.58	16.77	20.05	19.41	20.41	18.09		
	MAMMA1002466	9.48	9.89	14.22	14.58	15.75	13.93		
	MAMMA1002470	1.39	1.51	5.13	3.54	5.01	3.73		
	MAMMA1002475	0.72	1.85	5.03	3.86	5.17	4.65		
	MAMMA1002480	0.66	1.21	2.31	1.68	2.84	2.03		
	MAMMA1002485	29.98	27.24	46.09	64.83	74.9	80.68	**	+
55	MAMMA1002494	2	2	4.11	4.48	5.12	5.13	*	+

EP 1 130 094 A2

	MAMMA1002498	0.97	2.57	3.16	2.07	3.18	1.55
5	MAMMA1002524	3.04	2.96	6.43	5.18	7.34	6.1
	MAMMA1002530	2.5	3.24	4.88	3.17	4.41	2.55
	MAMMA1002538	2.34	2.38	5.62	5.46	5.13	4.91
	MAMMA1002545	2.37	2.64	6.26	4.56	6.49	4.56
	MAMMA1002554	1.96	1.42	5.43	5.3	6.01	7.81
	MAMMA1002556	1.3	1.9	3.6	3.73	5.75	3.89
10	MAMMA1002561	2.3	2.99	7.19	8.13	10.46	7.98
	MAMMA1002565	1.22	2.15	3.52	2.57	4.51	2.55
	MAMMA1002566	0.98	1.87	6.21	1.65	4.7	3.9
	MAMMA1002571	0.53	1.8	3.06	1.43	3.1	4.3
	MAMMA1002573	2.14	1.86	7.06	4.54	5.66	5.97
15	MAMMA1002576	118.77	131.84	363.97	348.62	471.73	358.66
	MAMMA1002584	3.52	2.27	11.91	12.86	17.82	13.46
	MAMMA1002585	0.76	1.86	4.38	1.85	3.6	5.26
	MAMMA1002586	1.98	2.55	3.85	4.12	5.02	3.3
	MAMMA1002589	1.08	1.26	2.44	2.36	5.06	3.19
20	MAMMA1002590	1.01	1.57	5.87	2.58	6.75	4.57
	MAMMA1002593	2.48	2.48	4.89	4.18	4.07	3.04
	MAMMA1002597	2.47	2.52	7.25	8.06	9.48	8.78 * +
	MAMMA1002598	12.12	13.52	30.83	37.28	48.14	38.91 * +
	MAMMA1002603	1.2	1.39	3.69	3.25	6.24	4.35
25	MAMMA1002612	3.51	3.39	12.6	7.66	7.78	9.76
	MAMMA1002617	4.3	3.41	10.15	6.3	7.29	10.05
	MAMMA1002618	1.68	2.27	4.02	2.76	3.59	3.91
	MAMMA1002619	2.96	2.8	5.24	3.22	5.88	3.49
	MAMMA1002622	2.51	2.12	8.02	7.1	7.18	7.15
30	MAMMA1002623	2.31	2.21	6.27	5.89	6.17	6.19
	MAMMA1002625	1.32	1.3	3.23	2.3	6.42	2.6
	MAMMA1002627	0.98	0.82	2.93	0.6	1.29	0.21
	MAMMA1002629	1.8	2.23	6.09	5.03	6.74	7.02
	MAMMA1002631	1	1.86	3.61	3.07	4.55	2.97
35	MAMMA1002633	6.61	7.44	21.47	19.33	24.55	21.53
	MAMMA1002636	1.02	2.46	6.97	6.79	8.77	9.25
	MAMMA1002637	1.05	1.4	4.66	3.39	4.85	4.28
	MAMMA1002646	1.69	0.8	3.32	2.33	2.86	1.53
40	MAMMA1002648	10.51	14.07	21.18	42.29	31.45	39.76 ** +
	MAMMA1002650	1.33	0.56	1.62	1.76	2.08	0.57
	MAMMA1002652	1.76	2.82	7.31	7.5	7.41	9.79
	MAMMA1002655	1.7	2.11	3.65	2.54	4.23	3.78
	MAMMA1002662	0.84	2.24	4.33	3.57	5.68	4.13
45	MAMMA1002665	3.61	3.57	10.05	13.42	17.97	19.59 * +
	MAMMA1002671	2.84	3.63	10.17	17.04	16.47	19.3 ** +
	MAMMA1002673	1.32	2.14	4.93	4.07	5.03	2.82
	MAMMA1002684	2.95	3.11	3.84	6.61	8.19	7.54 ** +
	MAMMA1002685	0.68	1.49	2.57	2.05	3.74	2.97
50	MAMMA1002692	1.28	1.96	5.45	2.46	4.14	3.62
	MAMMA1002693	1.84	4.18	8	4.63	7.68	6.61
	MAMMA1002698	0.99	1.91	4.05	2.92	4.42	3.3
	MAMMA1002699	2	2.35	4.43	4.05	5.22	3.64
	MAMMA1002701	2.41	2.56	8.46	6.72	8.94	8.93
55	MAMMA1002708	1.51	1.55	5.38	4.08	6.16	6.18

EP 1 130 094 A2

	MAMMA1002711	1.58	2.08	7.04	4.37	7.35	5.81		
5	MAMMA1002712	3.05	3.13	6.98	4.88	7.12	7.39		
	MAMMA1002716	0.56	1.75	3.39	2.38	6.29	2.9		
	MAMMA1002721	2.11	2.01	5.57	3.72	6.34	4.59		
	MAMMA1002723	2.43	2.46	4.91	3.85	5.98	4.88		
	MAMMA1002727	3.85	5.55	5.78	5.29	4.45	6.22		
	MAMMA1002728	21.35	22.03	57.81	49.09	54.73	65.13		
10	MAMMA1002742	4.12	4.39	10.35	7.92	8.63	7.61		
	MAMMA1002743	4.12	3.89	6.17	13.81	14.09	13.46	**	+
	MAMMA1002744	2.07	3.15	9.18	9.33	12.98	13.16		
	MAMMA1002746	0.93	1.28	3.09	2.29	4.31	1.68		
	MAMMA1002748	2.71	2.65	4.52	7.15	5.86	4.72	*	+
15	MAMMA1002754	1.12	2.41	5.56	5.05	5.65	6.26		
	MAMMA1002758	0.71	1.66	2.55	1.57	4.41	1.69		
	MAMMA1002762	11.3	11.14	36.64	38.42	34.23	48.71		
	MAMMA1002764	1.83	3.2	5.95	5.11	6.06	4.26		
	MAMMA1002765	1.19	1.63	4.29	4.63	5.26	2.67		
20	MAMMA1002769	7.4	6.44	13.04	13.78	8.03	12.41		
	MAMMA1002771	1.41	2.41	3.31	3.54	5.39	4.39		
	MAMMA1002775	4.56	4.48	19.79	22.54	29.77	24.29	*	+
	MAMMA1002780	2.59	1.83	3.03	2.11	4.89	3.78		
	MAMMA1002782	1.43	2.49	3.85	2.51	4.79	4.11		
25	MAMMA1002795	1.89	2.03	3.46	6.45	7.68	5.35	**	+
	MAMMA1002796	4.35	3.97	7.51	7.2	8.09	8.17		
	MAMMA1002805	6.61	11.12	16.52	15.95	24.7	16.5		
	MAMMA1002806	1.47	2.02	3.51	2.28	4.62	2.17		
	MAMMA1002807	1.63	2.4	6.77	6.78	9.66	6.4		
30	MAMMA1002814	3.43	3.52	7.92	9.58	12.39	10.66	*	+
	MAMMA1002817	1.28	1.56	2.87	2.89	5.43	2.91		
	MAMMA1002820	1.66	1.93	2.61	2.52	4.77	2.21		
	MAMMA1002830	67.67	70.46	130.59	165.92	139.33	187.18	*	+
35	MAMMA1002833	4.16	2.88	9.4	8.22	10.68	10.58		
	MAMMA1002835	0.77	1.87	4.03	1.73	3.97	2.79		
	MAMMA1002838	1.85	2.66	5.31	2.91	4.44	3.93		
	MAMMA1002842	1	3.83	3.84	3.32	4.63	5.15		
	MAMMA1002843	1.72	2.92	2.33	4.09	4.81	3		
40	MAMMA1002844	3.05	3.64	6.52	5.26	7.3	4.09		
	MAMMA1002845	1.25	1.57	2.45	3.59	3.55	4.67	*	+
	MAMMA1002857	92.1	106.97	208.17	209.17	202.29	249.13		
	MAMMA1002858	317.94	188.78	378.89	560.7	620.76	724.33	**	+
	MAMMA1002863	2.17	2.83	6.91	3.51	5.12	3.96		
45	MAMMA1002868	2.73	3.7	6.26	6.35	9.53	10.25	*	+
	MAMMA1002869	5.43	6.83	26.64	22.68	30.03	29.85		
	MAMMA1002871	0.61	1.7	1.78	1.9	3.8	1.97		
	MAMMA1002875	1.9	2.59	3.99	4.48	6.35	4.06		
	MAMMA1002879	8.42	9.2	14.19	22.55	23.63	27.96	**	+
50	MAMMA1002880	1.23	2.02	2.12	1.48	5.42	2.03		
	MAMMA1002881	1.21	1.43	1.84	3.01	5.43	2.46		
	MAMMA1002885	0.96	1.59	2.71	2.6	3.26	1.59		
	MAMMA1002886	2.63	2.52	3.9	6.01	5.37	7.05	**	+
	MAMMA1002887	1.28	1.83	2.78	2.98	5.14	4.32	*	+
55	MAMMA1002890	0.79	1.7	4.05	4.39	4.8	4.01		

EP 1 130 094 A2

	MAMMA1002892	1.35	2.45	4.98	6.64	6.24	5.84	*	+
5	MAMMA1002893	4.52	3.58	5.4	7.6	8.03	8.43	**	+
	MAMMA1002895	1.43	1.31	3.28	1.81	3.89	1.64		
	MAMMA1002898	0.53	1.67	4.15	2.69	4.72	1.42		
	MAMMA1002905	1.32	1.58	2.51	4.1	5.01	3.87	**	+
	MAMMA1002906	15.12	10.76	15.42	19.47	13.76	15.58		
10	MAMMA1002908	0.99	1.24	4.28	3.53	4.24	4.07		
	MAMMA1002909	1.92	2.64	5.67	6.82	8.18	6.57	*	+
	MAMMA1002918	2.75	2.69	5.42	5.27	7.26	6.58		
	MAMMA1002925	92.88	85.77	163.7	127.31	122.97	178.98		
	MAMMA1002926	6.08	6.31	16.25	16.64	19.48	19.9		
15	MAMMA1002930	1.21	1.59	5.67	4.88	8.91	4.21		
	MAMMA1002937	4.91	3.87	30.71	40.45	75.17	61.59	*	+
	MAMMA1002938	1.67	1.86	2.42	2.35	3.2	3.56		
	MAMMA1002941	0.49	1.48	2.78	2.53	3.59	2.24		
	MAMMA1002947	2.24	2.59	4.55	6	6.8	7.94	*	+
	MAMMA1002964	1.73	2.9	5.91	6.91	7.24	7.16	*	+
20	MAMMA1002967	1.94	1.59	2.28	2.9	4.19	2.79		
	MAMMA1002970	2.72	1.77	6	7.59	7.28	8.96	*	+
	MAMMA1002971	1.52	1.6	2.9	2.51	7.27	3.93		
	MAMMA1002972	1	1.32	2.95	1.74	4.56	2.12		
	MAMMA1002973	1.38	2.45	6.73	4.36	6.72	6.78		
25	MAMMA1002979	55.6	60.16	121.72	134.02	101.19	107.19		
	MAMMA1002982	0.53	1.98	2.28	2.04	3.28	1.9		
	MAMMA1002987	1.56	2.11	5.56	3.14	5.55	4.14		
	MAMMA1003003	0.77	2.18	4.78	4.46	6.47	5.08		
30	MAMMA1003004	1.65	1.86	3.7	3.64	3.59	3.16		
	MAMMA1003007	0.69	1.16	2.73	1.88	3.7	2.32		
	MAMMA1003011	1.56	1.8	3.67	3.77	5.41	3.94		
	MAMMA1003013	3.67	5.57	39.41	47.56	59.11	54.29	*	+
	MAMMA1003015	1.16	1.8	2.21	2.54	2.9	2.19		
35	MAMMA1003019	0.6	1.61	2.1	3.12	4.61	2.63		
	MAMMA1003020	2.96	4.19	5.34	11.31	10.33	10.09	**	+
	MAMMA1003026	1.29	1.56	2.95	2.66	4.25	2.25		
	MAMMA1003031	0.61	1.71	5.64	4.13	5.85	5.89		
	MAMMA1003033	1.34	1.65	4.13	2.84	5.11	3.64		
40	MAMMA1003035	1.66	2.5	5.44	5.12	7.03	4.9		
	MAMMA1003039	0.95	0.75	3.31	2.15	4.73	2.48		
	MAMMA1003040	1.38	2.54	5.32	4.57	7.47	7.43		
	MAMMA1003044	2.36	2.96	6.52	4.29	6.41	5.99		
	MAMMA1003047	1.82	3.67	7.61	5.74	7.05	7.13		
45	MAMMA1003049	0.47	1.72	2.03	1.08	1.56	1.45		
	MAMMA1003055	1.24	1.67	4.92	3.77	5.14	3.44		
	MAMMA1003056	0.9	0.91	1.85	1.22	2.26	1.02		
	MAMMA1003057	2.53	3.34	6.76	7.25	9.2	5.01		
	MAMMA1003066	1.65	2.06	4.73	4.1	7.08	5.07		
50	MAMMA1003075	1.11	1.71	3.16	1.85	4.37	2.32		
	MAMMA1003089	1.69	2.11	7.13	7.85	8.66	7.43		
	MAMMA1003092	1.25	1.79	3.21	2.62	4.08	1.76		
	MAMMA1003095	2.27	3.33	5.4	7.24	8.57	5.34		
	MAMMA1003099	1.88	2.51	4.95	4.09	6.45	4.35		
55	MAMMA1003102	1.33	2.04	2.88	3.2	3.27	2.39		

EP 1 130 094 A2

	MAMMA1003104	0.64	1.07	3.17	2.15	3.25	1.56		
5	MAMMA1003113	4.22	4.21	6.98	9.22	7.02	7.07		
	MAMMA1003126	12.93	14.72	20.89	19.28	12	15.63		
	MAMMA1003127	2.95	3.14	5.91	3.88	6.12	5.19		
	MAMMA1003131	2.82	3.51	4.86	3.82	5.91	5.88		
	MAMMA1003135	3.66	4.65	7.61	2.33	4.04	2.64		
10	MAMMA1003140	0.73	2.01	3.59	2.3	3.32	1.89		
	MAMMA1003146	2.08	2.24	3.89	3.17	5.09	3.3		
	MAMMA1003150	1.18	1.8	3.01	3.37	4.29	3.45	*	+
	MAMMA1003154	0.54	1.41	2.29	2.21	3.57	2.34		
	MAMMA1003155	8.08	9.18	20.88	21.41	17.68	20.56		
15	MAMMA1003157	5.94	4.82	6.07	5.18	7.05	7.89		
	MAMMA1003163	1.74	1.69	4.23	2.55	5.46	3.08		
	MAMMA1003164	2.94	4.56	6.23	4.08	9.9	8.18		
	MAMMA1003166	3.62	3.5	5.77	6.24	8.66	6.12		
	NB9N31000010	2.5	3.88	7.58	9.63	12.26	9.5	*	+
	NB9N31000016	0.73	2.8	5.21	4.04	4.41	3.15		
20	NB9N31000043	8.1	8.88	19.71	12.51	12.3	12.64		
	NB9N31000045	167.24	153.32	255.96	401.78	320.53	296.06	*	+
	NB9N31000054	7.29	4.42	11.75	11.15	11.87	13.43		
	NB9N31000076	2.31	1.94	3.51	4.5	6.35	4.44	*	+
	NB9N31000086	2.62	2.65	6.23	3.61	9.71	7.69		
25	NT2RM1000001	2.56	2.45	6.24	5.7	7.05	6.32		
	NT2RM1000018	3.84	4.69	10.6	6.58	9.09	6.92		
	NT2RM1000032	1.12	2.64	3.88	2.28	4.92	3.21		
	NT2RM1000035	1.72	3.68	5.53	5.44	5.21	5.98		
	NT2RM1000037	1.38	2.98	2.75	2.41	4.15	2.11		
30	NT2RM1000039	3.45	5.13	5.9	6.51	7.26	8.4	*	+
	NT2RM1000042	33.96	32.7	65.25	57.46	67.15	64.39		
	NT2RM1000055	0.85	1.74	3.34	1.16	3.55	1.16		
	NT2RM1000059	3.26	3.16	7.66	4.69	5.97	5.78		
	NT2RM1000062	1.13	1.21	1.9	3.47	4.33	2.46	*	+
35	NT2RM1000065	23.8	16.41	34.06	36.15	35.1	51.38		
	NT2RM1000066	4.13	4.31	8.98	7.23	10.95	9.81		
	NT2RM1000071	49.63	37.81	86.71	73.04	63.32	84.05		
	NT2RM1000080	1.37	2.04	3.8	5.1	5.94	4.5	*	+
	NT2RM1000086	4.04	4.65	4.08	5.01	6.23	5.58	*	+
40	NT2RM1000092	6.17	6.93	15.76	14.48	25.91	15.13		
	NT2RM1000118	0.63	1.12	1.22	0.63	1.7	0.44		
	NT2RM1000119	1.32	2.27	1.96	1.84	3.38	2.99		
	NT2RM1000121	1.13	1.84	1.76	2.92	3.84	2.78	*	+
	NT2RM1000122	3.5	3.78	7.34	5.5	8.86	9.57		
45	NT2RM1000127	0.69	1.34	1.47	2.14	3.36	3.32	*	+
	NT2RM1000131	0.71	1.7	1.47	1.36	3.02	2.53		
	NT2RM1000132	3.2	4.88	4.83	6.86	6.46	6.31	*	+
	NT2RM1000153	1.75	1.9	3.68	2.38	4.45	4.84		
50	NT2RM1000184	72.82	77.46	151.91	106.39	163.07	125.55		
	NT2RM1000186	1.55	1.46	4.32	2.67	4.72	3.94		
	NT2RM1000187	3.11	1.96	5.16	10.09	9.1	8.78	**	+
	NT2RM1000199	1.12	1.37	2.11	2.41	3.51	2.72	*	+
	NT2RM1000213	1.32	1.75	2.38	2.66	2.71	2.22		
55	NT2RM1000215	10.95	11.07	17.21	19.51	22.84	15.14		

EP 1 130 094 A2

	NT2RM1000218	9.72	9.95	23.71	26.94	24.74	29.21		
5	NT2RM1000224	8.8	8.63	15.2	15.51	21.29	17.61		
	NT2RM1000236	30.38	24.19	61.14	72.86	82.44	71.5	*	+
	NT2RM1000242	0.23	1.17	1.32	0.39	2.27	0.12		
	NT2RM1000244	1.41	1.48	3.43	6.9	3.69	6.7	*	+
	NT2RM1000252	1.75	1.5	3.4	3.4	3.06	3.18		
10	NT2RM1000256	7.88	5.89	9.46	26.12	29.45	36.8	**	+
	NT2RM1000257	1.98	3.01	5.09	4.64	6.83	6.65		
	NT2RM1000260	7.9	7.01	13.32	9.18	12.49	11.77		
	NT2RM1000269	3.87	2.87	5.12	6.63	9.78	3.87		
	NT2RM1000271	0.71	0.8	1.87	0.46	2.47	0.51		
	NT2RM1000272	117.67	92.26	202.95	249.32	333.98	356.74	*	+
15	NT2RM1000273	10.03	9.45	20.12	22.32	16.68	15.76		
	NT2RM1000274	63.11	66.41	123.01	137.14	91.97	104.48		
	NT2RM1000280	3.95	4.18	8.18	6.71	8.72	7.93		
	NT2RM1000295	0.49	1	2.2	1.12	3.16	0.87		
20	NT2RM1000300	1.51	1.87	2.78	3.63	5.75	3.09		
	NT2RM1000304	58.38	98.72	161.87	187.58	185.55	204.78	*	+
	NT2RM1000314	1.8	2.12	3.6	3.84	4.07	4.33		
	NT2RM1000318	12.6	14.04	20.81	35.01	29.96	29.8	**	+
	NT2RM1000335	2.76	2.57	4.34	6.29	5.41	4.09		
	NT2RM1000341	0.46	1.27	1.95	1.41	2.33	0.99		
25	NT2RM1000350	3.04	3.47	5.52	7.32	5.63	6.44		
	NT2RM1000354	0.55	1.31	1.31	5.43	7.2	5.72	**	+
	NT2RM1000355	30.24	31.5	56.85	74.62	50.25	61.33		
	NT2RM1000361	3.63	3.87	7.23	14.39	20.29	18.78	**	+
	NT2RM1000365	0.58	1.08	1.71	1.27	1.82	0.52		
30	NT2RM1000372	14.99	19.56	30.06	42.71	46.67	45.44	**	+
	NT2RM1000377	2.04	2.18	9.66	13.38	14.74	13.48	*	+
	NT2RM1000388	0.35	1.57	3.01	2.2	3.8	2.42		
	NT2RM1000394	0.45	1.31	1.87	1.43	2.72	0.69		
	NT2RM1000399	0.53	1.57	3.25	1.98	3.2	1.81		
35	NT2RM1000407	1.13	1.52	2.17	1.02	2.7	1.51		
	NT2RM1000421	0.84	0.57	2.78	1.06	1.77	1.13		
	NT2RM1000422	20.65	23.31	54.69	87.5	82.91	79.47	*	+
	NT2RM1000430	1.22	1.57	2.01	3.2	3.67	2.95	**	+
	NT2RM1000462	1.55	2.33	7.32	5.59	7.28	8.16		
40	NT2RM1000499	1.36	2.09	4.74	5	6.16	6.37	*	+
	NT2RM1000512	12.49	13.22	19.22	10.54	14.15	19.84		
	NT2RM1000519	33.96	37.54	55.78	31.14	29.25	47.55		
	NT2RM1000527	7.97	8.92	37.68	55.15	60.19	46.68	*	+
	NT2RM1000539	3.45	3.59	12.93	15.52	17.01	18.1	*	+
45	NT2RM1000542	0.85	1.05	2.99	1.17	2.35	1.02		
	NT2RM1000553	3.7	2.42	22.32	42.83	42.96	34.5	*	+
	NT2RM1000555	11.3	11.6	23.97	34.11	29.67	22.76		
	NT2RM1000558	2.09	5.34	9.74	9.56	16.24	14.29		
	NT2RM1000563	1.47	2.42	3.36	4.07	5.58	3.95	*	+
50	NT2RM1000566	0.88	1.57	3.5	3.62	6.01	2.79		
	NT2RM1000570	96.92	77.32	137.63	167.35	105.47	174.1		
	NT2RM1000571	13.21	11.87	22.51	43.87	40.18	28.45	*	+
	NT2RM1000574	0.84	2.15	2.55	2.15	3.07	1.67		
55	NT2RM1000580	1.37	2.18	4.07	5.15	7.98	2.96		

EP 1 130 094 A2

	NT2RM1000620	2.61	2.95	8.2	8.35	9.58	7.26		
5	NT2RM1000623	1.25	1.2	2.38	1.75	2.81	0.62		
	NT2RM1000630	0.79	2.28	2.39	1.68	3.51	1.67		
	NT2RM1000633	30.97	39.36	36.34	54.43	44.6	43.59	*	+
	NT2RM1000634	1.91	4.16	8.12	2.56	7.05	5.57		
	NT2RM1000642	3.85	5.37	8.13	8.21	8.56	8.52		
	NT2RM1000647	41.3	39.09	62.11	57.72	68.29	62.69		
10	NT2RM1000648	2.49	2.65	4.61	6.14	5.63	4.51		
	NT2RM1000650	2.46	3.05	7.6	5.4	6.07	6		
	NT2RM1000661	4.48	5.7	15.82	15.48	13.45	13.18		
	NT2RM1000666	1	1.77	1.99	1.37	2.8	0.71		
	NT2RM1000669	3.51	2.76	4.67	3.63	5.42	3.28		
15	NT2RM1000672	2.23	3.95	7.81	3.98	8.47	7.22		
	NT2RM1000681	99.53	86.09	118.7	105.41	90.59	124.14		
	NT2RM1000691	2.02	2.61	5.74	3.61	7.69	3.76		
	NT2RM1000698	1.11	1.43	4	6.42	6.29	4.11	*	+
	NT2RM1000699	1.85	2.86	3.17	3.67	4.35	4.15	*	+
20	NT2RM1000702	3.71	4.64	9.47	9.31	9.72	11.4		
	NT2RM1000703	11.56	12.36	25.24	26.72	20.42	21.06		
	NT2RM1000704	24.48	23	32.91	46.54	24.13	40.82		
	NT2RM1000725	60.92	59.45	88.28	94.89	82.36	105.67		
	NT2RM1000726	1.85	2.02	5.75	1.97	4.8	4		
25	NT2RM1000731	1.11	2.24	4.98	2.45	3.47	3.43		
	NT2RM1000741	1.38	1.87	3.16	2.69	4.15	2.9		
	NT2RM1000742	2.61	4.6	7.41	9.55	10.94	9.84	*	+
	NT2RM1000744	2.1	3.61	7.14	4.05	5.24	5.05		
	NT2RM1000746	2.25	2.47	2.95	2.22	4.01	3.89		
30	NT2RM1000747	23.34	23.92	46.23	44.66	50.12	55.15		
	NT2RM1000752	3.83	2.36	4.62	3.95	4.88	3.46		
	NT2RM1000767	4.14	7.27	35.27	25.27	38.02	28.81		
	NT2RM1000770	2.97	3.08	6.36	4.71	6.71	5.67		
	NT2RM1000772	0.76	0.7	1.07	1.34	1.69	0.44		
35	NT2RM1000779	13.03	12.11	42.22	53.91	45.61	66.73	*	+
	NT2RM1000780	1.16	2.9	3.74	3.09	4.32	3.01		
	NT2RM1000781	1.07	0.98	1.71	2.58	4.4	1.93		
	NT2RM1000789	5.28	5.15	29.74	29.63	46.72	36.53		
	NT2RM1000800	2.87	2.63	6.37	5.66	9.57	6.96		
40	NT2RM1000802	2.44	2.99	7.5	4.34	5.47	4.82		
	NT2RM1000811	1.78	1.6	2.13	2.26	4.96	2.76		
	NT2RM1000826	6.06	6.36	13.34	14.42	20.73	20.98	*	+
	NT2RM1000829	3.91	2.87	6.39	6.73	8.48	8.41	*	+
	NT2RM1000831	81.54	64.45	185.14	182.43	179.79	197.27		
45	NT2RM1000833	14.58	13.33	42.25	76.74	73.25	67.48	**	+
	NT2RM1000834	4.06	3.09	6.2	8.49	9.42	10.49	**	+
	NT2RM1000841	12.34	10.01	21.15	34.98	36.63	30.81	**	+
	NT2RM1000848	4.79	4.42	6.44	9.36	12.74	10.45	**	+
50	NT2RM1000850	2.66	3.42	13.41	8.55	11.79	9.74		
	NT2RM1000852	1.34	1.94	3.23	3.01	5.76	2.61		
	NT2RM1000853	1.19	2.85	2.15	3.11	3.26	3.23		
	NT2RM1000855	29.27	24.82	45.19	52.48	45.32	58.45		
	NT2RM1000857	4.63	5	10.67	8.76	11.3	10.76		
55	NT2RM1000858	7.3	7.6	15.86	9.09	11.56	10.93		

EP 1 130 094 A2

	NT2RM1000867	19.42	15.85	28.1	32.52	35.03	24.06		
5	NT2RM1000874	3.15	2.65	7.03	5.17	9.62	5.31		
	NT2RM1000882	2.36	1.37	3.71	5.39	9.31	5.45	*	+
	NT2RM1000883	5.21	3.34	7.42	5.18	11.3	7.9		
	NT2RM1000885	3.86	4.43	9.4	7.59	8.15	9.8		
	NT2RM1000893	3.15	3.41	8.14	7.73	6.17	8.39		
10	NT2RM1000894	3.29	4.4	6.18	8.14	6.11	6.61		
	NT2RM1000898	3.72	7.33	10.02	13.4	17.51	12.41	*	+
	NT2RM1000899	1.02	2.22	3.07	3.68	7.49	4.69		
	NT2RM1000905	11.92	17.41	30.36	37.19	45.16	37.3	*	+
	NT2RM1000910	7.5	8.78	20.16	36.37	36.98	37.5	**	+
15	NT2RM1000914	6.46	7.69	19.74	14.28	17.33	17.77		
	NT2RM1000919	6.1	3.92	9.91	14.61	17.49	15.37	**	+
	NT2RM1000921	0.72	1.9	3.69	2.79	4.27	3.32		
	NT2RM1000922	4.7	6.11	8.09	9.03	5.21	6.36		
	NT2RM1000924	0.89	3.03	3.04	3.08	2.89	3		
20	NT2RM1000927	1.35	1.78	2.85	3.07	4.72	3.46		
	NT2RM1000951	7.95	11.33	26.73	32.33	34.46	31.18	*	+
	NT2RM1000956	7.91	6.36	13.35	23.61	27.46	21.91	**	+
	NT2RM1000960	12.48	10.27	29.06	34.95	37.47	38.96	*	+
	NT2RM1000961	3.28	3.61	7.45	9.44	13.18	8.11		
	NT2RM1000962	4.14	3.5	8.18	7.59	10.15	9.86		
25	NT2RM1000973	16.71	15.79	29.32	31.15	11.56	27.73		
	NT2RM1000978	0.57	1.46	1.58	0.95	2.64	0.44		
	NT2RM1000982	2.34	2.29	3.52	3.57	4.94	4.54	*	+
	NT2RM1000991	1.61	1.78	4.25	3.88	5.56	5.23		
30	NT2RM1000994	6.36	6.16	12.57	16.52	16.64	14.53	*	+
	NT2RM1001002	5.11	6.69	15.34	21.78	22.69	22.28	*	+
	NT2RM1001003	5.42	5.15	11.98	16.24	9.06	8.46		
	NT2RM1001008	1.4	2.22	2.48	1.83	4.34	4.33		
	NT2RM1001011	6.29	5.43	7.86	14.4	10.46	14.72	*	+
35	NT2RM1001013	2.9	2.75	4.75	8.29	7.96	5.81	*	+
	NT2RM1001017	1	1.82	3.44	3.28	4.86	3.92		
	NT2RM1001018	65.15	74.45	146.86	134.65	125.46	113.93		
	NT2RM1001026	1.37	2.64	3.17	2.99	4.61	3.31		
	NT2RM1001028	0.98	1.73	2.91	1.74	1.89	0.76		
40	NT2RM1001043	4.47	3.64	8.42	11.43	12.7	8.01		
	NT2RM1001044	2.23	3.17	4.92	5.03	5.51	3.93		
	NT2RM1001059	1.47	3.72	4.12	4.05	6.11	3.02		
	NT2RM1001063	4.11	3.29	6.1	4.22	5.64	5.6		
	NT2RM1001066	0.86	1.85	2.44	2.23	3.99	2.85		
45	NT2RM1001072	1.8	2.8	4.33	1.94	3.74	1.52		
	NT2RM1001074	1.66	2.38	5.18	5.18	4.19	2.67		
	NT2RM1001076	1.39	2.2	4.94	3.43	4.42	1.72		
	NT2RM1001082	1.79	2.6	5.23	5.31	5.92	4.57		
	NT2RM1001085	1.25	1.65	2.81	1.16	3.27	1.17		
50	NT2RM1001092	3.82	4.2	5.57	9.34	7.94	9.82	**	+
	NT2RM1001102	1.7	2.3	4.4	2.49	5.94	4.64		
	NT2RM1001103	4.37	3.88	7.18	6.25	10.28	8.08		
	NT2RM1001105	1.77	2.02	4.63	2.49	5.11	3.51		
	NT2RM1001112	2.68	2.66	3.69	3.85	4.75	2.43		
55	NT2RM1001115	1.44	1.57	4.72	3	6.46	3.73		

EP 1 130 094 A2

	NT2RM1001122	2.84	3.35	7.3	9.43	9.75	9.54	*	+
5	NT2RM1001136	0.88	1.41	2.71	2.31	3.87	1.59		
	NT2RM1001139	3.9	3.7	5.38	5.33	11.18	6.77		
	NT2RM2000003	2.45	3.33	2.4	4.5	6.29	4.88	*	+
10	NT2RM2000006	2.34	2.95	7.25	5.12	7.11	6.24		
	NT2RM2000010	12.79	13.03	22.58	20.2	17.11	21.83		
	NT2RM2000013	8.1	9.44	50.36	68.75	95.32	74.36	*	+
15	NT2RM2000030	4.8	2.21	23.41	26.33	32.15	28.69		
	NT2RM2000032	2.76	2.92	8.53	10.01	12.19	10.67	*	+
	NT2RM2000039	3.94	4.67	4.75	6.42	5.78	4.99		
20	NT2RM2000042	3.5	4.9	11.69	17.71	17.4	15.02	*	+
	NT2RM2000092	1	2.38	1.98	1.29	4.69	2.25		
25	NT2RM2000093	8.37	6.63	11.41	9.02	12.23	10.18		
	NT2RM2000101	9.2	9.94	40	61.09	76.38	69.62	*	+
	NT2RM2000104	6.82	8.02	46.75	51.34	68.83	43.48		
30	NT2RM2000124	1.54	2.23	6.33	7.73	8.84	8.47	*	+
	NT2RM2000155	5.08	3.77	5.8	9.45	11.58	12.51	**	+
	NT2RM2000191	3.33	5.68	28.62	26.54	34.38	31.6		
	NT2RM2000192	1.03	1.29	2.45	6.3	4.75	3.83	*	+
	NT2RM2000239	1.92	2.79	3.09	2.85	5.02	3.1		
	NT2RM2000240	32.78	29.59	74.35	61.15	60.54	61.71		
35	NT2RM2000241	4.49	5.9	6.35	8.24	11.72	6.78		
	NT2RM2000250	1.29	1.54	4.16	2.09	5.05	2.54		
	NT2RM2000259	3.06	3.42	3.59	6.38	8.44	6.74	**	+
	NT2RM2000260	2.53	2.05	3.12	4.23	4.07	5.79	*	+
40	NT2RM2000265	0.91	1.55	0.99	1.43	2.4	1.09		
	NT2RM2000287	4.7	4.23	10.82	10.69	11.54	14.73		
	NT2RM2000306	12.24	9.36	10.48	23.63	14	20.79	*	+
	NT2RM2000312	19.4	17.81	25.01	38.39	31.27	24.8		
	NT2RM2000322	1.93	1.82	4.48	3.79	7.05	3.32		
45	NT2RM2000343	7.74	8.38	41.34	63.81	79.6	71.12	*	+
	NT2RM2000359	3.67	2.86	4.95	4.93	9.55	4.72		
	NT2RM2000362	20.09	18.2	62.29	94.88	111.25	95.66	*	+
	NT2RM2000363	1.08	1.89	2.97	4.2	4.32	3.33	*	+
	NT2RM2000368	2.84	2.4	4.74	6.15	5.98	5.29	*	+
50	NT2RM2000371	76.64	65.68	119.32	135.82	125	44.64		
	NT2RM2000374	1.68	1.92	5.75	3.34	4.8	3.58		
	NT2RM2000387	8.98	9.83	11.92	20.02	25.18	17.11	*	+
	NT2RM2000393	1.7	1.63	3.75	3.31	7.65	3.28		
	NT2RM2000395	1.07	1.51	1.98	1.72	4.34	2.23		
55	NT2RM2000402	12.38	11	15.78	25.15	18.31	22.51	*	+
	NT2RM2000405	1.33	1.25	2.2	1.52	3.08	3.16		
	NT2RM2000407	0.76	1.78	2.49	1.89	2.72	2.89		
	NT2RM2000410	0.79	1.94	2.23	1.98	2.84	2.09		
	NT2RM2000420	3.09	2.52	4.43	4.24	4.5	3.26		
	NT2RM2000422	3.22	2.44	5.81	3.61	6.17	2.87		
	NT2RM2000423	1.91	1.96	5.69	3.89	7.64	4.18		
	NT2RM2000452	3.46	3.18	4.31	7.35	8.65	9.57	**	+
	NT2RM2000469	3.28	3.28	4.44	1.87	2.33	2.46	*	-
	NT2RM2000490	6.03	6.03	9.18	5.55	6.16	6.9		
	NT2RM2000497	3.29	3.29	4.59	3.15	5.48	2.43		
	NT2RM2000502	4.69	4.69	10.24	5.87	7.08	7.02		

EP 1 130 094 A2

	NT2RM2000504	7.37	7.37	12.93	10.83	4.49	11.2
5	NT2RM2000514	2.75	2.75	6.23	3.11	3.32	3.8
	NT2RM2000522	1.9	1.9	3.27	1.94	1.18	1.13
	NT2RM2000540	6.02	6.02	9.53	9.12	8.96	8.14
	NT2RM2000556	2.09	2.09	2.8	1.24	2.33	0.93
	NT2RM2000565	3.35	3.35	6.02	3.27	4.14	3.72
10	NT2RM2000566	6.59	6.59	15.8	9.09	9.21	9.57
	NT2RM2000567	2.16	2.16	5.64	2	5.67	3.82
	NT2RM2000569	4.69	4.69	7.93	5.77	8.18	4.7
	NT2RM2000577	11.08	11.08	15.39	11.79	14.95	14.48
	NT2RM2000581	4.64	4.64	6.49	5.98	7.97	6.85
15	NT2RM2000582	5.23	5.23	10.34	8.34	9.14	7.19
	NT2RM2000588	21.84	21.84	65.91	40.15	44.01	45.21
	NT2RM2000589	3.98	3.98	11.35	7.96	7.6	8.64
	NT2RM2000594	1.87	1.87	4.38	1.62	2.71	1.92
	NT2RM2000599	6.34	6.34	16.12	17.82	14.5	15.44
20	NT2RM2000609	4.61	4.61	6.77	3.76	5.81	5.48
	NT2RM2000612	3.52	3.52	6.4	5.93	7.47	4.55
	NT2RM2000622	16.6	16.6	56.24	53.07	75.02	55.48
	NT2RM2000623	2.66	2.66	7.1	7.92	6.03	5.58
	NT2RM2000624	4.18	4.18	10.6	7.33	14.39	7.56
25	NT2RM2000632	2.8	2.8	6.73	4.1	6.4	4.73
	NT2RM2000635	3.42	3.42	8.09	5.41	6.29	5.31
	NT2RM2000636	2.61	2.61	6.28	3.99	4.39	3.72
	NT2RM2000639	3.73	3.73	8.26	5.42	7.79	5.99
	NT2RM2000649	6.03	6.03	9.69	9.4	9.17	8.05
30	NT2RM2000658	6.49	6.49	13.18	15.17	14.66	15.83 * +
	NT2RM2000660	11.45	11.45	18.34	17.03	7.1	20.16
	NT2RM2000669	3.6	3.6	6.51	5.28	4.28	6.69
	NT2RM2000689	31.07	31.07	59.7	37.03	16.51	70.9
	NT2RM2000691	2.09	2.09	5.73	4.83	7.13	4.27
35	NT2RM2000714	3.41	3.41	10.97	11.46	14.54	11.3
	NT2RM2000718	4.08	4.08	7.15	2.88	5.42	4.33
	NT2RM2000732	5.38	5.38	14.81	9.49	14.18	8.25
	NT2RM2000735	3.72	3.72	6.16	4.27	6.55	6.49
	NT2RM2000740	2.26	2.26	6.2	4.27	3.01	3.71
40	NT2RM2000743	2.26	2.26	7.89	5.65	3.24	3.89
	NT2RM2000772	6.43	6.43	8.48	5.24	6.72	9.47
	NT2RM2000773	8.17	8.17	19.56	19.18	17.96	18.29
	NT2RM2000776	13.96	13.96	17.16	24.24	9.95	26.76
	NT2RM2000784	6.64	6.64	8.8	8.74	9.02	10.5
45	NT2RM2000795	4.35	4.35	13.56	7.44	8.66	10.45
	NT2RM2000796	2.27	2.27	4.64	1.71	2.31	1.38
	NT2RM2000798	25.81	25.81	160.08	158.19	136.83	188.99
	NT2RM2000801	45.09	45.09	161.29	160.44	152.13	189.56
50	NT2RM2000821	7.53	7.53	12.33	7.37	7.77	11.87
	NT2RM2000829	5.76	5.76	13.01	8.05	10.13	11.75
	NT2RM2000837	3.29	3.29	7.28	4.27	6.08	4.18
	NT2RM2000924	9.96	9.96	36.74	43.24	57.8	35.84
	NT2RM2000930	10.64	10.64	18.29	24.45	27.78	28.34 ** +
55	NT2RM2000937	4.35	4.35	8.62	5.08	6.66	6.56
	NT2RM2000939	1.12	1.12	2.37	2.67	1.84	1.82

EP 1 130 094 A2

	NT2RM2000942	124.8	124.8	253.61	161.4	118.61	210.11
5	NT2RM2000951	1.01	1.01	2.6	2.13	3.12	1.6
	NT2RM2000952	2.53	2.53	5.31	5.98	6.41	6.86 * +
	NT2RM2000966	19.69	19.69	111.88	95.61	137.32	135.9
	NT2RM2000973	23.45	23.45	16.81	39.12	39.51	33.8 ** +
	NT2RM2000983	10.07	10.07	18.59	30.68	39.13	27.52 * +
10	NT2RM2000984	6.48	6.48	7.71	4.88	5.64	5.26 * -
	NT2RM2000994	8.27	8.27	16.47	13.2	8.36	21.81
	NT2RM2001004	6.01	6.01	48.58	47.51	54.15	46.8
	NT2RM2001022	101.09	101.09	350.92	239.63	304.37	490.04
	NT2RM2001035	10.75	10.75	24.98	24.17	24.54	34.51
15	NT2RM2001038	5.77	5.77	9.86	10.48	11.75	7.9
	NT2RM2001043	4.45	4.45	10.02	5.1	7.41	6.74
	NT2RM2001050	2.71	2.71	6.89	4.72	5.83	4.03
	NT2RM2001055	3.78	3.78	5.89	4.24	6.31	4.7
	NT2RM2001065	6.17	6.17	15.91	8.51	12.12	14.21
20	NT2RM2001075	39.81	39.81	188.21	154.65	156.72	168.68
	NT2RM2001083	2.23	2.23	5.57	4.01	5.8	3.01
	NT2RM2001100	10.38	10.38	93.67	95.8	113.9	97.52
	NT2RM2001105	6.34	6.34	8.27	11.35	5.34	11.8
	NT2RM2001109	6.81	6.81	9.4	11.88	12.47	14.53 * +
25	NT2RM2001110	7.67	7.67	21.63	21.2	30.71	23.29
	NT2RM2001126	6.1	6.1	6.53	5.32	6.44	7.27
	NT2RM2001131	5.52	5.52	40.22	21.93	29.37	20.14
	NT2RM2001141	1.64	1.64	6.84	7.09	6.4	5.45
	NT2RM2001152	1.63	1.63	3.27	4.42	5.77	3.02
30	NT2RM2001177	3.42	3.42	7.23	10.28	7.25	8.24
	NT2RM2001194	2.74	2.74	7.51	6.68	5.77	8.17
	NT2RM2001195	3.7	3.7	8.8	6.37	7.13	6.89
	NT2RM2001196	5.24	5.24	6.35	5.19	6.46	4.64
	NT2RM2001201	14.45	14.45	25.36	20.02	21.68	22.38
35	NT2RM2001221	4.22	4.22	8.61	11.69	13.61	16.63 * +
	NT2RM2001238	2.87	2.87	5.65	3.91	3.88	1.96
	NT2RM2001243	5.39	5.39	8.98	9.81	6.13	6.53
	NT2RM2001244	3.91	3.91	10.63	6.58	9.24	6.41
	NT2RM2001247	14.94	14.94	121.59	110.47	140.27	118.79
40	NT2RM2001256	3.84	3.84	5.23	3.15	3.26	2.96
	NT2RM2001269	4.4	4.4	5.98	4.8	5.63	4.74
	NT2RM2001278	5.28	5.28	7.37	8.45	8.56	5.35
	NT2RM2001291	3.05	3.05	5.18	3.24	4.62	2.9
	NT2RM2001294	12.47	12.47	24.39	20.08	15.43	17.81
45	NT2RM2001295	2.56	2.56	8.82	4.54	4.43	4.99
	NT2RM2001302	2.38	2.38	4.55	2.3	4.5	2.81
	NT2RM2001306	3.51	3.51	7.62	4.1	4.46	5.14
	NT2RM2001312	2.34	2.34	3.72	1.92	2.84	1.68
	NT2RM2001319	2.76	2.76	3.93	3.61	5.29	4.11
50	NT2RM2001324	3.73	3.73	8.29	5.48	4.9	5.71
	NT2RM2001345	8.53	8.53	10.01	6.83	11.12	14.14
	NT2RM2001360	4.02	4.02	6.36	5.67	5.9	5.46
	NT2RM2001370	5.75	5.75	14.53	8.56	9.86	11.69
	NT2RM2001391	1.79	1.79	6.07	1.85	5.04	1.65
55	NT2RM2001393	4.49	4.49	6.39	5.12	7.91	7.14

EP 1 130 094 A2

	NT2RM2001420	2.94	2.94	4.61	2.61	3.62	3.14		
5	NT2RM2001423	5.44	5.44	9.53	8.64	11.95	11.36		
	NT2RM2001424	5.88	5.88	15.09	11.77	10.31	11.63		
	NT2RM2001482	2.24	2.24	6.48	3.5	6.06	3.63		
	NT2RM2001499	1.4	1.4	5.81	2.84	4.3	2.17		
10	NT2RM2001504	3.63	3.63	6.99	3.2	4.54	1.68		
	NT2RM2001524	2.51	2.51	5.81	2.34	2.22	3.51		
	NT2RM2001530	2.56	2.56	4.42	2.68	4.35	3.52		
	NT2RM2001533	5.06	5.06	9.09	8.2	9.18	7.84		
	NT2RM2001540	5.77	5.77	8.36	14.57	17.99	27.1	*	+
	NT2RM2001544	2.4	2.4	6.12	3.7	3.72	2.31		
15	NT2RM2001547	6.6	6.6	15.29	8.44	7.61	8.24		
	NT2RM2001558	1.53	1.53	3.44	1.76	4.87	1.71		
	NT2RM2001575	2.45	2.45	4.57	3.36	4.38	2.29		
	NT2RM2001582	2.99	2.99	4.98	2.2	5.16	3.06		
	NT2RM2001588	3.69	3.69	8.8	6.39	9.14	6.6		
20	NT2RM2001592	2.66	2.66	6.2	3.1	5.24	4.64		
	NT2RM2001603	4.74	4.74	8.7	10.42	12.03	11.77	*	+
	NT2RM2001605	1.74	1.74	4.52	3.08	1.51	2.39		
	NT2RM2001611	2.28	2.28	8.63	3.74	3.34	3.51		
	NT2RM2001613	14.91	14.91	32.53	21.51	13.13	27.42		
25	NT2RM2001626	2.45	2.45	3.08	2.1	4.28	2.06		
	NT2RM2001632	4.93	4.93	7.07	4.67	4.88	5.42		
	NT2RM2001633	4.45	4.45	10.39	3.74	5.15	5.43		
	NT2RM2001635	4.33	4.33	9.54	4.3	5.81	4.7		
	NT2RM2001636	4.88	4.88	7.35	12.75	18.11	13.34	**	+
30	NT2RM2001637	1.25	1.25	6.48	4.18	3.68	2.51		
	NT2RM2001639	3.98	3.98	9.32	4.67	4.33	3.29		
	NT2RM2001641	1.63	1.63	4.69	4.84	6.02	2.71		
	NT2RM2001643	2.78	2.78	7.46	4.79	4.4	2.83		
	NT2RM2001648	12.97	12.97	18.91	20.13	17.07	25.5		
35	NT2RM2001652	6.32	6.32	5.65	4.29	8.13	4.46		
	NT2RM2001659	5.78	5.78	9.17	5.73	5.28	6.95		
	NT2RM2001660	3.44	3.44	3.86	2.08	2.29	2.63	**	-
	NT2RM2001664	1.24	1.24	6.12	4.51	4.89	4.8		
	NT2RM2001668	3.72	3.72	8.16	7.66	5.72	7.02		
40	NT2RM2001670	1.62	1.62	4.11	2.88	3.96	3.56		
	NT2RM2001671	2.67	2.67	5.57	3.9	6.46	4.85		
	NT2RM2001675	1.94	1.94	4.28	1.97	3.73	0.64		
	NT2RM2001681	2.47	2.47	5.91	3.13	4.64	3.39		
	NT2RM2001685	4.58	4.58	5.68	1.29	2.72	1.14	**	-
45	NT2RM2001688	5.46	5.46	4.14	3.11	3.82	2.46	*	-
	NT2RM2001695	15.09	15.09	35.18	17.41	19.26	34.51		
	NT2RM2001696	2.74	2.74	6.64	7.15	6.7	6.8		
	NT2RM2001698	1.44	1.44	3	4.06	3.49	1.65		
50	NT2RM2001699	1.63	1.63	5.03	4.19	3.75	5.48		
	NT2RM2001700	1.65	1.65	4.13	2.56	3.37	3.91		
	NT2RM2001704	2.68	2.68	5.46	3.89	3.85	3.99		
	NT2RM2001706	4.29	4.29	6.77	3.33	3.13	3.32		
	NT2RM2001714	6.48	6.48	6.64	5.62	7.33	5.18		
	NT2RM2001716	0.97	0.97	3.7	3.03	5.49	2.92		
55	NT2RM2001718	1.91	1.91	3.47	5	3.5	3		

EP 1 130 094 A2

	NT2RM2001723	2.09	2.09	5.48	5.1	5.21	5.71		
5	NT2RM2001727	3.08	3.08	6.25	7.51	7.28	5.7		
	NT2RM2001730	3.52	3.52	7.15	5.04	5.43	3.85		
	NT2RM2001738	4.56	4.56	6.2	6.71	10.25	9.08	*	+
	NT2RM2001743	2.95	2.95	5.81	4.39	5.02	4.46		
	NT2RM2001753	5.98	5.98	7.55	5.72	6.09	4.54		
	NT2RM2001755	0.89	0.89	2.82	2.4	2.83	2.67		
10	NT2RM2001760	14.77	14.77	33.17	27.49	25.48	36.23		
	NT2RM2001765	1.35	1.35	1.71	2.45	3.12	2.03	*	+
	NT2RM2001767	12.04	12.04	120.66	148.84	168.4	146.29	*	+
	NT2RM2001768	2.1	2.1	3.59	3.41	4.21	3.05		
15	NT2RM2001771	4.82	4.82	5.65	7.15	5.97	5.05		
	NT2RM2001778	2.89	2.89	4.09	2.34	3.24	1.48		
	NT2RM2001782	5.32	5.32	7.32	4.96	7.71	7.57		
	NT2RM2001784	0.84	0.84	2.19	2.81	2.5	1.41		
	NT2RM2001785	1.35	1.35	4.11	5.5	5.02	2.76		
20	NT2RM2001792	6.03	6.03	8.53	5.49	5.54	5.76		
	NT2RM2001795	3.97	3.97	6.15	7.62	5.96	8.9		
	NT2RM2001797	2.82	2.82	3.78	5	5.94	2.71		
	NT2RM2001800	3.46	3.46	4.26	5.01	4.03	5.24		
	NT2RM2001803	3.5	3.5	6.61	4.46	7.34	2.44		
	NT2RM2001805	3.65	3.65	3.21	2.53	4.2	1.71		
25	NT2RM2001806	7.34	7.34	17.96	15.62	15.23	21.11		
	NT2RM2001813	1.54	1.54	2.05	2.54	1.88	2.32		
	NT2RM2001814	2.46	2.46	4.71	3.52	2.89	4.42		
	NT2RM2001818	1.21	1.21	2.66	0.97	1.48	0.27		
30	NT2RM2001823	1.4	1.4	3.24	1.87	2.46	1.37		
	NT2RM2001825	14.79	14.79	36.08	34.68	34.2	35.81		
	NT2RM2001832	5.93	5.93	6.1	5.19	5.48	2.93		
	NT2RM2001839	67.48	67.48	123.46	152.63	157.11	121.35		
	NT2RM2001840	3.04	3.04	7.13	4.61	5.11	5.37		
35	NT2RM2001851	3.92	3.92	7.61	3.78	4.74	6.49		
	NT2RM2001855	8.21	8.21	11.51	10.22	12.06	15.41		
	NT2RM2001867	2.82	2.82	5.01	2.83	5.62	3.74		
	NT2RM2001869	60.8	60.8	90.58	101.19	79.67	105.32		
	NT2RM2001879	3.01	3.01	6.99	2.55	3.19	2.66		
40	NT2RM2001883	1.52	1.52	3.26	0.98	2.28	0.73		
	NT2RM2001886	1.57	1.57	4.56	2.48	3.51	2.42		
	NT2RM2001887	3.78	3.78	7.66	4.48	4.97	5.73		
	NT2RM2001896	274.2	274.2	378.57	325.68	216.52	497.31		
	NT2RM2001902	1.92	1.92	4.28	1.31	2.92	2.14		
45	NT2RM2001903	16.25	16.25	42.55	35.47	31.71	37.22		
	NT2RM2001930	2.11	2.11	6.3	2.3	5.86	5.44		
	NT2RM2001935	4.16	4.16	5.04	3.16	4.42	5.87		
	NT2RM2001936	2.81	2.81	4.9	2.99	3.44	4		
	NT2RM2001939	3.56	3.56	3.34	1.82	3.01	3.16		
50	NT2RM2001941	1.84	1.84	4.29	2.84	2.82	2.72		
	NT2RM2001950	4.66	4.66	10	6.01	6	8.69		
	NT2RM2001952	2.67	2.67	4.78	2.49	4.55	5.37		
	NT2RM2001976	11.48	11.48	18.2	14.58	11.46	35.27		
	NT2RM2001982	1.85	1.85	3.91	2.04	2.47	1.88		
55	NT2RM2001983	4.45	4.45	8.36	4.18	6.49	7.54		

EP 1 130 094 A2

	NT2RM2001984	7.74	7.74	8.88	20.06	27.05	22.95	**	+
5	NT2RM2001989	2.72	2.72	3.68	2.99	4.26	3.7		
	NT2RM2001996	7.51	7.51	8.09	4.8	8.01	5.29		
	NT2RM2001997	3.65	3.65	7.29	3.18	5.09	6.78		
	NT2RM2001998	2.24	2.24	5.07	3.33	6.53	3.96		
	NT2RM2001999	4.86	4.86	7.69	6.88	6.02	4.01		
10	NT2RM2002003	11.33	11.33	18.17	10.15	11	14.9		
	NT2RM2002004	1.99	1.99	5.79	2.51	2.09	1.9		
	NT2RM2002009	5.35	5.35	9.03	9.85	11.04	11.09	*	+
	NT2RM2002014	2.62	2.62	3	3.65	4.47	4.03	**	+
	NT2RM2002019	25.1	25.1	38.52	19.47	14.2	16.35		
	NT2RM2002029	12.92	12.92	19.01	10.82	4.88	14.74		
15	NT2RM2002030	4.15	4.15	5.8	13.54	9.71	21.98	*	+
	NT2RM2002034	22.05	22.05	31.76	24.83	20.89	21.04		
	NT2RM2002049	7.4	7.4	12.12	9.76	10.42	13.22		
	NT2RM2002055	2.8	2.8	8.01	1.91	4.03	2.52		
	NT2RM2002072	9.26	9.26	12.88	12.28	19.12	12.82		
20	NT2RM2002088	4.82	4.82	13.85	11.35	11.7	15.28		
	NT2RM2002091	4.98	4.98	8.44	5.92	3.82	4.61		
	NT2RM2002100	3.26	3.26	6.05	4.82	4.24	3.19		
	NT2RM2002109	1.31	1.31	3.57	2.57	4.88	4.92		
	NT2RM2002126	21.41	21.41	32.24	35.28	22.31	31.52		
25	NT2RM2002128	3.7	3.7	5.17	2.74	3.86	2.41		
	NT2RM2002129	6.43	6.43	11.48	8.53	13.03	10.66		
	NT2RM2002142	5.72	5.72	9.74	5.26	8.91	6.4		
	NT2RM2002144	3.27	3.27	3.76	1.85	1.73	1.62	**	-
	NT2RM2002145	2.63	2.63	8.69	6.1	5.18	5.98		
30	NT2RM2002153	2.61	2.61	6.37	6.31	7.62	5.75		
	NT2RM2002163	0.97	0.97	3.41	1.87	3.4	0.64		
	NT2RM2002170	3.28	3.28	7.03	6.62	7.5	7.65		
	NT2RM2002178	3.99	3.99	3.67	3.5	5.48	2.9		
	NT2RM2002179	7.82	7.82	8.69	6.17	8.15	6.02		
35	NT2RM2002270	4.51	4.51	4.56	2.28	1.76	1.67	**	-
	NT2RM2002326	2.47	2.47	3.86	2.13	3.69	2.34		
	NT2RM2002337	1.88	1.88	3.97	5.4	4.22	4.79	*	+
	NT2RM2002339	2.83	2.83	6.29	5.26	5.22	3.85		
	NT2RM2002345	5.16	5.16	6.03	4.04	4.2	4.21	*	-
40	NT2RM2002368	2.43	2.43	5.86	6.05	7.01	4.96		
	NT2RM2002381	2.23	2.23	5.16	3.47	3.65	2.8		
	NT2RM2002424	4.64	4.64	7.1	6.69	8.5	6.3		
	NT2RM2002450	4.17	4.17	3.87	2.29	2.39	1.87	**	-
	NT2RM2002482	3.93	3.93	4.65	2.66	3.2	3.79		
45	NT2RM2002492	9.39	9.39	24.31	29.13	24.65	29.29		
	NT2RM2002575	3.26	3.26	5.23	5.99	6.03	5.07		
	NT2RM2002580	4.23	4.23	4.68	4.82	7.79	7.42		
	NT2RM2002592	7.7	7.7	12.59	13.07	15.28	14.69	*	+
50	NT2RM2002608	27.33	27.33	45.49	57.07	65.96	48.3	*	+
	NT2RM2002615	6.01	6.01	9.38	13.15	20.32	14.42	*	+
	NT2RM2002622	14.35	14.35	16.22	18.38	24.99	13.44		
	NT2RM2002630	4.86	4.86	6.63	8.05	7.37	6.7		
	NT2RM2002634	1.72	1.72	4.66	4.71	4.6	3.94		
55	NT2RM2002645	27.02	27.02	68.46	30.66	14.59	31.46		

EP 1 130 094 A2

	NT2RM2002646	12.09	12.09	25.03	29.45	22.88	34.8
5	NT2RM2002647	7.68	7.68	17.56	19.5	17.74	23.44
	NT2RM2002652	5.11	5.11	4.71	4.3	6.43	3.73
	NT2RM2002692	4.59	4.59	4.48	2.5	2.86	2.02 **
	NT2RM2002721	30.26	30.26	46.01	62.71	84.18	61.02 * +
	NT2RM2002748	18.37	18.37	43.62	87.35	119.27	102.35 ** +
10	NT2RM2002764	2.28	2.28	5.3	5.05	5.95	4.07
	NT2RM2002772	3.15	3.15	9.32	9.66	7.81	5.44
	NT2RM2002811	5.79	5.79	12.3	14.01	9.18	10.45
	NT2RM2002818	2.03	2.03	7.94	5.86	5.42	7.13
	NT2RM2002879	4.21	4.21	7.17	8.39	7.87	9.11 * +
15	NT2RM2002979	11.79	11.79	19.66	24.49	23.23	21.79 * +
	NT2RM2002981	4.42	4.42	3.78	3.58	4.95	2.63
	NT2RM2002995	5.13	5.13	3.29	3.42	3.74	3.5
	NT2RM2003031	1.37	1.37	2.63	3	2.58	1.9
	NT2RM2003042	4.1	4.1	10.77	10.59	6.02	6.07
20	NT2RM2003044	1.88	1.88	4.11	2.13	5.11	1.2
	NT2RM2003090	4.4	4.4	7.64	9.36	7.91	10.68 * +
	NT2RM2003095	11.98	11.98	25.25	15.63	16.43	19.04
	NT2RM2003116	11.16	11.16	16.09	17.96	21.43	22.08 * +
	NT2RM2003222	3.98	3.98	3.63	2.67	3.64	2.35
25	NT2RM2003224	11.29	11.29	15.33	24.29	29.77	20.76 * +
	NT2RM2003250	14.18	14.18	86.06	85.79	96.6	94.15
	NT2RM2003258	4.59	4.59	6.32	6.54	5.11	5.69
	NT2RM2003262	5.07	5.07	7.33	5.06	7.76	5.72
	NT2RM4000023	2.15	2.15	7.02	3.57	4.91	4.29
30	NT2RM4000024	2.28	2.28	6.78	3.17	4.98	4.33
	NT2RM4000027	4.74	4.74	7.77	4.85	6.94	11.32
	NT2RM4000030	2.95	2.95	5.73	3.16	4.9	2.64
	NT2RM4000033	2.51	2.51	4.77	2.36	3.89	4.61
	NT2RM4000034	1.93	1.93	5.35	3.74	4.84	6.09
35	NT2RM4000046	1.37	1.37	3.79	1.57	3.5	2.32
	NT2RM4000052	1.82	1.82	3.55	1.72	2.96	1.98
	NT2RM4000054	10.43	10.43	13.85	12.07	12.83	24.7
	NT2RM4000061	1.65	1.65	4.17	1.66	4.54	0.83
	NT2RM4000074	15.83	15.83	43.57	27.9	34.24	30.79
40	NT2RM4000085	5.35	5.35	10.1	8.41	10.19	10.17
	NT2RM4000086	3.06	3.06	4.5	3.84	5.25	3.71
	NT2RM4000100	6.62	6.62	15.05	12.74	15.6	14.84
	NT2RM4000101	3.77	3.77	9.11	7.17	7.71	8.78
	NT2RM4000102	32.35	32.35	42.47	27.24	19.34	70.54
45	NT2RM4000104	2.78	2.78	7.13	3.41	5.12	4.3
	NT2RM4000115	2.87	2.87	6.1	3.91	5.86	4.08
	NT2RM4000129	2.17	2.17	4.75	2.62	3.48	2.18
	NT2RM4000139	3.17	3.17	3.31	3.58	4.82	6.49
	NT2RM4000149	2.74	2.74	1.49	2.41	2.55	7.32
50	NT2RM4000155	2.73	2.73	5.5	2.13	4.51	3.71
	NT2RM4000156	5.94	5.94	16.74	20.45	21	21.96 * +
	NT2RM4000167	1.36	1.36	2.58	2.61	4.34	1.75
	NT2RM4000169	9.95	9.95	36.53	29.12	24.89	23.57
	NT2RM4000191	4.29	4.29	7.56	5.49	5.57	5.66
55	NT2RM4000197	2.73	2.73	4.78	1.83	3.86	2.2

EP 1 130 094 A2

	NT2RM4000198	3.38	3.38	7.42	5.26	5.45	4.21				
5	NT2RM4000199	2	2	3.51	2.8	4	3.76				
	NT2RM4000200	0.67	0.67	3.19	2.25	1.84	1.2				
	NT2RM4000202	1	1	3.24	2.11	2.42	1.84				
	NT2RM4000210	1.46	1.46	3.72	2.41	3.08	2.21				
	NT2RM4000215	2.54	2.54	5.43	3.3	4.09	3.06				
10	NT2RM4000220	6.42	6.42	10.52	8.68	11.08	15.14				
	NT2RM4000229	3.26	3.26	6.62	1.46	2.34	1.76				
	NT2RM4000231	6.37	6.37	7.06	6.13	7.85	6.24				
	NT2RM4000233	4.83	4.83	17.3	11.9	14.34	13.4				
	NT2RM4000244	2.35	2.35	5.22	3.86	4.14	5.17				
15	NT2RM4000251	3.85	3.85	10.97	4.82	6.52	4.59				
	NT2RM4000255	2.28	2.28	4.7	3.79	4.89	1.42				
	NT2RM4000265	2.23	2.23	5.69	4.29	8.21	1.99				
	NT2RM4000283	18.14	18.14	26.21	37.17	39.88	44.79	**	+		
	NT2RM4000284	13.85	13.85	33.72	31.96	42.88	40.67				
20	NT2RM4000290	6.31	6.31	7.76	3.77	4.92	4	*	-		
	NT2RM4000295	2.36	2.36	2.16	2.32	2.13	0.88				
	NT2RM4000306	3.79	3.79	7.76	7.1	6.14	5.02				
	NT2RM4000307	5.04	5.04	9.13	9.95	9.99	11.72	*	+		
	NT2RM4000309	2.48	2.48	5.34	3.92	6.52	5.52				
25	NT2RM4000313	3.92	3.92	9.61	5.75	7.77	8.52				
	NT2RM4000318	3.38	3.38	6.87	4.35	6.36	3.28				
	NT2RM4000324	4.93	4.93	5.93	2.79	4.98	2.12				
	NT2RM4000326	5.32	5.32	4.61	2.59	2.45	2.01	**	-		
	NT2RM4000327	4.97	4.97	10.95	7.94	10.32	7.71				
30	NT2RM4000344	5.46	5.46	16.67	11.16	10.17	19.18				
	NT2RM4000349	3.68	3.68	9.99	11.87	10.88	13.8	*	+		
	NT2RM4000354	1.65	1.65	3.13	4.2	4.31	3.1				
	NT2RM4000356	1.5	1.5	3.11	2.5	4.07	1.64				
	NT2RM4000366	15.75	15.75	44.48	38.81	44.07	58.06				
35	NT2RM4000368	3.04	3.04	5.9	4.36	5.48	3.48				
	NT2RM4000373	6.49	6.49	12.29	12.72	15.96	16.47	*	+		
	NT2RM4000386	4.92	4.92	4.71	3.81	4.57	4.6				
	NT2RM4000395	2.7	2.7	4.69	6.36	6.51	5.68	*	+		
	NT2RM4000414	1	1	2.76	2.38	2.9	2.19				
40	NT2RM4000417	1.66	1.66	2.83	3.9	3.95	3.25	*	+		
	NT2RM4000421	2.99	2.99	5.17	4.96	5.47	4.13				
	NT2RM4000425	10.56	10.56	26.8	26.49	31.48	45.28				
	NT2RM4000433	2.78	2.78	5.39	1.67	2.21	1.79				
	NT2RM4000436	3.8	3.8	9.47	11.84	16.75	16.38	*	+		
45	NT2RM4000444	4.51	4.51	12.97	7.29	8.54	7.38				
	NT2RM4000457	3.35	3.35	8.69	13.35	12.38	13.25	*	+		
	NT2RM4000471	1.73	1.73	4.01	4.17	4.87	2.49				
	NT2RM4000472	2.2	2.2	7.62	6.64	7.61	5.39				
	NT2RM4000486	2.98	2.98	5.92	6.85	7.54	6				
50	NT2RM4000490	3.85	3.85	6.41	7.16	5.1	5.86				
	NT2RM4000496	3.68	3.68	3.86	2.16	2.36	2.04	**	-		
	NT2RM4000505	26.85	26.85	60.33	68.9	80.59	70.67	*	+		
	NT2RM4000511	22.8	22.8	45.35	64.6	89.95	75.97	*	+		
	NT2RM4000514	2.61	2.61	6.75	10.47	7.53	9.25	*	+		
55	NT2RM4000515	3.75	3.75	8.81	7.27	7.94	4.66				

EP 1 130 094 A2

	NT2RM4000517	34.51	34.51	74.2	76.45	53.07	79.47		
5	NT2RM4000520	2.24	2.24	3.08	3.21	3.3	5.49		
	NT2RM4000531	2.76	2.76	5.71	4.41	5.5	4.22		
	NT2RM4000532	3.03	3.03	5.56	2.72	3.54	2.39		
	NT2RM4000533	3.55	3.55	5.43	4.73	6.98	3.23		
	NT2RM4000534	5.17	5.17	2.92	2.73	4.62	1.94		
10	NT2RM4000563	5.21	5.21	16.69	17.05	16.8	19.36		
	NT2RM4000566	1.79	1.79	4.6	7.14	5.27	7.91	*	+
	NT2RM4000568	10.48	10.48	19.4	28.18	22.91	33.06	*	+
	NT2RM4000585	1.97	1.97	2.52	0.82	1.99	1.26		
	NT2RM4000587	3.88	3.88	6.15	6.66	5.75	5.15		
15	NT2RM4000590	3.73	3.73	4.12	1.64	2.48	2.3	**	-
	NT2RM4000593	4.46	4.46	7.83	10.21	12.36	7.45		
	NT2RM4000595	3.94	3.94	3.91	2.27	4.36	2.45		
	NT2RM4000603	4.18	4.18	6.98	6.95	7.23	7.26		
	NT2RM4000611	9.81	9.81	18.02	17.1	17.38	25.49		
20	NT2RM4000616	2.05	2.05	6.19	2.73	4.14	4.53		
	NT2RM4000621	26.04	26.04	70.86	57.5	62.2	59.07		
	NT2RM4000648	2.78	2.78	7.83	2.66	2.67	3.88		
	NT2RM4000649	5.53	5.53	11.03	7.34	8.4	13.12		
	NT2RM4000658	3.22	3.22	8.18	4.22	6.14	8.14		
	NT2RM4000661	57.68	57.68	140.68	141.09	135.49	177.49		
25	NT2RM4000673	3.02	3.02	5.72	3.69	3.8	4.59		
	NT2RM4000674	2.23	2.23	4.27	2.89	2.63	2.99		
	NT2RM4000689	3.81	3.81	6.47	5.34	6.36	7.74		
	NT2RM4000698	14.85	14.85	20.92	25.12	23.66	26.39	*	+
	NT2RM4000700	2.39	2.39	5.53	2.41	6.95	5.61		
30	NT2RM4000701	10.07	10.07	54.36	61.81	67.75	63.17		
	NT2RM4000712	3.5	3.5	7.9	5.97	8.03	9.55		
	NT2RM4000717	2.14	2.14	6.66	3.67	2.94	4.3		
	NT2RM4000733	4.37	4.37	7.8	4.16	6.93	11.03		
35	NT2RM4000734	2.17	2.17	5.92	2.35	5.23	4.7		
	NT2RM4000741	2.14	2.14	6.11	3.59	4.75	4.66		
	NT2RM4000744	1.76	1.76	7.05	2.76	4.4	10.18		
	NT2RM4000749	15.53	15.53	23.13	26.26	27.8	34.67	*	+
	NT2RM4000751	2.88	2.88	6.54	6.23	6.11	5.94		
40	NT2RM4000752	4.11	4.11	4.88	4.78	5.12	38.58		
	NT2RM4000760	3.5	3.5	9.69	4.54	6.31	5.26		
	NT2RM4000761	237.9	237.9	478.3	219.65	302.54	336.34		
	NT2RM4000764	66.05	66.05	178	212.33	205.98	232.75	*	+
	NT2RM4000768	6.11	6.11	11.21	15.56	10.14	21.17		
45	NT2RM4000778	1.6	1.6	4.7	4.27	5.18	6.18		
	NT2RM4000779	4.52	4.52	8.28	6.87	7.19	7.33		
	NT2RM4000787	2.55	2.55	7.49	3.64	4.9	4.53		
	NT2RM4000790	2.99	2.99	5.03	5.47	5.82	12.06		
	NT2RM4000795	1.99	1.99	3.67	2.36	1.2	2.51		
50	NT2RM4000796	3.26	3.26	5.86	4.29	3.48	4.28		
	NT2RM4000798	1.77	1.77	5.53	3.72	3.08	3.47		
	NT2RM4000800	4.15	4.15	8.16	8.7	9.44	9.06		
	NT2RM4000813	3.31	3.31	8.79	7.14	7.95	10.09		
	NT2RM4000820	4.89	4.89	9.14	5.39	6.27	5.44		
55	NT2RM4000827	7.1	7.1	18.55	16.3	15.8	17.88		

EP 1 130 094 A2

	NT2RM4000830	3.27	3.27	7.35	5.28	7.8	8.38
5	NT2RM4000833	2.51	2.51	6.84	4.48	3.35	4.87
	NT2RM4000841	4	4	15	10.57	8.84	10.1
	NT2RM4000846	1.66	1.66	8.83	4.74	6.83	5.09
	NT2RM4000848	2.61	2.61	5.75	4.15	6.32	3.12
10	NT2RM4000852	3.89	3.89	9.81	8.16	8.67	8.29
	NT2RM4000855	5.12	5.12	7.64	5.99	6.08	7.19
	NT2RM4000859	11.18	11.18	16.28	16.48	19.12	17.62
	NT2RM4000868	3.06	3.06	6.47	5.23	6.91	7.05
15	NT2RM4000870	4	4	9.82	7.06	3.87	6.59
	NT2RM4000879	1.67	1.67	6	4.15	3.31	3.11
	NT2RM4000882	18.99	18.99	28.36	20.33	16.5	12.55
20	NT2RM4000887	2.16	2.16	6.01	3.53	4.91	1.6
	NT2RM4000895	2.33	2.33	5.33	3.16	5.9	3.08
	NT2RM4000897	5.78	5.78	6.99	8.89	9.73	7.02
	NT2RM4000901	5.22	5.22	6.41	4.37	6.2	6.12
	NT2RM4000950	4.04	4.04	5.09	3.57	4.06	2.91
25	NT2RM4000965	2.89	2.89	4.54	5.98	4.04	6.18
	NT2RM4000971	2.49	2.49	4.78	4.84	4.29	7.62
	NT2RM4000979	5.16	5.16	12.71	10.23	10.46	7.87
	NT2RM4000987	1.9	1.9	4.59	3.64	4.22	3.21
	NT2RM4000989	2.51	2.51	5.17	4.2	5.16	4.99
30	NT2RM4000991	3.1	3.1	4.83	2.87	3.53	8.73
	NT2RM4000992	3.39	3.39	5.41	3.6	4.54	3.19
	NT2RM4000996	6.22	6.22	7.86	7.14	8	7.28
	NT2RM4000997	3.53	3.53	13.96	9.81	10.96	10.89
	NT2RM4001001	26.06	26.06	55.43	37.67	34.22	54.29
35	NT2RM4001002	5.13	5.13	11.03	11.54	11.33	19.44
	NT2RM4001016	1.63	1.63	2.73	4.07	5.31	3.76 * +
	NT2RM4001025	65.77	65.77	133.97	148.39	181.87	171.5 * +
	NT2RM4001027	2.49	2.49	3.66	1.67	1.77	4.31
	NT2RM4001032	2.55	2.55	6.74	4.94	5.46	3.84
40	NT2RM4001047	3.87	3.87	3.7	2.61	2.73	2.7 ** -
	NT2RM4001049	3.97	3.97	10.12	18.29	20.63	26.25 ** +
	NT2RM4001051	2.72	2.72	12.54	11.17	10.12	13.68
	NT2RM4001052	14.95	14.95	72.14	75.49	75.01	79.12
	NT2RM4001053	14.96	14.96	39.3	41.36	28.95	25.87
45	NT2RM4001054	3.13	3.13	5.17	5.34	5.69	5.01
	NT2RM4001059	3.65	3.65	6.37	4.91	3.52	4.48
	NT2RM4001071	4.03	4.03	7.35	6.8	7.34	6.55
	NT2RM4001084	8.04	8.04	6.52	9.49	10.53	9.53 * +
	NT2RM4001092	12.61	12.61	109.97	76.93	98.78	73.14
50	NT2RM4001100	6.72	6.72	20.93	22.35	15.18	18.98
	NT2RM4001116	1.17	1.17	2.5	2.77	2.96	2.16
	NT2RM4001119	1.74	1.74	4.82	4.72	4.22	4.15
	NT2RM4001140	2.65	2.65	7.49	8.27	7.78	9.03
	NT2RM4001148	6.59	6.59	13.68	12.1	12.92	15.83
55	NT2RM4001151	3.7	3.7	4.31	1.94	3.65	1.68
	NT2RM4001155	5.51	5.51	6.36	3.55	5.37	4.63
	NT2RM4001157	1.68	1.68	4.95	4.86	2.81	3.82
	NT2RM4001160	1.57	1.57	3.39	2.99	1.9	2.41
	NT2RM4001163	42.35	42.35	86.27	106.63	52.13	98.56

EP 1 130 094 A2

	NT2RM4001187	2.64	2.64	7.25	3.96	4.87	5.2
5	NT2RM4001191	3.2	3.2	9.95	8.59	6.36	8.72
	NT2RM4001200	3.83	3.83	6.35	5.52	4.41	4.11
	NT2RM4001203	9.93	9.93	20.29	22.65	25.36	21.82
	NT2RM4001204	3.23	3.23	3.59	3.17	2.83	2.6
	NT2RM4001217	4.62	4.62	12.16	11.26	13.39	13.72
10	NT2RM4001245	7.31	7.31	17.14	13.76	14.49	17.16
	NT2RM4001247	3.23	3.23	9.1	5.73	6.57	5.03
	NT2RM4001256	2.51	2.51	6.39	3.57	5.48	4.14
	NT2RM4001258	8.2	8.2	24.68	25.02	24.16	22.89
	NT2RM4001267	3.43	3.43	4.83	3.93	4.3	8.08
15	NT2RM4001273	4.23	4.23	8.38	7.39	6.96	8.77
	NT2RM4001281	4	4	10.54	10.15	9.05	10
	NT2RM4001286	345.27	345.27	526.77	215.2	220.51	552.53
	NT2RM4001290	23.51	23.51	61.5	56.51	48.6	59.58
	NT2RM4001309	2.64	2.64	6.81	3.17	5.42	4.05
20	NT2RM4001313	2.63	2.63	8.62	3.81	6.36	7.03
	NT2RM4001316	3.14	3.14	6.12	3.39	3.85	5.25
	NT2RM4001320	2.4	2.4	6.43	2.83	3.16	5.6
	NT2RM4001321	3.98	3.98	8.62	6.17	7.03	6.24
	NT2RM4001325	2.54	2.54	5.2	4.76	2.93	5.25
25	NT2RM4001333	8.65	8.65	18.06	8.57	10.76	9.51
	NT2RM4001340	4.81	4.81	12.27	6.99	7.72	11.24
	NT2RM4001344	4.09	4.09	4.69	3.04	3.44	4.93
	NT2RM4001347	6.49	6.49	9.8	10.53	9.72	17.71
	NT2RM4001357	7.59	7.59	12.09	8.58	11.68	9.37
30	NT2RM4001360	2.79	2.79	5.11	3.82	2.85	3.07
	NT2RM4001371	4.71	4.71	8.57	6.58	13.16	12.93
	NT2RM4001377	8.01	8.01	13.74	8.66	9.23	10.58
	NT2RM4001382	17.31	17.31	56.74	35.57	28.32	38.22
	NT2RM4001384	2.17	2.17	4.11	2.35	3.34	3.75
35	NT2RM4001400	3.78	3.78	5.76	4.87	4.66	5.07
	NT2RM4001409	2.55	2.55	6.82	4.82	4.63	5.27
	NT2RM4001410	5.48	5.48	21.69	17.34	21.09	18.91
	NT2RM4001411	2.66	2.66	6.5	5.86	6.64	6.77
	NT2RM4001412	1.75	1.75	3.33	2.39	2.52	2.79
40	NT2RM4001414	2.18	2.18	4.83	2.45	2.4	3.77
	NT2RM4001436	8.35	8.35	16.65	10.45	10.13	15.55
	NT2RM4001437	2.77	2.77	8.85	8.31	11.26	7.67
	NT2RM4001444	11.57	11.57	25.93	21.1	18.36	18.42
	NT2RM4001454	3.62	3.62	7.89	6.16	5.03	4.79
45	NT2RM4001455	5.85	5.85	22.19	18.03	25.08	26.16
	NT2RM4001483	4.37	4.37	8.77	4.97	5.43	6.46
	NT2RM4001489	3.12	3.12	7.04	3.64	4.19	5.46
	NT2RM4001495	1.35	1.35	5.13	2.85	3.29	3.37
	NT2RM4001499	1.74	1.74	4.98	3.65	2.77	3.3
50	NT2RM4001515	0.95	0.95	3.38	2.65	5.38	3.41
	NT2RM4001519	1.86	1.86	4.6	2.24	4.38	2.85
	NT2RM4001522	3.8	3.8	7.66	5.36	7.42	9.13
	NT2RM4001523	5.46	5.46	9.11	4.82	7.58	5.79
	NT2RM4001550	11.9	11.9	17.38	16.49	16.76	15.01
55	NT2RM4001553	7.88	7.88	13.4	23.26	23.53	23.87 ** +

EP 1 130 094 A2

	NT2RM4001554	0.86	0.86	1.74	1.85	1.11	2.2		
5	NT2RM4001557	2.5	2.5	6.33	5.05	3.36	4.89		
	NT2RM4001565	1.87	1.87	4.05	2.46	3.34	3.23		
	NT2RM4001566	3.23	3.23	8.57	8.91	10.49	11.42		
	NT2RM4001569	1.47	1.47	5.4	3.35	4.15	1.56		
10	NT2RM4001579	6.57	6.57	16.69	19.23	23.83	18.22		
	NT2RM4001582	4.06	4.06	5.97	2.16	3.17	2.67	*	-
	NT2RM4001589	21.51	21.51	37.16	42.45	55.76	47.57	*	+
	NT2RM4001592	1.37	1.37	2.96	3.02	2.14	3.71		
	NT2RM4001594	1.98	1.98	4.09	5.4	5.24	5.67	*	+
15	NT2RM4001597	2.65	2.65	5.64	5.17	4.97	4.33		
	NT2RM4001605	2.7	2.7	6.18	5.71	5.92	5.93		
	NT2RM4001609	23.65	23.65	45	61.08	78.89	77.31	*	+
20	NT2RM4001610	48.1	48.1	69.16	132.54	132.39	115.22	**	+
	NT2RM4001611	3.31	3.31	4.56	2.33	2.32	2.02	*	-
	NT2RM4001618	7.05	7.05	7.95	6.68	8.98	12.95		
	NT2RM4001622	13.53	13.53	19.88	14.67	24.67	28.46		
25	NT2RM4001624	1.6	1.6	3.02	3.92	2.66	4.43		
	NT2RM4001625	4.89	4.89	39.6	41.63	47.1	46.46		
	NT2RM4001629	3.82	3.82	8.82	12.09	12.08	13.38	*	+
	NT2RM4001632	15.28	15.28	24.55	31.07	26.16	25.6		
	NT2RM4001642	3.29	3.29	4.17	2.89	3.62	2.1		
30	NT2RM4001647	4.44	4.44	6.83	4.04	5.48	4.67		
	NT2RM4001650	4.96	4.96	4.94	2.66	2.87	3.79	**	-
	NT2RM4001662	2.18	2.18	5.47	8.31	6.54	9.39	*	+
	NT2RM4001666	2.28	2.28	6.5	6.24	6.17	8.14		
	NT2RM4001670	3.52	3.52	10.77	11.16	10.82	14.91		
35	NT2RM4001682	12.66	12.66	31.6	33.03	26.04	37.07		
	NT2RM4001710	6.7	6.7	38.5	40.58	58.41	40.31		
	NT2RM4001712	4.06	4.06	7.61	10.19	10.7	9.98	*	+
	NT2RM4001714	10.88	10.88	19.37	18.67	19.3	17.65		
40	NT2RM4001715	10.77	10.77	11.6	13.55	16.86	12.99		
	NT2RM4001727	3.41	3.41	5.92	4.83	5.89	7.6		
	NT2RM4001731	2.6	2.6	10.72	13.46	11.23	11.73		
	NT2RM4001735	12.84	12.84	21.53	22.01	20.88	34.93		
	NT2RM4001739	2.46	2.46	7.3	8.13	5.17	7.14		
45	NT2RM4001741	14.41	14.41	29.88	26.98	27.21	32.35		
	NT2RM4001746	3.65	3.65	6.76	6.89	6.5	5.33		
	NT2RM4001754	3.16	3.16	4.17	3.39	3.62	3.84		
	NT2RM4001757	5.02	5.02	5.78	4.7	6.31	7.97		
	NT2RM4001758	1	1	0.76	1.98	0.65	1.46		
50	NT2RM4001768	4.83	4.83	10.19	8.48	6.91	7.83		
	NT2RM4001775	3.23	3.23	2.76	1.9	1.85	1.71	**	-
	NT2RM4001776	2.56	2.56	4.77	2.47	2.68	2.69		
	NT2RM4001783	2.88	2.88	3.22	3.12	3.48	3.68		
	NT2RM4001793	4.67	4.67	11.44	12.02	9.6	10.75		
55	NT2RM4001810	3.31	3.31	4.46	3.33	3.63	3.11		
	NT2RM4001813	3.9	3.9	4.15	4.71	4.19	5.36		
	NT2RM4001818	4.06	4.06	11.34	10.43	8.67	10.53		
	NT2RM4001819	2.35	2.35	5.6	2.37	3.02	4.58		
	NT2RM4001823	1.76	1.76	4.48	2.47	4.04	4.27		
	NT2RM4001828	5.01	5.01	11.49	5.67	7.54	7.51		

EP 1 130 094 A2

	NT2RM4001835	9.75	9.75	18.65	21.12	16.5	26.55		
5	NT2RM4001836	3.27	3.27	8.32	3.65	3.54	5.58		
	NT2RM4001841	7.94	7.94	15.82	20.15	20.96	23.33	*	+
	NT2RM4001842	2.1	2.1	4.44	3.5	3.35	4.85		
	NT2RM4001843	5.65	5.65	14.54	13.34	12.25	14.94		
	NT2RM4001856	4.42	4.42	7.16	7.65	4.71	16.83		
10	NT2RM4001858	5.91	5.91	15.86	16.09	17.03	16.93		
	NT2RM4001861	2.91	2.91	9.57	6.31	8.66	9.28		
	NT2RM4001863	8.06	8.06	9.5	15.16	15.68	11.77	*	+
	NT2RM4001865	5.04	5.04	11.25	7.44	10.24	9.03		
	NT2RM4001869	5.1	5.1	5.96	5.22	8.45	21.88		
15	NT2RM4001873	9.62	9.62	18.43	13.33	15.49	19.21		
	NT2RM4001876	2.24	2.24	6.94	3.65	4.39	7.25		
	NT2RM4001880	3.6	3.6	8.57	5.13	5.41	7.67		
	NT2RM4001885	5.71	5.71	11.11	7.11	6.56	11.98		
	NT2RM4001889	10.25	10.25	18.24	16.31	15.85	21.33		
20	NT2RM4001894	2.61	2.61	6.07	3.58	3.65	3.49		
	NT2RM4001897	7.87	7.87	20.24	18.41	20.4	23.46		
	NT2RM4001899	3.36	3.36	7.43	4.92	8.19	8.54		
	NT2RM4001905	3	3	4.84	3.3	4.53	7.1		
	NT2RM4001922	2.55	2.55	6.05	3.97	4.84	5.11		
25	NT2RM4001930	2.64	2.64	8.9	2.88	6.53	6.38		
	NT2RM4001938	2.65	2.65	4.91	5.09	5.65	6.43		
	NT2RM4001940	2.73	2.73	6.17	5.91	4.46	5.48		
	NT2RM4001942	37.36	37.36	32.02	53.86	59.28	82.77	*	+
	NT2RM4001953	4.65	4.65	9.68	5.04	6.79	4.91		
30	NT2RM4001965	4.96	4.96	8.82	10.18	8.54	8.39		
	NT2RM4001966	3	3	5.14	6.3	7.45	8.19	*	+
	NT2RM4001969	2.22	2.22	7.29	5.01	2.95	4.5		
	NT2RM4001974	1.19	1.19	4.61	1.89	2.96	4.83		
35	NT2RM4001979	2.09	2.09	6.37	3.39	4.65	7.36		
	NT2RM4001980	4.3	4.3	7.59	7.58	8.02	9.33		
	NT2RM4001984	2.31	2.31	5.36	2.68	3.49	4.57		
	NT2RM4001987	3.36	3.36	9.66	2.92	4.6	5.01		
	NT2RM4002013	6.62	6.62	15.13	13.47	17.16	19.8		
40	NT2RM4002018	2.31	2.31	5.15	4.09	5.53	7.1		
	NT2RM4002033	3.19	3.19	8.16	4.91	3.27	5.93		
	NT2RM4002034	1.89	1.89	6.19	4.82	4.38	4.03		
	NT2RM4002044	7.71	7.71	17.9	18.75	12.3	18.5		
	NT2RM4002047	3.88	3.88	5.19	2.68	5.38	9.2		
	NT2RM4002054	4.54	4.54	6.97	2.56	4.3	3.89		
45	NT2RM4002055	13.72	13.72	74.75	60.51	91.27	61.53		
	NT2RM4002059	23.73	23.73	31.85	48.05	63.09	52.61	**	+
	NT2RM4002061	3.72	3.72	5.32	3.59	3.69	4.81		
	NT2RM4002062	1.9	1.9	5.41	3.66	2.84	4.26		
50	NT2RM4002063	2.21	2.21	8.1	7.64	7.35	3.79		
	NT2RM4002066	2.07	2.07	5.29	4.42	6.32	4.07		
	NT2RM4002067	2.51	2.51	4.27	3.07	5.19	4.41		
	NT2RM4002073	3.73	3.73	7.24	5.51	7.69	5.16		
	NT2RM4002074	5.19	5.19	7.35	5.67	7.47	4.49		
55	NT2RM4002075	5.13	5.13	5.9	3.16	3.18	2.91	**	-
	NT2RM4002076	3.13	3.13	3.05	1.94	2.52	1.71	*	-

EP 1 130 094 A2

	NT2RM4002078	10.3	10.3	28.06	23.95	20.81	26.64		
5	NT2RM4002081	10.47	10.47	30.87	19.18	17.8	18.22		
	NT2RM4002082	1.25	1.25	3.02	3.85	2.58	1.23		
	NT2RM4002093	2.82	2.82	3.9	4.79	4.66	4.79	*	+
	NT2RM4002109	4.42	4.42	11.51	13.95	15.12	15.21	*	+
10	NT2RM4002115	2.86	2.86	4.51	4.81	4.8	2.52		
	NT2RM4002118	4.48	4.48	6.14	4.3	4.86	4.27		
	NT2RM4002128	3.78	3.78	4.57	2.84	3.31	3.13	*	-
	NT2RM4002137	3.96	3.96	8.14	10.27	7.51	8.92		
	NT2RM4002139	3.78	3.78	8.98	7.03	7.84	7.87		
15	NT2RM4002140	4.04	4.04	9.45	8.87	7.81	10.17		
	NT2RM4002145	5.99	5.99	17.51	25.81	31.07	24.47	*	+
	NT2RM4002146	4.51	4.51	8.23	8.56	9	8.92		
	NT2RM4002161	2.33	2.33	4.97	1.38	3.15	5.3		
	NT2RM4002174	4.86	4.86	8.02	3.12	4.53	6.15		
20	NT2RM4002178	7.3	7.3	24.43	28.61	33.13	29.27	*	+
	NT2RM4002180	3.47	3.47	11.93	9.27	10.02	11.28		
	NT2RM4002185	5.94	5.94	35.51	31.59	32.34	31.69		
	NT2RM4002189	1.6	1.6	3.24	3.68	5.59	4.91	*	+
	NT2RM4002194	9.3	9.3	25.94	37.2	29.64	38.23	*	+
	NT2RM4002198	6.09	6.09	7.61	9.37	8.4	10.04	*	+
25	NT2RM4002205	4.01	4.01	9.05	6.76	7.86	8.76		
	NT2RM4002213	5.36	5.36	8.79	8.05	11.99	14.41		
	NT2RM4002216	7.35	7.35	12.58	16.58	23.93	18.16	*	+
	NT2RM4002226	3.84	3.84	9.71	20.85	16.65	16.5	**	+
	NT2RM4002237	4.19	4.19	10.13	10.37	7.64	13.22		
30	NT2RM4002240	1.96	1.96	3.64	3.73	3.71	7.59		
	NT2RM4002251	2.11	2.11	6.2	7.87	5.48	5.17		
	NT2RM4002256	4.38	4.38	10.68	10.7	9.46	9.64		
	NT2RM4002262	2.85	2.85	6.25	3.34	4.43	9.66		
	NT2RM4002266	3.93	3.93	4.76	2.76	3.55	4.47		
35	NT2RM4002276	11.23	11.23	15.55	16.5	28.25	20.64		
	NT2RM4002278	1.89	1.89	4.59	4.33	3.99	5.11		
	NT2RM4002281	17.71	17.71	59.08	62.68	51.19	59.89		
	NT2RM4002287	2.08	2.08	3.84	2.46	4.21	3.32		
	NT2RM4002294	3.19	3.19	6.99	6.28	6.09	8.69		
40	NT2RM4002298	18.59	18.59	60.14	86.09	89.9	88.75	*	+
	NT2RM4002301	3.2	3.2	6.85	4.63	5.94	4.02		
	NT2RM4002306	4.71	4.71	8.24	4.99	5.31	4.2		
	NT2RM4002323	3.9	3.9	4.06	4.11	4.39	3.11		
	NT2RM4002334	11.54	11.54	20.76	17.92	20.72	16.95		
45	NT2RM4002339	1.78	1.78	3.52	1.33	1.3	1.38		
	NT2RM4002344	2.36	2.36	5.74	2.87	3.57	7.92		
	NT2RM4002345	3.56	3.56	10.59	5.06	4.63	7.5		
	NT2RM4002352	2.04	2.04	7.67	3.99	5.14	3.74		
	NT2RM4002362	20.38	20.38	24.92	11.23	14.32	15.17	*	-
50	NT2RM4002373	2.1	2.1	3.96	3.21	2.55	3.63		
	NT2RM4002374	2.28	2.28	4.39	2.29	3.58	4.3		
	NT2RM4002376	4.02	4.02	6.03	3.31	2.97	5.52		
	NT2RM4002383	2.8	2.8	8.49	4.76	5.79	4.28		
	NT2RM4002390	3.03	3.03	6.01	4.06	5.27	7.37		
55	NT2RM4002398	5.16	5.16	43.18	33.97	50.73	30.41		

EP 1 130 094 A2

	NT2RM4002409	2.11	2.11	5.93	3.37	4.29	1.9
5	NT2RM4002414	4.73	4.73	6.21	7.37	9.12	14.53
	NT2RM4002438	2.07	2.07	5.28	3.03	4.38	7.18
	NT2RM4002440	2.99	2.99	6.92	5.78	5.32	9.49
	NT2RM4002446	2.23	2.23	6.08	2.95	4.45	5.7
	NT2RM4002450	3.36	3.36	10.01	6.15	7.75	7.24
10	NT2RM4002452	2.13	2.13	6.3	3.67	5.15	7.23
	NT2RM4002457	2.68	2.68	4.44	2.66	3.26	4.52
	NT2RM4002458	3.06	3.06	5.77	3.32	5.34	4.04
	NT2RM4002460	2.43	2.43	3.68	1.57	2.45	1.43
	NT2RM4002464	5.4	5.4	12.62	14.39	13.72	14.3
15	NT2RM4002479	4.66	4.66	6.69	4.91	7.98	11.54
	NT2RM4002482	4.26	4.26	16.18	10.19	11.5	12.2
	NT2RM4002489	6.74	6.74	16.91	8.79	5.81	11.68
	NT2RM4002493	1.35	1.35	3.22	1.96	3.51	2.73
	NT2RM4002499	34.96	34.96	72.9	59.42	52.07	54.3
20	NT2RM4002504	5.15	5.15	10.68	10.57	13.51	9.8
	NT2RM4002506	4.77	4.77	9.4	4.93	7.59	8.53
	NT2RM4002510	2.03	2.03	3.27	1.66	2.97	2.48
	NT2RM4002527	1.57	1.57	3.14	1.83	2.31	4.47
	NT2RM4002532	2.45	2.45	7.75	5.88	3.37	5.19
25	NT2RM4002534	1.79	1.79	4.8	2.1	3.45	2.94
	NT2RM4002535	2.5	2.5	6.51	5.89	8.1	6.37
	NT2RM4002554	3.29	3.29	5.31	3.31	5.47	3.12
	NT2RM4002558	6.91	6.91	32.57	32.58	41.54	25.61
	NT2RM4002565	5.38	5.38	13.6	8.22	9.85	10.53
30	NT2RM4002567	3.34	3.34	5.43	4.21	4.49	7.22
	NT2RM4002571	4.48	4.48	15.61	11.95	16.47	15.24
	NT2RM4002572	5.57	5.57	17.2	13.7	9.59	13.48
	NT2RM4002577	7.76	7.76	15.25	6.59	5.87	5.65
	NT2RM4002583	1.08	1.08	3.58	2.28	4.83	2.44
35	NT2RM4002584	1.64	1.64	5.67	3.24	5.74	5.56
	NT2RM4002593	3.29	3.29	5.17	2.75	3.91	4.61
	NT2RM4002594	11.26	11.26	46.5	38.21	55.32	43.58
	NT2RM4002604	4.83	4.83	4.64	1.77	2.03	2.89 ** -
40	NT2RM4002614	3.48	3.48	3.48	2.52	3.66	2.81
	NT2RM4002616	1.07	1.07	2.73	2.88	2.71	2.38
	NT2RM4002623	1.39	1.39	4.89	3.92	3.72	5.06
	NT2RM4002634	1.41	1.41	4.38	3.42	4.91	2.96
	NT2RM4002636	2.22	2.22	3.93	3.92	4.18	4.12
45	NT2RP1000002	8.82	8.82	52.94	75.1	92.89	81.45 * +
	NT2RP1000006	4.68	4.68	6.28	4.25	4.48	2.56
	NT2RP1000015	4.86	4.86	5.27	2.74	1.99	2.28 ** -
	NT2RP1000018	5.45	5.45	5	5.55	4.83	4.96
	NT2RP1000034	18.22	18.22	49.95	38.04	30.76	50.07
50	NT2RP1000035	1.93	1.93	3.2	5.26	3.23	3.96
	NT2RP1000040	1.77	1.77	3.33	2.93	3.28	4.28
	NT2RP1000042	1.3	1.3	3.44	1.99	3.22	2.38
	NT2RP1000048	3.6	3.6	10.24	7.25	9.9	9
	NT2RP1000050	2.21	2.21	4.71	2.89	4	3.57
55	NT2RP1000056	4.03	4.03	3.74	1.09	0.61	1.96 ** -
	NT2RP1000058	3.49	3.49	2.03	1.84	2.07	2.48

EP 1 130 094 A2

	NT2RP1000063	1.77	1.77	3.65	4.09	4	3.83		
5	NT2RP1000068	1.89	1.89	3.99	3.12	3.33	2.43		
	NT2RP1000072	22.9	22.9	74.07	82.91	66.26	95.85		
	NT2RP1000073	2.18	2.18	2.45	2.68	3.69	3.86	*	+
10	NT2RP1000078	2.72	2.72	3.17	2.93	2.3	3.13		
	NT2RP1000079	4.13	4.13	5.32	3.6	4.48	2.5		
	NT2RP1000080	4.99	4.99	8.13	9.46	12.46	9.46	*	+
15	NT2RP1000086	4.15	4.15	3.63	1.31	2.1	3.75		
	NT2RP1000087	1.3	1.3	4.36	3.51	3.21	3.45		
	NT2RP1000089	4.5	4.5	9.98	12.69	11.3	14.93	*	+
	NT2RP1000090	45.76	45.76	96.6	94.37	53.44	93.42		
20	NT2RP1000100	2.17	2.17	4.05	5.23	4.13	3.66		
	NT2RP1000101	3.44	3.44	5.22	4.41	2.88	4.81		
	NT2RP1000111	3.24	3.24	5.56	4.51	3.9	3.69		
	NT2RP1000112	3.29	3.29	4.08	1.85	3.33	3		
25	NT2RP1000124	5.57	5.57	4.96	3.11	5.73	5.5		
	NT2RP1000125	7.28	7.28	19.39	13.69	10.68	16.86		
	NT2RP1000129	1.81	1.81	4.35	5.14	3.91	4.27		
	NT2RP1000130	2.31	2.31	4.11	5.31	5.62	16.86		
	NT2RP1000154	7.5	7.5	15.63	17.16	12.72	16.37		
	NT2RP1000163	2.42	2.42	3.51	2.72	2.99	3.59		
30	NT2RP1000170	3.42	3.42	4.2	4.96	5.17	5.85	*	+
	NT2RP1000174	3.5	3.5	3.42	1.3	2.38	2.12	**	-
	NT2RP1000181	6.14	6.14	7.22	10.97	14.98	9.38	*	+
	NT2RP1000191	1.08	1.08	5.61	4.94	3.59	5.71		
	NT2RP1000202	1.06	1.06	1.66	2.02	1.2	2.24		
35	NT2RP1000239	1.53	1.53	4.1	2.15	0.94	2.07		
	NT2RP1000243	2.37	2.37	2.04	1.31	1.14	1.64	**	-
	NT2RP1000255	1.94	1.94	3.02	2.11	2.26	1.78		
	NT2RP1000259	5.27	5.27	9.55	5.53	6.33	4.29		
	NT2RP1000261	2.76	2.76	4.4	2.07	1.64	2.64		
40	NT2RP1000269	5.16	5.16	5.01	7.7	10.51	7.39	*	+
	NT2RP1000271	7.79	7.79	15.88	13.16	15.11	18.48		
	NT2RP1000272	7.71	7.71	13.07	10.72	11.74	11.3		
	NT2RP1000279	2.19	2.19	5.24	2.23	3.91	2.62		
	NT2RP1000290	6.61	6.61	9.02	12.65	13.52	9.92	*	+
45	NT2RP1000293	6.86	6.86	10.91	9.75	8.45	10.92		
	NT2RP1000300	12.42	12.42	11.93	9.96	11.37	10.2	*	-
	NT2RP1000324	5.16	5.16	6	4.69	5.92	6.97		
	NT2RP1000325	54.42	54.42	101.4	70.46	57.52	78.6		
	NT2RP1000326	4.01	4.01	7.67	3.82	4.56	7.85		
50	NT2RP1000331	12.16	12.16	24.08	12.19	10.5	20.1		
	NT2RP1000333	4.18	4.18	7.52	6.66	6.53	6.98		
	NT2RP1000336	1.45	1.45	4.45	1.35	3.76	1.78		
	NT2RP1000347	3.05	3.05	8.75	7.26	8.31	6.38		
	NT2RP1000348	2.11	2.11	4.14	2.76	3	2.75		
55	NT2RP1000349	2.12	2.12	3.92	3	4.39	4.11		
	NT2RP1000353	40.87	40.87	83.5	51.49	47.8	66.02		
	NT2RP1000356	39.53	39.53	93.37	50.3	56.48	74.42		
	NT2RP1000357	3.89	3.89	9.63	8.43	8.7	8.72		
	NT2RP1000358	2.85	2.85	6.11	4.23	3.04	5.09		
	NT2RP1000360	11.04	11.04	19.39	12.08	18.42	19.44		

EP 1 130 094 A2

	NT2RP1000363	13.09	13.09	15.39	13.13	13.38	10.01				
5	NT2RP1000376	1.81	1.81	3.8	2.09	1.9	2.24				
	NT2RP1000386	118	118	191.31	146.98	187.97	155.47				
	NT2RP1000407	0.72	0.72	3.16	0.58	0.89	1.2				
	NT2RP1000409	2.05	2.05	5.39	2.84	6.59	3.83				
	NT2RP1000413	4.78	4.78	8.03	5.86	8.89	10.19				
10	NT2RP1000416	1.5	1.5	2.01	0.93	3.17	0.7				
	NT2RP1000418	2.27	2.27	6.69	5.08	6.67	4.85				
	NT2RP1000420	1.77	1.77	5.19	7.32	7.64	3.7				
	NT2RP1000434	1.48	1.48	4.39	1.27	3.12	1				
	NT2RP1000439	5.02	5.02	9.31	20.62	28.73	24.75	**	+		
15	NT2RP1000443	1.8	1.8	3.46	2.24	1.61	1.63				
	NT2RP1000447	2.21	2.21	5.57	2.49	2.87	3.1				
	NT2RP1000448	1.39	1.39	3.58	3.09	4.4	1.41				
	NT2RP1000451	4.2	4.2	6.37	5.72	7.27	7.04				
	NT2RP1000458	15.1	15.1	10.53	19.73	8.72	23.03				
20	NT2RP1000460	7.55	7.55	13.82	8.76	11.49	8.62				
	NT2RP1000465	4.58	4.58	20.97	20.41	19.98	22.46				
	NT2RP1000468	3.25	3.25	4.64	3.82	4.1	4.45				
	NT2RP1000470	2.38	2.38	5.67	3.99	2.35	3.8				
	NT2RP1000477	1.11	1.11	3.81	1.1	0.84	0.83				
25	NT2RP1000478	4.53	4.53	12.55	19.87	18.75	20.39	*	+		
	NT2RP1000481	1.23	1.23	3.89	2.48	4.09	1.2				
	NT2RP1000493	2.44	2.44	3.8	1.74	3.83	0.87				
	NT2RP1000513	13.07	13.07	16.37	17.06	17.57	18.97	*	+		
	NT2RP1000522	6.13	6.13	12.69	13.13	13.08	10.32				
30	NT2RP1000533	3.72	3.72	6.17	2.92	4.49	2.17				
	NT2RP1000544	1.53	1.53	2.45	1.38	1.24	1.44				
	NT2RP1000547	0.88	0.88	2.45	2	1.63	1.23				
	NT2RP1000551	1.7	1.7	2.62	2.13	3.2	1.1				
	NT2RP1000567	1.66	1.66	4.29	2.54	4.29	1.77				
35	NT2RP1000574	1.99	1.99	4.28	1.5	3.43	1.38				
	NT2RP1000577	3.14	3.14	6.01	3.16	5.31	2.05				
	NT2RP1000579	4.64	4.64	6.24	3.27	3.97	2.04				
	NT2RP1000581	5.22	5.22	3.58	2.07	1.61	0.93	**	-		
	NT2RP1000593	1.74	1.74	4.39	2.48	3.28	2.3				
40	NT2RP1000604	3.85	3.85	7.75	17.25	13.78	16.39	**	+		
	NT2RP1000609	1.15	1.15	2.21	2.84	2.61	1.55				
	NT2RP1000613	1.12	1.12	2.56	1.82	4.29	0.82				
	NT2RP1000622	5.94	5.94	15.9	14.91	19.42	15.46				
	NT2RP1000627	9.18	9.18	18.96	23.88	21.9	14.86				
45	NT2RP1000629	4.18	4.18	5.9	5.92	5.32	3.17				
	NT2RP1000630	6.54	6.54	7.84	7.21	7.67	7.92				
	NT2RP1000639	0.64	0.64	0.31	1.53	2.04	0.28				
	NT2RP1000640	130.14	130.14	307.77	227.5	176.05	232.29				
	NT2RP1000646	4.14	4.14	9.59	10.19	11.87	12.15	*	+		
50	NT2RP1000659	2.65	2.65	7	8.91	7.99	6.04				
	NT2RP1000674	13.48	13.48	28.08	43.62	45.82	56.95	**	+		
	NT2RP1000677	3.9	3.9	10.76	11.84	10.19	9.87				
	NT2RP1000679	2.38	2.38	3.76	2.3	2.35	1.05				
	NT2RP1000688	4.72	4.72	3.34	2.76	2.73	1.83	*	-		
55	NT2RP1000689	1.44	1.44	1.86	2.03	1.22	1.13				

EP 1 130 094 A2

	NT2RP1000695	1.11	1.11	2.5	2.09	2.44	1.52		
5	NT2RP1000701	0.89	0.89	1.08	2.62	2.74	1.71	*	+
	NT2RP1000702	1.12	1.12	2.28	3.74	4.07	3.15	*	+
	NT2RP1000713	2.29	2.29	2.79	2.8	3.56	2.38		
	NT2RP1000721	4.14	4.14	4.49	4.48	3.92	3.78		
	NT2RP1000730	3.5	3.5	4.83	2.61	4.5	2.41		
10	NT2RP1000733	6.08	6.08	6.56	4.91	8.12	5.65		
	NT2RP1000738	3.18	3.18	8.04	5.16	5.71	7.11		
	NT2RP1000739	1.11	1.11	2.65	4.02	3.09	2.86		
	NT2RP1000740	1.41	1.41	3.13	3.63	3.57	3.77	*	+
	NT2RP1000746	1.15	1.15	3.58	2.28	3.74	1.37		
15	NT2RP1000750	4	4	8.31	10.25	10.72	9.39	*	+
	NT2RP1000751	33.15	33.15	59.65	67.84	64.22	66.55		
	NT2RP1000767	3.8	3.8	3.64	1.7	2.62	0.62	*	-
	NT2RP1000769	9.31	9.31	13.98	7.42	8.59	7.19		
	NT2RP1000780	0.86	0.86	1.01	1.87	1.13	0.89		
20	NT2RP1000782	4.25	4.25	12.21	10.24	7.96	9.13		
	NT2RP1000796	3.17	3.17	2.69	4.23	2.99	2.86		
	NT2RP1000797	12.31	12.31	22.78	19.44	18.64	21.78		
	NT2RP1000800	1.13	1.13	3.74	2.46	2.66	1.46		
	NT2RP1000825	2.38	2.38	2.91	1.04	1.88	0.87	*	-
25	NT2RP1000833	2.5	2.5	2.85	0.92	2.39	1.26		
	NT2RP1000834	35.44	35.44	66.57	73.98	90.28	71.45		
	NT2RP1000836	1.83	1.83	3.43	1.01	2.39	1.04		
	NT2RP1000837	3.36	3.36	6.66	3.22	4.71	3.67		
	NT2RP1000846	1.29	1.29	5.48	1.67	2.84	1.4		
30	NT2RP1000847	1.99	1.99	5.49	2.15	5.12	1.64		
	NT2RP1000851	4.67	4.67	9.32	6.18	7.94	6.72		
	NT2RP1000856	14.31	14.31	17.45	20.38	23.22	19.37	*	+
	NT2RP1000860	2.09	2.09	4.54	4.02	2.74	4.04		
	NT2RP1000902	5.31	5.31	11.6	6.94	9.91	7.34		
35	NT2RP1000903	2.45	2.45	6.26	4.04	3.42	4.24		
	NT2RP1000905	1.76	1.76	4.87	5.36	5.66	10		
	NT2RP1000915	5.51	5.51	10.01	6.72	8.59	9.91		
	NT2RP1000916	2.31	2.31	5.51	1.78	3.82	2.09		
	NT2RP1000921	9.38	9.38	8.73	8.23	9.13	7.92		
40	NT2RP1000943	5.14	5.14	10.76	8.51	8.55	7.2		
	NT2RP1000944	1.59	1.59	2.21	1.78	1.74	1.15		
	NT2RP1000947	8.5	8.5	14.91	16.51	15.04	14.22		
	NT2RP1000954	2.11	2.11	4.96	2.74	5.55	3.04		
	NT2RP1000958	6.48	6.48	14.73	4.54	10.17	10.21		
45	NT2RP1000959	124.81	124.81	209.45	128.43	72.65	206.1		
	NT2RP1000966	9.96	9.96	12.96	14.28	15.36	21.39		
	NT2RP1000974	2.46	2.46	5.38	3.98	6.08	3.71		
	NT2RP1000980	3.07	3.07	5.5	4.04	4.53	4.02		
50	NT2RP1000981	4.3	4.3	8.09	5.68	7.26	5.27		
	NT2RP1000988	6.45	6.45	10.46	9.62	6.44	7.87		
	NT2RP1001002	2.8	2.8	7.36	3.94	4.57	4.3		
	NT2RP1001004	4.72	4.72	8.25	3.65	4.9	5.37		
	NT2RP1001007	1.42	1.42	3.42	1.69	3.84	2.03		
	NT2RP1001011	1.94	1.94	5.93	3.82	5.46	4.83		
55	NT2RP1001013	4.45	4.45	9.41	5.92	8.62	5.04		

EP 1 130 094 A2

	NT2RP1001014	2.21	2.21	5.89	3.76	6.64	3.49
5	NT2RP1001020	1.87	1.87	4.11	2.08	3.75	2.36
	NT2RP1001023	62.79	62.79	145.09	101.48	105.86	143.96
	NT2RP1001027	18.11	18.11	82.66	51.63	59.05	68.9
	NT2RP1001031	1.83	1.83	3.31	2.05	3.53	2.25
10	NT2RP1001033	2.43	2.43	6.09	5.68	5.98	4.27
	NT2RP1001042	2.94	2.94	6.47	2.99	3.85	2.04
	NT2RP1001045	15.95	15.95	23.24	40.66	47.04	44.53 ** +
	NT2RP1001073	6.64	6.64	10.57	8.32	10.46	7.33
	NT2RP1001079	2.91	2.91	6.37	2.16	2.58	1.48
	NT2RP1001080	2.16	2.16	4.89	6.88	4.2	4.56
15	NT2RP1001113	1.07	1.07	3.64	3.55	3.94	3.26
	NT2RP1001159	21.42	21.42	43.84	22.89	23.31	34.25
	NT2RP1001173	1.7	1.7	3.07	1.38	4.28	1.52
	NT2RP1001176	7.4	7.4	10.13	13	9.31	13.95
	NT2RP1001177	5.31	5.31	5.75	3.01	5.5	2.02
20	NT2RP1001185	6.42	6.42	9.37	3.79	4.63	2.73 * -
	NT2RP1001199	3.9	3.9	7.67	6.93	5.22	3.28
	NT2RP1001205	7.78	7.78	19.46	16.66	12.64	23.28
	NT2RP1001215	1.82	1.82	5.02	3.79	4.12	3.15
	NT2RP1001225	4.54	4.54	7.96	7.56	8.77	6.31
25	NT2RP1001245	7.27	7.27	10.86	19.68	21.03	22.13 ** +
	NT2RP1001247	2.04	2.04	4.01	1.77	2.89	1.67
	NT2RP1001248	2.81	2.81	6.79	3.94	4.63	2.4
	NT2RP1001253	5.02	5.02	6.39	4.48	4.38	3.32
	NT2RP1001286	6.18	6.18	7.69	3.79	3.88	4.12 ** -
30	NT2RP1001294	2.4	2.4	4.47	3.6	2.73	4.18
	NT2RP1001302	2.46	2.46	4.51	4.89	2.9	5.39
	NT2RP1001310	15.54	15.54	34.01	21.13	20.75	27.15
	NT2RP1001311	1.9	1.9	3.22	2.66	3.16	2.38
	NT2RP1001313	2.6	2.6	7.72	5.45	7.85	5.78
35	NT2RP1001324	2.47	2.47	5.3	3.34	4.17	2.35
	NT2RP1001349	3.3	3.3	6.29	3.63	3.92	2.14
	NT2RP1001361	19.41	19.41	18.28	23.28	28.33	24.16 * +
	NT2RP1001379	3.82	3.82	9.52	4.97	7.97	7.06
	NT2RP1001385	2.06	2.06	4.51	4.09	3.89	4.4
40	NT2RP1001395	4.96	4.96	7.86	6.01	6.32	8.13
	NT2RP1001410	8.75	8.75	20.39	15.74	15.66	9.94
	NT2RP1001424	2.39	2.39	3.34	3	3	1.73
	NT2RP1001432	4.33	4.33	3.86	2.19	1.76	2.05 ** -
	NT2RP1001449	6.23	6.23	7.5	6.29	8.21	4.63
45	NT2RP1001457	4.09	4.09	4.21	2.11	2.26	2.63 ** -
	NT2RP1001459	21.54	21.54	132.97	90.96	107.97	81.08
	NT2RP1001466	5.73	5.73	14.97	11.31	9.39	10.99
	NT2RP1001475	2.45	2.45	6.31	5.98	6.67	3.9
	NT2RP1001482	3.93	3.93	9.18	15.88	13.03	8.2
50	NT2RP1001494	1.61	1.61	4.6	4.34	4.18	2.25
	NT2RP1001500	3.39	3.39	8.13	8.09	8.65	7.42
	NT2RP1001517	5.11	5.11	7.37	4.41	5.38	2.36
	NT2RP1001540	4.74	4.74	5.03	4.6	4.86	3.11
	NT2RP1001543	1.02	1.02	1.83	1.49	1.12	0.98
55	NT2RP1001546	22.51	22.51	51.51	34.99	22.76	33.42

EP 1 130 094 A2

	NT2RP1001550	9.33	9.33	21.4	14.35	12.21	13.42		
5	NT2RP1001553	2.07	2.07	6.07	5.69	6.04	4.45		
	NT2RP1001555	36.28	36.28	58.55	41.1	53.63	54.35		
	NT2RP1001563	2.28	2.28	3.44	2.07	2.24	1.31		
	NT2RP1001569	9.43	9.43	16	17.31	18.21	13.04		
10	NT2RP1001584	15.6	15.6	19.66	28.1	32.53	25.83	**	+
	NT2RP1001599	1.18	1.18	1.95	1.27	1.19	1.24		
	NT2RP1001616	5	5	11.95	9.49	6.7	8.95		
15	NT2RP1001654	11.78	11.78	18.07	16.27	16.54	18.38		
	NT2RP1001665	2.77	2.77	4.72	2.73	2.05	2.05		
	NT2RP1001679	76.31	76.31	195.7	199.2	240.87	222.46		
	NT2RP1001681	10.11	10.11	15.1	20.39	21.03	23.99	**	+
20	NT2RP1001694	3.58	3.58	3.82	2.45	2.38	1.97	**	-
	NT2RP2000001	5.23	5.23	5.53	4.17	4.54	3.74	**	-
	NT2RP2000006	3.49	3.49	7.32	4.12	3.88	3.4		
	NT2RP2000007	3.18	3.18	6.56	4.68	5.66	4.92		
	NT2RP2000008	2.77	2.77	6.72	3.66	5.3	4.9		
25	NT2RP2000010	2.89	2.89	5.59	2.99	5.06	2.5		
	NT2RP2000011	7.08	7.08	17.96	14.55	14.74	15.15		
	NT2RP2000027	2.28	2.28	7.42	4.52	4.89	3.61		
	NT2RP2000028	22.93	22.93	62.54	46.48	51.47	53.47		
	NT2RP2000032	2.5	2.5	5.85	3.11	3.71	6.42		
30	NT2RP2000040	11.57	11.57	23.92	14.38	14.5	23.1		
	NT2RP2000042	5.28	5.28	10.32	6.89	7.21	12.64		
	NT2RP2000045	5.7	5.7	9.42	5.27	6.45	6.3		
	NT2RP2000051	3.16	3.16	6.29	9.23	9.96	9.53	**	+
	NT2RP2000054	2.55	2.55	6.42	3.81	5.42	2.53		
35	NT2RP2000056	3.68	3.68	6.23	5.67	6.89	5.8		
	NT2RP2000057	60.79	60.79	174.83	212.63	239.81	221.98	*	+
	NT2RP2000067	3.1	3.1	3.86	2.98	4.36	5.72		
	NT2RP2000070	2.91	2.91	6.27	5.7	5.95	8.21		
	NT2RP2000076	1.66	1.66	4.45	2.98	3.58	3.23		
40	NT2RP2000077	1.67	1.67	4.73	2.43	4.94	3.14		
	NT2RP2000079	3.76	3.76	9.24	5.15	4.81	5.47		
	NT2RP2000088	2.9	2.9	5.22	2.18	3.07	2.21		
	NT2RP2000091	5.84	5.84	6.54	6.62	8.28	6.72		
	NT2RP2000092	4.37	4.37	6.7	6.06	7.67	5.65		
45	NT2RP2000097	2.74	2.74	3.39	3.4	4.13	4.13	*	+
	NT2RP2000098	3.44	3.44	6.83	6.69	9.01	6.27		
	NT2RP2000108	1.93	1.93	7.24	4.8	6.31	6.68		
	NT2RP2000114	1.95	1.95	3.65	2.58	4.41	2.9		
50	NT2RP2000116	3.17	3.17	7.36	5.35	3.85	9.42		
	NT2RP2000119	3.14	3.14	7.16	4.58	7.96	5.6		
	NT2RP2000120	3.91	3.91	7.62	5.57	8.5	5.8		
	NT2RP2000126	2.86	2.86	4.86	3.88	5.1	3.44		
	NT2RP2000133	1.83	1.83	3.66	3.13	4.05	2.01		
55	NT2RP2000147	6.28	6.28	12.88	11.64	6.51	8.58		
	NT2RP2000153	4.61	4.61	9.55	10.57	6.49	12.05		
	NT2RP2000156	3.27	3.27	8.24	5.59	6.55	4.07		
	NT2RP2000157	3.7	3.7	6.33	6.57	5.02	4.15		
	NT2RP2000161	4.45	4.45	8.82	7.52	7.5	6.02		
	NT2RP2000168	4.22	4.22	12.63	3.94	6.03	3.88		

EP 1 130 094 A2

	NT2RP2000173	12.56	12.56	81.37	72.12	92.12	78.68
5	NT2RP2000175	1.9	1.9	3.78	2.03	3.33	4.43
	NT2RP2000178	2.06	2.06	6.06	3.23	3.01	3.81
	NT2RP2000183	1.64	1.64	7.82	5.82	6.21	6.03
	NT2RP2000195	3.1	3.1	6.65	6	6.71	3.22
10	NT2RP2000204	73.6	73.6	93.43	102.95	40.16	62.34
	NT2RP2000205	4	4	6.56	3.91	5.74	4.5
	NT2RP2000208	3.06	3.06	9.42	4.23	6.77	3.36
	NT2RP2000224	13.3	13.3	31.75	18.34	21.15	20.93
	NT2RP2000230	9.96	9.96	18.99	12.16	16.4	11.95
15	NT2RP2000231	4.3	4.3	7.41	4.24	3.43	4.54
	NT2RP2000232	1.08	1.08	2.75	1.53	2.45	0.74
	NT2RP2000233	8.04	8.04	60.44	47.2	64.72	52.31
	NT2RP2000239	3	3	4.7	8.93	8.93	7.01 ** +
	NT2RP2000240	2.01	2.01	5.25	2.49	3.41	1.45
	NT2RP2000248	4.29	4.29	6.09	2.82	2.39	0.96 *
20	NT2RP2000256	5.7	5.7	8.25	5.62	6.22	5.44
	NT2RP2000257	3.47	3.47	6.92	4.86	6.52	4.34
	NT2RP2000258	1.53	1.53	3.83	3.88	2.93	3.02
	NT2RP2000261	2.95	2.95	3.94	4.47	3.59	2.91
	NT2RP2000270	3.12	3.12	6.26	6.66	4.06	4.3
25	NT2RP2000274	1.78	1.78	3.87	3.48	5.16	2.56
	NT2RP2000277	2.18	2.18	6.13	3.19	4.02	2.98
	NT2RP2000279	2.26	2.26	4.92	2.43	2.52	2.17
	NT2RP2000283	5.75	5.75	27.65	21.53	27.32	24.78
	NT2RP2000288	6.29	6.29	7.46	8.9	10.89	8.64 * +
30	NT2RP2000289	1.12	1.12	2.79	3.09	2.77	1.93
	NT2RP2000297	2.57	2.57	5.7	4.8	4.53	6.09
	NT2RP2000298	3.61	3.61	9.64	8.51	7.66	8.24
	NT2RP2000310	1.43	1.43	2.3	2.46	3.41	1.7
	NT2RP2000327	2.12	2.12	3.96	3.13	3.49	1.57
35	NT2RP2000328	6.95	6.95	11.56	13.43	16.7	14.68 * +
	NT2RP2000329	10.73	10.73	10.17	17.55	23.92	18.52 ** +
	NT2RP2000333	6.35	6.35	6.4	6.83	7.17	4.64
	NT2RP2000337	2.05	2.05	5.16	4.43	5.32	5.31
	NT2RP2000346	2.55	2.55	5.18	7.2	5.63	4.95
40	NT2RP2000357	1.57	1.57	6.87	5.48	5.14	5.35
	NT2RP2000358	2.09	2.09	4.52	5.03	4.9	4.01
	NT2RP2000366	3.23	3.23	4.08	4.16	4.25	2.32
	NT2RP2000369	7.22	7.22	9.94	44.13	45.2	44.34 ** +
	NT2RP2000376	26.92	26.92	108.62	84.48	134.63	85.95
45	NT2RP2000394	6.49	6.49	5.92	5.08	8.52	4.21
	NT2RP2000396	2.71	2.71	6.55	7.52	6.8	5.02
	NT2RP2000412	4.48	4.48	23.45	21.42	24.93	20.49
	NT2RP2000414	8.03	8.03	18.69	23.83	18.98	23.37
	NT2RP2000420	1.12	1.12	4.11	3.54	3.25	1.97
50	NT2RP2000422	6.41	6.41	13.18	17.56	17.88	18.67 * +
	NT2RP2000426	21.59	21.59	80.94	87.94	110.97	74.98
	NT2RP2000428	24.92	24.92	43.91	34.21	35.59	30.95
	NT2RP2000438	5.06	5.06	5.17	5.62	6.94	5.11
	NT2RP2000447	4.14	4.14	9.68	7.3	7.08	7.16
55	NT2RP2000448	3.03	3.03	4.63	4.57	3.57	3.17

EP 1 130 094 A2

	NT2RP2000459	2.47	2.47	4.93	2.82	3.15	2.09		
5	NT2RP2000479	3.3	3.3	7.51	5.33	5.71	5.06		
	NT2RP2000498	3.07	3.07	6.25	4.48	5.09	3.9		
	NT2RP2000503	2.47	2.47	4.46	2.54	2.82	1.52		
	NT2RP2000510	4.01	4.01	6.19	5.08	6.45	3.7		
	NT2RP2000514	2.65	2.65	2.51	1.94	2.25	1.63	*	-
10	NT2RP2000516	4.72	4.72	9.77	4.92	5.29	5.18		
	NT2RP2000523	2.21	2.21	3.17	1.92	2.44	2.63		
	NT2RP2000533	17.82	17.82	29.05	22.57	27.56	30.78		
	NT2RP2000540	1.98	1.98	4.66	3.01	5.41	5.18		
	NT2RP2000547	3.1	3.1	5.26	4.38	5.27	3.71		
15	NT2RP2000557	4.26	4.26	6.96	4.34	6.5	3.32		
	NT2RP2000558	3.43	3.43	7.17	6.43	7.11	8.26		
	NT2RP2000564	3.04	3.04	7.2	3.49	8.03	4.77		
	NT2RP2000565	4.54	4.54	11.07	7.64	9.24	9.98		
	NT2RP2000583	14.8	14.8	44.9	49.6	34.93	49.08		
	NT2RP2000591	0.81	0.81	3.81	1.53	2.61	1.21		
20	NT2RP2000599	1.85	1.85	4.1	1.97	3.43	2.36		
	NT2RP2000601	1.78	1.78	4.67	1.28	2.48	1.3		
	NT2RP2000603	2.58	2.58	4.44	2.54	2.84	2.98		
	NT2RP2000610	3.77	3.77	7.23	6.32	7.62	5.53		
	NT2RP2000614	75.85	75.85	129.42	130.63	184.38	188.58	*	+
25	NT2RP2000616	1.81	1.81	4.89	3.9	5.1	3.83		
	NT2RP2000617	2.17	2.17	6.73	5.78	6.82	6.26		
	NT2RP2000623	3.1	3.1	5.36	3.46	5.1	3.49		
	NT2RP2000634	1.56	1.56	3.92	2.29	3.34	2.02		
	NT2RP2000636	3.78	3.78	8.64	6.27	7.6	6.62		
30	NT2RP2000638	4.37	4.37	8.91	4.57	7.41	5.69		
	NT2RP2000644	2.22	2.22	5.47	3.41	4.16	3.45		
	NT2RP2000649	8.96	8.96	15.76	13.65	17.22	13.07		
	NT2RP2000652	3.35	3.35	4.58	3.57	4.36	2.72		
	NT2RP2000656	3.73	3.73	6.93	4.83	3.91	4.08		
35	NT2RP2000658	1.08	1.08	2.64	1.51	3.18	1.43		
	NT2RP2000663	4.23	4.23	6.9	5.98	7.21	5.9		
	NT2RP2000664	4.24	4.24	10.24	12.72	12.54	16.44	*	+
	NT2RP2000668	7.49	7.49	26.84	16.92	20.41	17.17		
40	NT2RP2000678	1.77	1.77	3.19	1.77	2.09	1.13		
	NT2RP2000694	4.89	4.89	8.39	11.06	13	13.36	**	+
	NT2RP2000704	1.8	1.8	5.63	2.99	3.13	3.67		
	NT2RP2000710	4.51	4.51	9.96	6.72	8.08	7.23		
	NT2RP2000712	1.43	1.43	5.35	3.39	3.57	2.95		
45	NT2RP2000715	3.42	3.42	7.43	6.04	7.56	4.49		
	NT2RP2000720	4.92	4.92	11.76	7.24	8	7.11		
	NT2RP2000731	3.92	3.92	9.15	3.7	4.5	2.61		
	NT2RP2000739	3.23	3.23	5.67	2.62	3.32	5.65		
	NT2RP2000748	1.59	1.59	4.2	1.42	1.81	1.62		
50	NT2RP2000749	11.84	11.84	21.88	14.4	8.47	13.91		
	NT2RP2000758	1.6	1.6	3.17	2.65	6	1.17		
	NT2RP2000764	1.51	1.51	5.74	2.95	5.22	1.95		
	NT2RP2000766	9.08	9.08	52.24	45.37	59.37	52.89		
	NT2RP2000777	12.28	12.28	18.43	26.91	28.56	24.47	**	+
55	NT2RP2000786	21.32	21.32	73.91	55.85	67.59	58.16		

EP 1 130 094 A2

	NT2RP2000793	5.32	5.32	6.9	4.32	3.57	4.38	*	-
5	NT2RP2000796	5.32	5.32	7.41	7.38	9.17	6.66		
	NT2RP2000809	3.25	3.25	8.3	6.46	4.69	5.45		
	NT2RP2000812	6.65	6.65	17.51	16.43	14.35	16.89		
	NT2RP2000814	4.16	4.16	4.97	3.75	4.6	3.29		
	NT2RP2000816	1.84	1.84	5.64	4.64	5.19	3.58		
10	NT2RP2000818	3.28	3.28	5.19	3.18	3.66	1.95		
	NT2RP2000819	2.76	2.76	5.79	3.03	3.05	1.94		
	NT2RP2000841	4.35	4.35	4.51	2.17	2.48	1.65	**	-
	NT2RP2000842	7.8	7.8	9.57	13.62	14.25	12.66	**	+
	NT2RP2000845	2.52	2.52	8.31	7.51	6.76	6.93		
15	NT2RP2000863	2.45	2.45	3.48	3.82	3.37	2.47		
	NT2RP2000880	5.96	5.96	11.61	9.5	11.13	10.25		
	NT2RP2000892	4.3	4.3	6.43	6.54	6.97	5.01		
	NT2RP2000894	5.59	5.59	11.88	5.41	5.59	2.16		
	NT2RP2000903	5.71	5.71	9.12	10.73	11.92	7.44		
20	NT2RP2000906	4.56	4.56	5.39	2.63	3.78	2.19	*	-
	NT2RP2000910	4.34	4.34	4.26	2.9	2.7	1.68	**	-
	NT2RP2000931	10.97	10.97	18.36	20.51	19.28	24.6		
	NT2RP2000932	2.86	2.86	5.43	4.8	4.72	4.21		
	NT2RP2000938	18.41	18.41	42.99	35.71	30.01	43.52		
	NT2RP2000943	7.02	7.02	14.98	18.7	14.88	14.48		
25	NT2RP2000957	3.19	3.19	4.11	4.26	3.66	2.71		
	NT2RP2000958	7	7	6.84	10.43	12.36	7.8		
	NT2RP2000959	9.88	9.88	14.99	13.92	17.38	10.69		
	NT2RP2000965	5.05	5.05	7.82	15.73	18.97	16.02	**	+
30	NT2RP2000970	2.31	2.31	6.72	5.14	5	4.62		
	NT2RP2000973	0.9	0.9	1.47	2.56	2.64	1.57	*	+
	NT2RP2000985	2.69	2.69	6	9.28	6.29	13.98		
	NT2RP2000987	1.89	1.89	3.31	4.54	3.17	1.66		
	NT2RP2000997	13.83	13.83	23.99	38.12	29.73	40.96	*	+
35	NT2RP2001024	2.86	2.86	5.34	3.61	3.12	2.36		
	NT2RP2001028	4.66	4.66	4.2	2.65	4.09	0.99		
	NT2RP2001036	5.14	5.14	8.86	6.16	6.44	4.91		
	NT2RP2001039	1.08	1.08	3.18	3.47	1.14	2.24		
	NT2RP2001044	1.13	1.13	2.5	2.53	1.89	2.8		
40	NT2RP2001056	4.97	4.97	28.32	20.16	26.9	18.16		
	NT2RP2001065	2.38	2.38	6.24	7.45	7.4	5.69		
	NT2RP2001067	2.98	2.98	5.38	4.12	5.29	2.41		
	NT2RP2001070	3.3	3.3	7.63	4.72	6.17	3.58		
	NT2RP2001081	2.91	2.91	8.19	4.8	6.68	3.9		
45	NT2RP2001087	3.93	3.93	2.36	2.06	2.92	1.61		
	NT2RP2001094	0.69	0.69	1.37	1.25	1.15	1.04		
	NT2RP2001119	2.02	2.02	6.11	5.86	4.44	4.35		
	NT2RP2001127	1.53	1.53	4.04	2.69	1.85	2.1		
	NT2RP2001133	2.45	2.45	4.73	4.06	3.61	3.6		
50	NT2RP2001137	2.68	2.68	4.07	2.3	2.82	2.9		
	NT2RP2001142	3.88	3.88	7.47	3.37	2.83	2.42		
	NT2RP2001149	2.7	2.7	2.98	2.11	3.39	1.32		
	NT2RP2001168	6	6	7.81	6.8	7.01	5.75		
	NT2RP2001173	4.15	4.15	7.88	3.98	3.09	5.44		
55	NT2RP2001174	9.23	9.23	14.98	14.12	15.45	18.01		

EP 1 130 094 A2

	NT2RP2001184	2.78	2.78	5.46	4.21	7.18	4.64
5	NT2RP2001196	1.62	1.62	5.93	3.14	3.28	2.94
	NT2RP2001200	3.85	3.85	9.36	5.02	4.25	7.88
	NT2RP2001218	2.29	2.29	5.69	2.55	3.89	3.6
	NT2RP2001223	2.65	2.65	5.03	1.95	3.69	3.31
	NT2RP2001226	4.34	4.34	10.19	6.95	5.72	7.35
10	NT2RP2001227	4.45	4.45	6.12	3.2	3.62	6.01
	NT2RP2001232	6.44	6.44	13.95	7.13	9.79	13.66
	NT2RP2001233	4.02	4.02	10.57	7.04	7.77	8.01
	NT2RP2001245	4.21	4.21	8.03	9.47	11.82	11.16 *
	NT2RP2001246	6.3	6.3	9.84	9	11.28	11.57
	NT2RP2001268	6.19	6.19	18.1	17.61	16.26	18.55
15	NT2RP2001270	4.78	4.78	9.11	5.68	8.7	10.04
	NT2RP2001276	4.92	4.92	13.29	12.73	10.92	12.73
	NT2RP2001277	3.11	3.11	7.02	4.91	6.22	10.82
	NT2RP2001290	2.71	2.71	6.46	4.42	5.61	6.01
	NT2RP2001295	5.46	5.46	9.44	5.13	5.98	7.92
20	NT2RP2001297	118.17	118.17	120.73	139.11	97.16	145.76
	NT2RP2001301	9.12	9.12	18.56	15.89	19.62	14.24
	NT2RP2001312	2.7	2.7	5.68	5.6	4.59	6.04
	NT2RP2001327	4.73	4.73	5.69	6.39	8.53	11.86
	NT2RP2001328	8.44	8.44	20.87	16.32	23.25	23.16
25	NT2RP2001341	4.59	4.59	9.22	3.06	7.65	7.21
	NT2RP2001347	3.09	3.09	8.54	5.54	9.55	6.9
	NT2RP2001366	10.33	10.33	48.06	54.83	51.5	52.33
	NT2RP2001378	2.33	2.33	3.77	3.74	4.64	5.02
	NT2RP2001381	2.82	2.82	6.86	5.79	6.62	8.37
30	NT2RP2001388	3.25	3.25	6.71	4.54	5.11	5.2
	NT2RP2001391	443.52	443.52	734.13	742.83	990.71	747.95
	NT2RP2001392	2.98	2.98	6.43	4.58	3.16	4.18
	NT2RP2001394	3.3	3.3	8.55	8.35	6.09	10.15
	NT2RP2001397	5.04	5.04	6.79	7.33	5.68	12.2
35	NT2RP2001400	3.1	3.1	6.4	3.43	6.25	2.92
	NT2RP2001408	3.31	3.31	6.13	4.02	5.97	5.62
	NT2RP2001420	5.63	5.63	12.09	8.09	9.97	9.17
	NT2RP2001423	4.71	4.71	9.71	6.21	8.29	7.19
	NT2RP2001427	2.68	2.68	5.32	3.69	4.61	5.49
40	NT2RP2001428	2.71	2.71	7.13	5.49	3.78	3.03
	NT2RP2001436	4.27	4.27	8.85	5.84	2.85	4.84
	NT2RP2001440	2.89	2.89	7.34	10.24	10.15	11.98 *
	NT2RP2001445	2.43	2.43	6.75	5.86	5.55	5.89
45	NT2RP2001449	4.37	4.37	6.41	5	4.74	5.02
	NT2RP2001450	3.19	3.19	6.75	2.26	5.4	8.59
	NT2RP2001467	4.53	4.53	10.28	5.32	4.72	6.5
	NT2RP2001469	4.74	4.74	6.79	8.22	11.04	7.18
	NT2RP2001480	6.54	6.54	26.68	14.98	12.63	15.42
50	NT2RP2001495	5.86	5.86	11.96	3.16	9.04	10.39
	NT2RP2001499	8.25	8.25	16.78	10.05	14.46	9.66
	NT2RP2001506	2.79	2.79	7.24	5.32	8.19	5.33
	NT2RP2001508	10.59	10.59	13.66	18.74	20.49	21.92 **
	NT2RP2001511	6.41	6.41	9.74	6.08	8.63	6.53
55	NT2RP2001514	7.04	7.04	7.02	7.24	6.44	6.38

EP 1 130 094 A2

	NT2RP2001520	2.93	2.93	4.84	2.6	3.19	2.87		
5	NT2RP2001526	3.88	3.88	8.49	7.01	5.27	3.83		
	NT2RP2001529	9.87	9.87	53.78	44.74	55.72	60.88		
	NT2RP2001536	1.63	1.63	4.17	3.81	4.52	4.71		
	NT2RP2001538	83.44	83.44	178.68	132.75	146.73	155.87		
	NT2RP2001547	4.96	4.96	14.87	16.77	19.21	17.77	*	+
10	NT2RP2001560	6.28	6.28	21.64	25.41	28.19	27.75	*	+
	NT2RP2001562	5.56	5.56	5.57	5.94	6.75	4.64		
	NT2RP2001566	7.96	7.96	9.24	8.22	7.91	8.56		
	NT2RP2001569	4.26	4.26	8.71	6.09	5.65	8.28		
	NT2RP2001576	3.95	3.95	11.58	13.42	9	12.82		
	NT2RP2001581	47.15	47.15	130.15	121.19	112.28	129.54		
15	NT2RP2001597	3.73	3.73	7.88	8.57	8.3	13.3		
	NT2RP2001601	2.37	2.37	4.81	3.67	4.81	3.34		
	NT2RP2001613	2.74	2.74	4.87	2.83	2.72	4.15		
	NT2RP2001628	3.42	3.42	3.97	3.14	3.04	7.84		
	NT2RP2001634	8.64	8.64	13.94	16.57	23.67	17.67	*	+
20	NT2RP2001635	2.51	2.51	5.92	5.63	5.53	4.72		
	NT2RP2001660	4.27	4.27	16.91	5.9	5.54	10.06		
	NT2RP2001662	1.49	1.49	4.07	4.5	4.44	3.47		
	NT2RP2001663	2.82	2.82	5.09	10.37	8.21	9.74	**	+
	NT2RP2001672	3.28	3.28	3.82	3.88	4.09	4	*	+
25	NT2RP2001675	4.1	4.1	5.01	5.23	4.73	5.06		
	NT2RP2001677	9.58	9.58	18.2	20.9	26.67	19.74	*	+
	NT2RP2001678	4.84	4.84	6.73	4.6	4.83	4.5		
	NT2RP2001683	1.89	1.89	3.12	4.6	4.72	2.78		
	NT2RP2001699	3.15	3.15	6.16	5.5	5.84	4.88		
30	NT2RP2001707	1.24	1.24	3.19	3.42	4.13	4.8	*	+
	NT2RP2001720	1.47	1.47	3.6	3.91	3	2.72		
	NT2RP2001721	2.26	2.26	4.57	5.53	3.96	3.66		
	NT2RP2001740	12	12	60.21	52.38	79.71	54.73		
	NT2RP2001748	6.43	6.43	10.8	8.75	10.25	8.55		
35	NT2RP2001755	5.51	5.51	4.96	3.71	4.62	2.69	*	-
	NT2RP2001762	1.25	1.25	2.01	3.87	2.56	3.52	*	+
	NT2RP2001768	1.91	1.91	4.7	6.7	5.55	4.55		
	NT2RP2001769	3.06	3.06	5.86	10.42	5.06	11.86		
40	NT2RP2001784	3.62	3.62	6.23	7.06	6.02	6.91		
	NT2RP2001805	2.33	2.33	5.61	6.02	4.93	6.6		
	NT2RP2001813	2.75	2.75	3.73	1.84	1.98	1.94	*	-
	NT2RP2001817	3.16	3.16	4.49	4.03	5.32	3.45		
	NT2RP2001818	2.72	2.72	2.45	2.35	3.62	2.66		
45	NT2RP2001837	5.13	5.13	13.43	10.29	10.16	12.33		
	NT2RP2001839	17.02	17.02	83.84	60.14	71.06	82.26		
	NT2RP2001861	2	2	6.37	3.16	3.52	3.87		
	NT2RP2001869	2.64	2.64	6.54	4.35	5.77	8.84		
	NT2RP2001876	12.15	12.15	27.71	24.54	24.93	23.67		
50	NT2RP2001878	2.32	2.32	3.96	2.95	3.32	4.95		
	NT2RP2001881	3.72	3.72	5.4	9.67	12.64	12.16	**	+
	NT2RP2001883	2.63	2.63	6.8	4.33	5.42	6.35		
	NT2RP2001884	13.59	13.59	23.56	15.33	10.54	23.6		
	NT2RP2001885	3.27	3.27	5.49	2.88	4.39	4.82		
55	NT2RP2001898	10.76	10.76	80.37	69.48	88.43	73.46		

EP 1 130 094 A2

	NT2RP2001900	3.38	3.38	4.03	2.61	4.93	10.26		
5	NT2RP2001903	3.73	3.73	7.71	5.57	5.7	8.2		
	NT2RP2001907	3.1	3.1	8.56	5.05	7.56	6.72		
	NT2RP2001915	2.89	2.89	5.06	4.06	3.08	7.19		
	NT2RP2001921	4.04	4.04	10.3	13.02	12.45	19.33	*	+
	NT2RP2001926	2.75	2.75	8.25	3.55	5.3	5.64		
	NT2RP2001933	5.65	5.65	52.55	43.62	43.55	48.58		
10	NT2RP2001936	1.54	1.54	5.03	2.8	2.96	3.8		
	NT2RP2001943	25.33	25.33	49.4	47.71	40.48	51.65		
	NT2RP2001946	3.05	3.05	4.3	3.41	4.51	6.1		
	NT2RP2001947	3.18	3.18	3.44	3.93	3.21	6.88		
	NT2RP2001948	3.59	3.59	10.79	5.71	7.29	19.72		
15	NT2RP2001956	5.24	5.24	12.73	11.54	9.42	9.89		
	NT2RP2001969	4.05	4.05	7.82	3.24	5.7	6		
	NT2RP2001976	2.9	2.9	6.39	5.68	6.95	6.41		
	NT2RP2001978	3.26	3.26	6.08	4.18	4.83	6.03		
	NT2RP2001985	2.14	2.14	3.8	2.56	4.63	2.51		
20	NT2RP2001991	3.34	3.34	5.7	1.53	4.62	5.19		
	NT2RP2001997	3.16	3.16	8.43	5.31	7.47	6.98		
	NT2RP2002015	136.21	136.21	265.98	266.8	340.89	272.43		
	NT2RP2002017	3.24	3.24	6.06	2.06	3.3	2.57		
	NT2RP2002025	6.08	6.08	51.73	31.83	26.94	37.84		
25	NT2RP2002030	6.06	6.06	11.95	9.77	8.07	8.76		
	NT2RP2002032	2.31	2.31	4.95	2.39	3.81	2.55		
	NT2RP2002033	3	3	6.71	3.53	7.57	8.05		
	NT2RP2002041	3.5	3.5	6.37	2.76	3.15	9		
	NT2RP2002046	3	3	6.88	2.99	7.4	6.01		
30	NT2RP2002047	2.71	2.71	3.86	2.06	3.87	3.83		
	NT2RP2002050	7.67	7.67	11.66	9.78	6.47	7.77		
	NT2RP2002052	3.77	3.77	8.39	6.6	3.99	6.28		
	NT2RP2002058	2.07	2.07	4.11	3.1	4.82	3.39		
	NT2RP2002060	1.48	1.48	3.44	2.1	5.9	3.18		
35	NT2RP2002063	3.61	3.61	5.83	3.3	5.2	6.65		
	NT2RP2002066	10.11	10.11	13.47	5.47	9.88	9.73		
	NT2RP2002070	3.74	3.74	6.3	2.15	3.1	3.83		
	NT2RP2002076	3.72	3.72	5.1	3.35	5.58	3.63		
	NT2RP2002078	13.09	13.09	105.74	73.87	88.51	76.08		
40	NT2RP2002079	5.76	5.76	36.34	31.87	32.66	36.54		
	NT2RP2002099	4.19	4.19	5.82	4.7	6.75	6.03		
	NT2RP2002105	2.66	2.66	12.25	11.41	14.04	11.23		
	NT2RP2002115	1.63	1.63	5.21	1.98	3.42	1.52		
45	NT2RP2002124	3.66	3.66	6	4.56	5.38	3.88		
	NT2RP2002137	3.99	3.99	4.83	2.21	2.1	1.76	**	-
	NT2RP2002139	24.08	24.08	45.74	51.88	77.99	62.3	*	+
	NT2RP2002154	1.37	1.37	4.13	3.56	2.36	3.2		
	NT2RP2002155	351.63	351.63	869.83	623.53	501.61	620.68		
50	NT2RP2002172	1.5	1.5	3.33	2.78	3.53	5.13		
	NT2RP2002185	3.29	3.29	7.65	7.3	8.56	8.12		
	NT2RP2002188	1.74	1.74	5.95	4.15	4.31	4.95		
	NT2RP2002192	2.9	2.9	7.6	6.65	6.42	5.83		
	NT2RP2002193	5.21	5.21	5.22	4.76	4.95	5.75		
55	NT2RP2002208	5.96	5.96	7.31	4.7	5.67	5.14		

EP 1 130 094 A2

	NT2RP2002219	2.2	2.2	1.8	2.22	3.2	2.26		
5	NT2RP2002231	1.72	1.72	3.1	4.11	2.76	5.76		
	NT2RP2002232	2.59	2.59	5.17	3.93	4.7	6.08		
	NT2RP2002235	5.62	5.62	15.07	16.26	16.18	15.18		
	NT2RP2002239	37.02	37.02	67.99	72.09	67.21	63.77		
	NT2RP2002252	2.64	2.64	3.66	2.63	2.76	2.94		
	NT2RP2002256	4.62	4.62	15.3	11.37	16.99	12.91		
10	NT2RP2002257	7.01	7.01	22.77	18.65	25.09	20.6		
	NT2RP2002259	1.58	1.58	13.91	9.9	12.15	10.49		
	NT2RP2002264	0.6	0.6	3.14	3.2	3.12	3.92		
	NT2RP2002267	3.66	3.66	8.75	8.95	8.3	11.16		
15	NT2RP2002270	4.26	4.26	8.23	16.09	10.47	14.71	*	+
	NT2RP2002281	2.85	2.85	5.66	8.18	6.48	6.54	*	+
	NT2RP2002288	4.32	4.32	6.6	5.33	5.56	4.23		
	NT2RP2002292	5.42	5.42	8.4	6.64	8.08	6.95		
	NT2RP2002299	9.6	9.6	9.22	11.75	19.42	15.97	*	+
	NT2RP2002304	1.37	1.37	4.78	6.99	5.08	5.52		
20	NT2RP2002312	1.21	1.21	2.33	3.78	5.3	3.28	*	+
	NT2RP2002316	3.28	3.28	5.43	7.57	7.21	8.2	**	+
	NT2RP2002325	1.95	1.95	3.46	2.79	2.22	4.95		
	NT2RP2002333	2.13	2.13	3.03	3.53	4.86	5.69	*	+
	NT2RP2002371	5.43	5.43	9.14	9.72	12.07	11.65	*	+
25	NT2RP2002373	10.65	10.65	40.1	36.72	58.84	33.58		
	NT2RP2002381	4.68	4.68	2.35	2.66	3.19	3.71		
	NT2RP2002385	5.71	5.71	11.84	9.95	11.34	9.47		
	NT2RP2002394	0.94	0.94	1.52	1.24	0.96	1.26		
	NT2RP2002408	2.7	2.7	5.08	3.89	3.12	4.29		
30	NT2RP2002409	3.73	3.73	10.81	10.78	7.95	8.35		
	NT2RP2002424	2.98	2.98	4.22	5.84	6.22	7.85	*	+
	NT2RP2002426	6.44	6.44	11.38	7.59	8.46	8.93		
	NT2RP2002429	17.2	17.2	24.73	27.87	33.96	20.83		
	NT2RP2002437	4.61	4.61	5.98	4.83	6.47	4.79		
35	NT2RP2002439	3.83	3.83	6.69	2.68	3.22	4		
	NT2RP2002442	13.63	13.63	71.65	57.78	63.05	78.84		
	NT2RP2002457	3.27	3.27	5.31	4.35	4.87	5.82		
	NT2RP2002464	2.17	2.17	5.34	3.29	4.59	4.24		
	NT2RP2002475	3.11	3.11	7.88	5.3	2.83	5.43		
40	NT2RP2002479	3.09	3.09	4.25	1.95	2.99	1.93		
	NT2RP2002487	1.73	1.73	5.15	1.98	2.1	3.04		
	NT2RP2002498	1.52	1.52	2.2	2.62	2.82	4.47		
	NT2RP2002503	7.63	7.63	31.85	29.32	32.02	31.84		
45	NT2RP2002504	3.81	3.81	5.73	6	7.23	11.28		
	NT2RP2002510	2.65	2.65	8.92	4.68	6.59	6.85		
	NT2RP2002520	3.57	3.57	7.17	6.26	8.86	6.61		
	NT2RP2002527	5.18	5.18	6.02	9	12.37	11.22	**	+
	NT2RP2002533	3.34	3.34	6.27	4.83	6.94	5.88		
50	NT2RP2002537	3.22	3.22	4.02	4.09	5.91	10.08		
	NT2RP2002542	4.81	4.81	4.64	5.99	5.93	9.73		
	NT2RP2002546	4.31	4.31	5.85	6.5	4.91	5.24		
	NT2RP2002549	4.06	4.06	9.33	7.68	10.49	11.65		
	NT2RP2002564	4.11	4.11	11.18	10.67	9.21	9.29		
55	NT2RP2002591	2.45	2.45	7.03	3.31	4.79	5.79		

EP 1 130 094 A2

	NT2RP2002595	9.67	9.67	12.41	12.06	13.39	14.79			
5	NT2RP2002602	4.19	4.19	7.53	5.68	8.96	10.42			
	NT2RP2002606	1.27	1.27	2.93	2.26	2.97	3.95			
	NT2RP2002609	6.12	6.12	9.95	4.79	5.48	7.74			
	NT2RP2002618	2.74	2.74	6.83	4.2	6.34	5.44			
10	NT2RP2002621	4.24	4.24	10.22	6.58	7.52	9.79			
	NT2RP2002643	1.79	1.79	4.84	3.11	5.98	3.94			
	NT2RP2002672	4.48	4.48	9.23	8.03	9.37	9.87			
	NT2RP2002673	4.13	4.13	5.01	8	12.88	17.73	*	+	
	NT2RP2002674	2.4	2.4	4.06	2.78	2.37	1.84			
	NT2RP2002686	2.73	2.73	4.61	3.17	5.19	6.49			
15	NT2RP2002688	10.73	10.73	28.07	22.34	33.34	28.71			
	NT2RP2002695	2.62	2.62	7.03	5.26	4.34	5.52			
	NT2RP2002701	7.29	7.29	13.37	11.85	5.18	10.04			
	NT2RP2002706	3.02	3.02	5.58	6.47	8.14	6.19	*	+	
20	NT2RP2002710	11.2	11.2	36.97	39.43	33.9	42.75			
	NT2RP2002721	5.53	5.53	9.42	7.33	7.34	8.45			
	NT2RP2002727	3.56	3.56	6.87	2.17	3.96	3.52			
25	NT2RP2002734	3.59	3.59	6.65	5.71	7.65	7.54			
	NT2RP2002736	5.25	5.25	13.13	13.17	13.59	17.58			
	NT2RP2002740	2	2	5.11	3.18	2.81	3.13			
	NT2RP2002741	2.12	2.12	4.8	4.68	5.39	5.78			
30	NT2RP2002750	2.5	2.5	9.22	7.73	9.57	8.18			
	NT2RP2002752	4.59	4.59	10.39	7.93	7.66	8.03			
	NT2RP2002753	4.49	4.49	9.91	8.66	9.04	14.67			
	NT2RP2002760	4.79	4.79	10.31	3.56	4.5	4.13			
35	NT2RP2002769	4.42	4.42	6.06	3.89	5.67	6.43			
	NT2RP2002778	4.13	4.13	10.59	6.8	8.2	9.12			
	NT2RP2002791	8.89	8.89	54.27	48.75	53.08	50.19			
	NT2RP2002800	1.66	1.66	4.52	4	5.19	5.38			
	NT2RP2002805	3.38	3.38	5.46	4.75	6.44	3.81			
	NT2RP2002811	3.27	3.27	8.23	5.87	8.13	10.61			
40	NT2RP2002824	18.29	18.29	25.05	29.95	34.29	25.05			
	NT2RP2002839	13.26	13.26	31.21	16.09	23.42	16.27			
	NT2RP2002845	5.87	5.87	7.93	4.61	6.12	5.5			
	NT2RP2002857	2.95	2.95	3.6	2.35	4.23	2.99			
45	NT2RP2002862	4.56	4.56	12.49	12.55	9.84	11.34			
	NT2RP2002880	5.27	5.27	13.89	13.5	11.56	11.1			
	NT2RP2002885	8.6	8.6	17.12	7.56	10.07	10.02			
	NT2RP2002891	1.9	1.9	7.78	4.65	6.63	7.56			
	NT2RP2002907	2.95	2.95	6.91	5.95	5.5	4.9			
50	NT2RP2002925	5.67	5.67	6.73	10.04	11.6	8.45	*	+	
	NT2RP2002927	10.08	10.08	10.63	19.05	21.85	15.48	**	+	
	NT2RP2002928	4.32	4.32	4.56	2.65	2.34	2.51	**	-	
	NT2RP2002929	3.96	3.96	9.74	8.09	7.86	9.87			
	NT2RP2002934	1.5	1.5	1.4	2.81	3.01	2.49	**	+	
55	NT2RP2002939	2.96	2.96	5.09	5.15	6.71	4.91			
	NT2RP2002942	2.4	2.4	5.06	4.35	5.07	10.81			
	NT2RP2002954	5.41	5.41	11.46	7.21	9.1	8.65			
	NT2RP2002959	8.15	8.15	12.55	13.81	16.28	16.69	*	+	
	NT2RP2002974	5.03	5.03	6.53	4.7	3.45	4.54			
	NT2RP2002976	6.92	6.92	17.08	11.84	14.66	12.42			

EP 1 130 094 A2

	NT2RP2002979	4.41	4.41	8.12	7.03	8.66	7.6		
5	NT2RP2002980	6.44	6.44	15.09	15.56	11	17.45		
	NT2RP2002986	3.87	3.87	7.6	6.68	7.4	7.39		
	NT2RP2002987	3.52	3.52	8.23	11.1	9.18	9.4	*	+
	NT2RP2002988	14.96	14.96	22.92	30.07	31.87	31.36	**	+
	NT2RP2002993	2.97	2.97	4.18	3.8	3.84	2.84		
10	NT2RP2003000	4.88	4.88	8.34	6.97	9.62	9.97		
	NT2RP2003008	4.85	4.85	5.06	3.34	4.76	4.78		
	NT2RP2003020	4.45	4.45	44.26	28.35	46.52	34.33		
	NT2RP2003032	1.91	1.91	4.02	5.82	6.48	6.59	**	+
	NT2RP2003034	4.21	4.21	13.47	13.16	11.15	16.31		
	NT2RP2003042	2.15	2.15	3.81	4.57	3.65	4.92		
15	NT2RP2003050	2.32	2.32	3.56	2.55	2.17	1.83		
	NT2RP2003060	7.27	7.27	15.51	21.53	18.91	17.46	*	+
	NT2RP2003073	5.61	5.61	8.73	7.06	10.51	8.17		
	NT2RP2003099	5.05	5.05	3.67	3.21	3.73	2.84		
20	NT2RP2003108	3.6	3.6	4.23	5.29	3.91	6.62		
	NT2RP2003115	1.68	1.68	5	7.75	4.69	4.84		
	NT2RP2003117	2.71	2.71	5.69	3.6	4.66	4.13		
	NT2RP2003121	1.83	1.83	3.47	4.03	2.69	3.33		
	NT2RP2003125	4.13	4.13	11.44	15.42	12.55	13.66	*	+
	NT2RP2003127	2.36	2.36	3.94	1.53	1.66	1.75		
25	NT2RP2003129	3.43	3.43	7.09	6.08	6.05	5.42		
	NT2RP2003137	4.49	4.49	6.14	7.58	8.4	6.46	*	+
	NT2RP2003138	4.66	4.66	20.24	16.55	17.45	16.92		
	NT2RP2003146	6.2	6.2	24.78	18.5	23.25	25.96		
30	NT2RP2003148	3.09	3.09	6.73	3.06	4.6	4.04		
	NT2RP2003150	1.45	1.45	5.71	3.98	5.2	4.3		
	NT2RP2003157	6.93	6.93	34.27	34.29	31.85	32.84		
	NT2RP2003158	6.3	6.3	25.32	26.87	28.69	59.31		
	NT2RP2003161	2.73	2.73	3.36	2.51	2.82	6.12		
35	NT2RP2003164	1.96	1.96	2.1	1.28	1.87	2.46		
	NT2RP2003165	2.18	2.18	5.94	3.1	3.69	4.84		
	NT2RP2003177	1.63	1.63	4.37	2.79	3.03	4.42		
	NT2RP2003179	1.23	1.23	4.98	4.08	3.63	7.96		
	NT2RP2003194	4.04	4.04	7.2	5.73	6.29	14.77		
40	NT2RP2003206	1.59	1.59	4.47	1.64	3.52	1.44		
	NT2RP2003210	5.06	5.06	15.15	16.14	12.93	15.9		
	NT2RP2003227	1.62	1.62	3.97	2.04	3.66	6.28		
	NT2RP2003228	6.57	6.57	29.53	29.56	43.94	44.24		
	NT2RP2003230	3.51	3.51	7.91	4.49	8.04	8.46		
45	NT2RP2003231	2.22	2.22	5.59	2.46	3.23	3.83		
	NT2RP2003237	2.52	2.52	4.59	4.59	6.4	6.46	*	+
	NT2RP2003239	2.3	2.3	4.46	2.97	4.46	4.05		
	NT2RP2003243	2.16	2.16	4.13	2.38	3.28	3.98		
	NT2RP2003265	3.93	3.93	5.33	4.22	4.88	4.92		
50	NT2RP2003267	2.73	2.73	3.15	3.24	4.17	7.42		
	NT2RP2003272	6.03	6.03	14.8	16.93	23.85	32.58	*	+
	NT2RP2003277	3.85	3.85	11.29	5.53	8.39	6.39		
	NT2RP2003280	3.47	3.47	9.38	7.67	7.25	6.09		
	NT2RP2003286	2.18	2.18	4.23	4.13	5	9.61		
55	NT2RP2003293	2.98	2.98	6.9	5.66	7.05	7.94		

EP 1 130 094 A2

	NT2RP2003295	4.67	4.67	8.45	8.73	12.39	6.35		
5	NT2RP2003297	3.43	3.43	7.57	4.32	6.89	5.28		
	NT2RP2003300	20.38	20.38	32.04	45.7	53.51	48.07	**	+
	NT2RP2003302	2.88	2.88	4.52	3.46	3.81	7.26		
	NT2RP2003307	0.57	0.57	2.62	1.43	1.49	1.38		
	NT2RP2003308	1.44	1.44	4.5	2.77	4.44	5.44		
10	NT2RP2003311	4.18	4.18	5.83	7.35	4.25	8.2		
	NT2RP2003329	2.99	2.99	4.41	2.63	3.89	4.44		
	NT2RP2003339	3.06	3.06	7.01	3.76	4.92	3.64		
	NT2RP2003345	4.15	4.15	8.38	2.77	3.97	6.33		
	NT2RP2003347	2.55	2.55	4.23	2.08	1.98	3.46		
15	NT2RP2003367	2.15	2.15	4.65	2.7	1.98	1.44		
	NT2RP2003369	1.34	1.34	4.71	2.16	2.36	0.89		
	NT2RP2003383	4.05	4.05	6.75	7.66	7.17	6.99		
	NT2RP2003390	9.1	9.1	17.93	16.66	14.27	12.94		
	NT2RP2003391	9.39	9.39	12.9	11.96	9.91	12.84		
	NT2RP2003393	4.23	4.23	6.99	6.14	5.03	9.44		
20	NT2RP2003394	8.67	8.67	16.21	17.56	21.75	17.23		
	NT2RP2003401	4.39	4.39	5.97	3.52	3.72	2.9		
	NT2RP2003403	3.42	3.42	7.64	6.62	8.55	7.79		
	NT2RP2003433	3.02	3.02	15.54	13.62	13.5	13.08		
	NT2RP2003445	3.2	3.2	4.74	4.08	3.5	3.93		
25	NT2RP2003446	2.67	2.67	6.23	5.06	6.05	4.47		
	NT2RP2003456	2.04	2.04	6.57	4.26	5.89	3.81		
	NT2RP2003466	3.56	3.56	20.09	17.34	25.96	23.53		
	NT2RP2003469	6.2	6.2	5.65	6.19	7.53	6.33		
	NT2RP2003470	5.64	5.64	6.47	5.06	6.11	6.44		
30	NT2RP2003471	2.72	2.72	3.88	3.22	2.78	3.38		
	NT2RP2003480	7.15	7.15	20.74	19.77	19.89	21.14		
	NT2RP2003495	3.99	3.99	6.03	8.07	7.24	10.72	*	+
	NT2RP2003499	1.52	1.52	4.58	3.67	4.05	2.75		
	NT2RP2003505	0.98	0.98	3.21	2.62	3.88	1.4		
35	NT2RP2003506	2.54	2.54	6.53	5.65	5.36	4.78		
	NT2RP2003511	3.67	3.67	5.57	4.22	3.1	2.96		
	NT2RP2003513	3.79	3.79	6.01	5.49	5.57	5.71		
	NT2RP2003517	2.9	2.9	2.52	1.32	1.11	0.85	**	-
	NT2RP2003522	11.08	11.08	19.77	10.55	11.42	16.52		
40	NT2RP2003525	5.12	5.12	14.93	12.19	10.72	11.79		
	NT2RP2003533	3.36	3.36	10.44	12.12	10.72	12.94		
	NT2RP2003541	6.72	6.72	11.29	12.02	13.42	11.7		
	NT2RP2003543	2.48	2.48	5.96	4.17	3.55	6.54		
	NT2RP2003545	2.59	2.59	4.85	2.22	3.6	1.85		
45	NT2RP2003559	4.92	4.92	4.81	3.97	3.84	3.37	**	-
	NT2RP2003564	4.46	4.46	3.93	2.53	1.97	2.42	**	-
	NT2RP2003565	4.94	4.94	50.48	41.12	48.32	37.82		
	NT2RP2003567	3.51	3.51	16.65	16.25	19.43	16.05		
	NT2RP2003575	4.44	4.44	18.78	19.56	22.63	20.7		
50	NT2RP2003576	102.12	102.12	203.44	206.62	128.42	171.89		
	NT2RP2003579	11.45	11.45	26.58	38.62	39.51	39.88	*	+
	NT2RP2003581	3.85	3.85	6.1	4.33	4.38	3.96		
	NT2RP2003587	8.37	8.37	11.47	13.35	14.11	12.14	*	+
55	NT2RP2003590	7.15	7.15	9.08	11.06	13.15	14.91	*	+

EP 1 130 094 A2

	NT2RP2003593	1.58	1.58	4.57	7.84	4.43	8.59		
5	NT2RP2003596	4.86	4.86	10.86	14.43	13.12	17.96	*	+
	NT2RP2003599	6.49	6.49	12.46	14.29	10.17	11.98		
	NT2RP2003600	1.88	1.88	2.95	3.02	3.64	6.36		
	NT2RP2003604	7.09	7.09	8.97	16.39	13.03	16.68	**	+
	NT2RP2003629	3.72	3.72	5.25	3.11	4.56	2.38		
10	NT2RP2003630	4.09	4.09	6.66	4.79	6.78	3.84		
	NT2RP2003643	5.49	5.49	4.88	7.15	9.8	8.51	*	+
	NT2RP2003655	4.27	4.27	11.12	7.52	6.38	7.59		
	NT2RP2003664	12.29	12.29	24.31	17.9	18.07	17.11		
	NT2RP2003668	2.52	2.52	5.01	3.3	3.18	3.62		
15	NT2RP2003687	1.61	1.61	2.77	1.63	2.42	1.71		
	NT2RP2003691	3.03	3.03	5.07	3.7	4.21	4.57		
	NT2RP2003702	3.99	3.99	6.14	2.89	3.02	2.89		
	NT2RP2003704	3.31	3.31	4.12	2.65	3.84	1.99		
	NT2RP2003706	2.44	2.44	1.24	1.72	1.42	1.6		
20	NT2RP2003713	4.11	4.11	5.49	4.16	3.89	3.87		
	NT2RP2003714	3.39	3.39	7.8	5.19	5.31	5.32		
	NT2RP2003727	3.96	3.96	11.63	4.81	6.08	10.46		
	NT2RP2003737	2.52	2.52	8.58	4.88	6.47	4.6		
	NT2RP2003751	1.66	1.66	4.84	1.24	1.67	1.37		
25	NT2RP2003760	2.52	2.52	5.47	3.87	4.19	5.45		
	NT2RP2003764	2.1	2.1	2.81	1.44	1.87	4.62		
	NT2RP2003769	5.52	5.52	11.45	7.41	8.17	10.64		
	NT2RP2003770	7.43	7.43	12.42	7.17	5.67	12.82		
	NT2RP2003777	3.44	3.44	6.78	5.01	5.6	9.57		
30	NT2RP2003781	4.93	4.93	15.85	13.04	11.91	13.48		
	NT2RP2003785	9.69	9.69	13.44	11.1	10.68	8.99		
	NT2RP2003793	9.32	9.32	9.5	8.29	13.22	10.51		
	NT2RP2003806	5.6	5.6	12.03	8.54	8.75	12.97		
	NT2RP2003825	10.73	10.73	62.01	57.88	71.84	82.78		
35	NT2RP2003840	3.19	3.19	6.07	3.86	4.44	4.71		
	NT2RP2003857	4.02	4.02	4.94	3.15	4.61	6.12		
	NT2RP2003859	1.82	1.82	6	3.35	4.16	4.21		
	NT2RP2003871	5.22	5.22	9.43	5.1	4.59	7.79		
	NT2RP2003876	3.82	3.82	8.8	5.92	5.87	7.92		
40	NT2RP2003878	3.38	3.38	6.49	3.8	4.9	4.11		
	NT2RP2003885	2.46	2.46	3.09	1.66	3.29	2.37		
	NT2RP2003898	5.39	5.39	8.91	12.3	12.73	18.25	*	+
	NT2RP2003902	5.09	5.09	10.78	8.24	8.23	10.42		
	NT2RP2003912	3.83	3.83	14.48	5.91	7.43	6.74		
45	NT2RP2003931	1.81	1.81	6.03	3.95	6.86	4.42		
	NT2RP2003940	2.31	2.31	9.51	7.1	6.2	7.3		
	NT2RP2003950	2.81	2.81	5.48	3.84	5.57	2.98		
	NT2RP2003952	1.86	1.86	5.63	2.58	4.23	2.98		
	NT2RP2003968	4.82	4.82	7.38	9.86	11.76	13.51	*	+
50	NT2RP2003976	5.35	5.35	9.56	12.56	12.6	13.2	*	+
	NT2RP2003981	3.27	3.27	7.41	4.62	2.03	4.07		
	NT2RP2003984	5.57	5.57	15.87	10.21	4.25	10.34		
	NT2RP2003986	2.79	2.79	6.22	6.29	6.32	5.17		
	NT2RP2003988	2.36	2.36	6.84	4.51	7.42	5		
55	NT2RP2004013	8.46	8.46	13.75	14.68	13.19	17		

EP 1 130 094 A2

	NT2RP2004014	4.24	4.24	10.07	4.06	5.12	4.08
5	NT2RP2004036	6.88	6.88	14.85	14.08	19.02	16.03
	NT2RP2004041	2.77	2.77	5.02	3.96	4.43	5.19
	NT2RP2004042	1.99	1.99	4.6	4.41	2.02	4.09
	NT2RP2004049	4.68	4.68	19.13	14.24	15.5	16.3
10	NT2RP2004060	5.7	5.7	10.41	7.09	8.67	10.84
	NT2RP2004066	2.17	2.17	4.31	3.05	4.83	3.65
	NT2RP2004069	3.99	3.99	7.24	3.54	6	4.26
15	NT2RP2004076	3.73	3.73	5.82	1.92	4.2	3.61
	NT2RP2004080	4.21	4.21	9.26	4.45	6.47	6.15
	NT2RP2004081	3.27	3.27	5.39	3.51	3.71	4.5
	NT2RP2004098	2.32	2.32	6.48	5.4	3.1	5.75
20	NT2RP2004108	3.82	3.82	9.56	7.18	5.89	7.56
	NT2RP2004124	3.13	3.13	5.9	3.68	5.82	3.92
	NT2RP2004130	3.67	3.67	9.32	5.51	9.12	8.4
	NT2RP2004133	2.05	2.05	6.41	3.69	6.54	6.25
	NT2RP2004141	5.72	5.72	7.15	5.14	7.05	7.05
25	NT2RP2004142	5.33	5.33	8.1	4.18	5.45	3.93
	NT2RP2004152	3.34	3.34	4.78	5.7	7.49	4.39
	NT2RP2004165	3.71	3.71	8.3	5.87	5.92	6.54
	NT2RP2004170	1.86	1.86	5.97	5.37	4.17	4.94
	NT2RP2004172	2.93	2.93	5.24	4.69	5.58	4.26
30	NT2RP2004176	3.45	3.45	8.4	7.77	10.21	8.98
	NT2RP2004179	4.01	4.01	9.17	3.94	5.07	4.15
	NT2RP2004187	3.16	3.16	6.36	3.87	3.88	4.59
	NT2RP2004190	5.1	5.1	5.46	5.49	7.33	9.98
	NT2RP2004194	7.54	7.54	14.57	18.5	23.44	19.83 * +
35	NT2RP2004196	4.28	4.28	13.77	10.02	7.87	14.61
	NT2RP2004205	2.67	2.67	8.14	8.64	6.62	7.81
	NT2RP2004207	2.57	2.57	4.38	4.15	4.97	3.59
	NT2RP2004226	2.09	2.09	4.95	4.11	6.15	5.33
40	NT2RP2004232	2.79	2.79	6.52	6	6.59	5.33
	NT2RP2004239	3.57	3.57	4.49	2.71	3.97	5.6
	NT2RP2004240	7.07	7.07	12.57	13	15.8	8.95
	NT2RP2004242	3.87	3.87	6.52	5.77	6.94	7.27
	NT2RP2004245	1.74	1.74	3.47	2.42	3.29	3.15
45	NT2RP2004270	9.77	9.77	33.78	28.39	27.43	29.48
	NT2RP2004300	2	2	5.22	4.34	4.52	3.26
	NT2RP2004304	6.46	6.46	15.37	17.41	12.33	13.9
	NT2RP2004313	3.17	3.17	3.78	5.51	4.18	4.63 * +
50	NT2RP2004316	3.46	3.46	5.84	4.9	4.96	4.04
	NT2RP2004321	4.71	4.71	6.06	6.79	7.43	6.29 * +
	NT2RP2004336	4.19	4.19	4.97	2.73	4.28	4.53
	NT2RP2004339	5.3	5.3	20.89	17.11	18.07	15.39
	NT2RP2004347	1.39	1.39	3.99	4.78	5	4.19
	NT2RP2004364	2.26	2.26	6.52	5.08	6.72	4.76
	NT2RP2004365	3.18	3.18	6.58	6.68	6.34	7.7
	NT2RP2004366	2.49	2.49	6.06	4.49	4.71	3.08
55	NT2RP2004373	8.17	8.17	14.38	7.1	7.22	5.91
	NT2RP2004375	9.27	9.27	13.98	20.89	26.85	20.68 ** +
	NT2RP2004389	5.25	5.25	5.62	5.01	6.26	5.61
	NT2RP2004392	8.88	8.88	23.7	13.04	19.48	20.89

EP 1 130 094 A2

	NT2RP2004396	1.98	1.98	6.27	6.65	4.98	6.17			
5	NT2RP2004399	5.24	5.24	8.12	12.56	7.74	9.52			
	NT2RP2004400	2.07	2.07	3.55	2.36	3.47	2			
	NT2RP2004404	15.79	15.79	46	45.56	40.89	41.74			
	NT2RP2004410	16.64	16.64	24.04	27.99	33.46	32.69	*	+	
	NT2RP2004412	5.84	5.84	6.74	7.37	9.71	7.37			
10	NT2RP2004414	4.27	4.27	5.09	3.81	4.89	3.8			
	NT2RP2004425	3.71	3.71	6.53	3.73	3.18	4.04			
	NT2RP2004447	1.93	1.93	5.68	2.75	5.22	3.56			
	NT2RP2004463	13.57	13.57	16.23	16.84	16.25	20.26			
15	NT2RP2004476	9.11	9.11	12.69	11.89	12.66	15.87			
	NT2RP2004488	3.82	3.82	8.52	4.59	6.02	5.37			
	NT2RP2004490	2.88	2.88	3.86	2.31	2.96	4.1			
	NT2RP2004495	35.59	35.59	88.76	96.31	109.31	123.5	*	+	
	NT2RP2004512	4.25	4.25	7.62	5.84	6.41	7.12			
	NT2RP2004523	5.18	5.18	11.04	8.44	7.56	10.21			
20	NT2RP2004524	2.19	2.19	6.33	4.97	5.32	5.56			
	NT2RP2004536	8.99	8.99	16.96	14.1	14.51	17.51			
	NT2RP2004538	8.03	8.03	24.44	20.15	25.59	22.24			
	NT2RP2004548	4.45	4.45	9.92	7.39	9.1	10.51			
	NT2RP2004551	4.95	4.95	5.62	7.17	9.98	6.21			
25	NT2RP2004556	83.73	83.73	210.17	226.48	298.92	241.84			
	NT2RP2004568	5.19	5.19	11.18	6.52	9.16	9.99			
	NT2RP2004580	3.98	3.98	7.71	5.71	7.88	7.04			
	NT2RP2004585	11.28	11.28	49.82	36.69	46.91	64.56			
	NT2RP2004587	1.85	1.85	4.16	2.07	2.89	3			
30	NT2RP2004594	4.56	4.56	9.24	11.47	12.21	28.18			
	NT2RP2004600	3.49	3.49	5.76	2.22	3.22	3.09			
	NT2RP2004602	4.62	4.62	6.32	6	8.49	6.26			
	NT2RP2004606	392.21	392.21	581.19	612.4	897.5	764.63	*	+	
	NT2RP2004614	2.92	2.92	4.73	2.69	3.63	3.81			
35	NT2RP2004648	2.52	2.52	4.96	3.24	5.01	4.12			
	NT2RP2004655	5.69	5.69	10.1	8.37	6.76	9.46			
	NT2RP2004664	3.64	3.64	5.35	3.59	4.62	5.97			
	NT2RP2004670	1.98	1.98	3.81	1.98	3.71	4.27			
	NT2RP2004675	3.37	3.37	9.29	4.08	5.87	5.33			
40	NT2RP2004681	3.46	3.46	7.56	5.72	8.92	7.55			
	NT2RP2004689	2.63	2.63	5.75	5.75	4.73	7.87			
	NT2RP2004709	3.93	3.93	7.79	4.46	2.89	5.25			
	NT2RP2004710	3.15	3.15	8.37	5.63	4.61	6.88			
	NT2RP2004721	1.79	1.79	5.99	3.39	4.41	2.78			
45	NT2RP2004736	3.26	3.26	5.81	6.11	4.79	4.63			
	NT2RP2004743	4.94	4.94	7.96	5.94	6.67	7.36			
	NT2RP2004750	6.21	6.21	17.46	11.9	15.49	11.01			
	NT2RP2004755	11.65	11.65	19.9	14.84	22.87	19.91			
	NT2RP2004767	3.54	3.54	9	4.05	5.8	4.81			
50	NT2RP2004768	3.48	3.48	29.51	18.48	18.73	19.6			
	NT2RP2004775	4.68	4.68	5.68	7.71	5.62	8.26			
	NT2RP2004791	7.23	7.23	16.58	9.33	10.24	11.68			
	NT2RP2004794	14.01	14.01	25.74	23.04	16.86	22.78			
	NT2RP2004795	5.15	5.15	7.97	6.96	5.67	11.2			
55	NT2RP2004799	6.74	6.74	10.99	5.35	8.58	6.3			

EP 1 130 094 A2

	NT2RP2004802	6.35	6.35	11.79	6.1	7.62	6.24		
5	NT2RP2004810	3.44	3.44	8.83	7.37	7.84	6.03		
	NT2RP2004816	5.58	5.58	12.1	11.22	8.76	11.15		
	NT2RP2004837	4.13	4.13	9.89	10.43	7.23	12.98		
	NT2RP2004841	0.91	0.91	2.86	3.69	4.03	8.87		
	NT2RP2004847	3.25	3.25	13.75	13.82	13.87	17.16		
10	NT2RP2004861	2.3	2.3	5.23	2.33	4.23	2.46		
	NT2RP2004897	3.35	3.35	6.43	4.26	3.27	3.35		
	NT2RP2004932	6.64	6.64	10.16	7.96	8.53	6.91		
	NT2RP2004933	4.63	4.63	3.41	2.98	2.93	3.2 *	-	
	NT2RP2004936	3.69	3.69	6.41	4.56	4.42	7.53		
15	NT2RP2004951	2.98	2.98	10.48	5.09	5.22	19.28		
	NT2RP2004959	3.13	3.13	6.61	6.43	6.26	6.5		
	NT2RP2004961	2.1	2.1	4.79	4.89	6.49	5.44		
	NT2RP2004962	2.27	2.27	7.28	4.5	5.57	4.47		
	NT2RP2004966	2.26	2.26	6.07	4.1	4.1	2.97		
	NT2RP2004967	3.87	3.87	6.16	4.07	4.82	3.26		
20	NT2RP2004974	5.27	5.27	5.43	3.59	3.47	3.89 **	-	
	NT2RP2004978	2.68	2.68	5.26	4.17	6.39	5.09		
	NT2RP2004982	0.57	0.57	1.82	2.2	1.94	1.72		
	NT2RP2004985	16.03	16.03	45.34	44.65	46.12	54.4		
	NT2RP2004999	2.21	2.21	5.64	4.27	8.86	10.34		
25	NT2RP2005000	3.62	3.62	5.76	4.33	4.76	4.65		
	NT2RP2005001	5.41	5.41	7.91	8.26	9.15	8.32		
	NT2RP2005003	3.8	3.8	7.2	6.11	7.91	6.2		
	NT2RP2005012	6.61	6.61	20.14	18.41	20.96	17.87		
30	NT2RP2005018	1.9	1.9	4.24	3.29	2.24	2.91		
	NT2RP2005020	6.12	6.12	23.58	19.97	19.94	22.96		
	NT2RP2005022	1.65	1.65	5.01	5.09	7.24	4.77		
	NT2RP2005027	5.96	5.96	38.61	42.51	40.08	33.77		
	NT2RP2005031	1.54	1.54	4.99	3.94	4.53	3.92		
35	NT2RP2005035	44.19	44.19	94.82	116.52	107.36	106.69 *	+	
	NT2RP2005037	4.28	4.28	5.87	7.91	10.26	7.09 *	+	
	NT2RP2005038	4.86	4.86	4.84	1.85	2.29	3.1 **	-	
	NT2RP2005048	9.92	9.92	30.91	30.14	33.38	32.48		
	NT2RP2005069	16.01	16.01	34.88	21.99	20.63	27.64		
40	NT2RP2005073	7.36	7.36	30.35	29.36	28.24	30.33		
	NT2RP2005097	2.39	2.39	5.6	5.27	5.2	4.6		
	NT2RP2005108	1.76	1.76	3.95	2.84	4.21	7.12		
	NT2RP2005116	3.53	3.53	5.96	6.27	5.42	5.89		
	NT2RP2005126	5.88	5.88	8.31	8.9	14.96	8.51		
45	NT2RP2005135	5.08	5.08	5.22	4.65	6.59	5.47		
	NT2RP2005139	1.94	1.94	2.77	1.87	1.81	2.45		
	NT2RP2005140	3.82	3.82	4.86	12.39	6.72	8.55 *	+	
	NT2RP2005144	4.04	4.04	6.31	6.69	5.97	9.7		
	NT2RP2005147	2.23	2.23	5.49	5.61	6.15	6.25		
50	NT2RP2005148	2.86	2.86	5.63	3.83	6.65	4.83		
	NT2RP2005159	3.92	3.92	5.6	4.94	6.38	7.41		
	NT2RP2005162	3.23	3.23	5.56	4.57	5.4	4.21		
	NT2RP2005163	9.15	9.15	20.61	24.53	28.92	23.77 *	+	
	NT2RP2005168	2.87	2.87	6.14	5.24	4.79	4.88		
55	NT2RP2005181	2.64	2.64	5.42	3.4	2.11	1.98		

EP 1 130 094 A2

	NT2RP2005204	5.4	5.4	7.81	9.08	11.94	11.81	*	+
5	NT2RP2005219	4.61	4.61	9.64	7.09	10.28	8.7		
	NT2RP2005227	3.59	3.59	10.43	7.55	5.36	9.97		
	NT2RP2005237	26.49	26.49	94.81	86.96	105.8	93.92		
	NT2RP2005239	2.24	2.24	6.07	2.62	4.27	4.34		
10	NT2RP2005247	10.63	10.63	37.59	35.58	46.1	46.95		
	NT2RP2005254	4.35	4.35	9.14	5.7	6.44	6.93		
	NT2RP2005270	9.06	9.06	17.44	10.82	9.28	17.11		
	NT2RP2005276	7.19	7.19	11.53	10.88	11.68	15.71		
	NT2RP2005287	7.98	7.98	11.97	8.37	7.7	13.36		
	NT2RP2005288	2.51	2.51	5.14	2.89	5.59	5.22		
	NT2RP2005289	4.26	4.26	8.48	6.68	9.08	7.49		
15	NT2RP2005293	5	5	6.93	13.68	14.37	15.66	**	+
	NT2RP2005315	5.79	5.79	10.64	8.04	12.95	16.68		
	NT2RP2005322	5.05	5.05	15.42	18.91	11.33	22.43		
	NT2RP2005325	8.45	8.45	18.4	15.57	13.63	20.01		
	NT2RP2005336	1.71	1.71	6.68	4.18	5.74	5.3		
20	NT2RP2005343	2.44	2.44	7.48	3.91	4.11	5.89		
	NT2RP2005344	3.39	3.39	4.83	2.37	2.67	3.32		
	NT2RP2005347	3.14	3.14	3.61	3.34	2.96	3.53		
	NT2RP2005354	6.49	6.49	11.79	10.37	13	11.38		
	NT2RP2005358	35.87	35.87	109.04	101.37	134.72	117.96		
25	NT2RP2005360	2.93	2.93	5	3.59	4.97	3.84		
	NT2RP2005378	5.27	5.27	13.12	7.54	8.7	13.93		
	NT2RP2005391	3.06	3.06	5.41	4.21	6.76	7.72		
	NT2RP2005393	1.61	1.61	6.34	4.86	6.16	4.07		
	NT2RP2005407	2.59	2.59	5.71	4.28	5.65	4.64		
30	NT2RP2005419	2.65	2.65	9.05	6.37	8.5	6.77		
	NT2RP2005425	5.63	5.63	18.38	15.27	18.89	15.46		
	NT2RP2005429	3.23	3.23	5.85	5.41	6.65	5.64		
	NT2RP2005436	4.65	4.65	10.5	7.02	4.28	4.97		
	NT2RP2005441	2.28	2.28	5.62	3.36	3.77	5.79		
35	NT2RP2005442	24.92	24.92	40.66	34.62	25.56	41.66		
	NT2RP2005444	10.72	10.72	19.24	21.92	21.07	25.56	*	+
	NT2RP2005453	2.79	2.79	7.44	2.63	4.09	3.15		
	NT2RP2005457	15.12	15.12	23.21	28.69	37.38	31.61	*	+
	NT2RP2005458	2.47	2.47	5.27	3.55	4.16	4.95		
40	NT2RP2005463	7.73	7.73	15.23	15.65	22.11	25.05	*	+
	NT2RP2005464	5.96	5.96	11.91	9.22	4.67	10.35		
	NT2RP2005465	1.81	1.81	6.69	3.86	3.75	3.74		
	NT2RP2005472	10.98	10.98	32.59	28.21	27.9	25.85		
	NT2RP2005476	5.01	5.01	8.99	7.01	6.98	6.08		
45	NT2RP2005490	7.51	7.51	21.09	18.18	25.55	23.45		
	NT2RP2005491	4.99	4.99	12.47	8.63	10.12	8.78		
	NT2RP2005495	3.56	3.56	5.77	3.38	4.55	4.3		
	NT2RP2005496	4.84	4.84	18.25	11.3	13.16	11.28		
	NT2RP2005498	2.92	2.92	7.45	5.18	5.03	4.98		
50	NT2RP2005501	2.04	2.04	5.54	3.12	4.34	2.46		
	NT2RP2005506	124.3	124.3	217.82	139.27	121.83	104.81		
	NT2RP2005509	6.97	6.97	10.45	11.4	9.61	15.73		
	NT2RP2005514	3.93	3.93	6	4.06	7.05	4.39		
	NT2RP2005520	14.95	14.95	32.39	27.11	39.97	33.03		

EP 1 130 094 A2

	NT2RP2005525	6.19	6.19	7.01	7.81	7.68	4.79			
5	NT2RP2005531	2.18	2.18	3.33	1.67	2.12	1.9			
	NT2RP2005535	4.66	4.66	9.09	9.34	7.79	8.91			
	NT2RP2005539	3.39	3.39	6.22	6.43	5.84	7.45			
	NT2RP2005540	3.2	3.2	7.15	4.79	5.58	6.59			
10	NT2RP2005541	21.25	21.25	39.57	25.85	38.31	39.61			
	NT2RP2005549	2.69	2.69	7.66	6.72	4.85	7.11			
	NT2RP2005555	7.97	7.97	10.1	14.96	16.19	15.37	**	+	
	NT2RP2005557	4.89	4.89	8.47	4.03	6.52	6.26			
15	NT2RP2005581	3.93	3.93	9.61	6.32	7.95	6.89			
	NT2RP2005586	1.56	1.56	3.18	3.21	2.92	4.74			
	NT2RP2005597	2.77	2.77	2.93	2.98	4.1	3.84			
	NT2RP2005600	1.81	1.81	3.71	4.03	4.29	4.44	*	+	
20	NT2RP2005605	4.93	4.93	14.29	13.17	15.14	15.75			
	NT2RP2005614	3.06	3.06	5.62	3.68	4.11	2.45			
	NT2RP2005620	3.47	3.47	6.26	3.6	3.92	3.11			
	NT2RP2005622	6.14	6.14	5.07	6.21	7.43	4.61			
25	NT2RP2005632	5.72	5.72	10.95	11.57	10.42	14.89			
	NT2RP2005635	2.22	2.22	19.06	18.14	23.77	18.14			
	NT2RP2005637	1.53	1.53	8	3.73	3.71	4.14			
	NT2RP2005640	1.72	1.72	7.22	7.49	8.73	6.06			
30	NT2RP2005645	4.68	4.68	11.8	10.61	11.47	9.67			
	NT2RP2005651	3.45	3.45	7.88	7.64	6.78	10.15			
	NT2RP2005654	4.08	4.08	4.14	3.02	2.52	3.8			
	NT2RP2005666	4.91	4.91	5.27	4.34	7.7	4.74			
	NT2RP2005669	7.15	7.15	7.95	7.05	11.14	8.21			
35	NT2RP2005670	2.35	2.35	6.91	7.77	5.04	5.2			
	NT2RP2005671	3.12	3.12	7.83	10.77	8.9	9.78	*	+	
	NT2RP2005675	7.32	7.32	37.84	34.46	40.94	40.02			
	NT2RP2005683	2.56	2.56	7.01	7.16	5.19	7.16			
	NT2RP2005690	2.84	2.84	4.48	2.82	3.74	3.4			
40	NT2RP2005694	4.07	4.07	5.49	3.77	6.26	3.54			
	NT2RP2005701	5.97	5.97	8.82	10.39	10.35	9.52	*	+	
	NT2RP2005712	5.67	5.67	5.28	4.83	7.94	6.33			
	NT2RP2005719	1.86	1.86	3.26	4.42	3.8	3.76	*	+	
	NT2RP2005722	4.16	4.16	11.13	13.39	15.7	15.94	*	+	
45	NT2RP2005723	2.71	2.71	4.2	3.65	4.58	3.67			
	NT2RP2005726	2.55	2.55	4.13	2.86	4.01	3.22			
	NT2RP2005729	4.64	4.64	9.94	10.21	10.7	10.62			
	NT2RP2005731	3.05	3.05	3.39	2.51	2.16	1.27	*	-	
	NT2RP2005732	9.41	9.41	57.73	48.37	75.21	41.64			
50	NT2RP2005737	10.75	10.75	22.28	27.16	25.02	17.59			
	NT2RP2005741	3.03	3.03	5.35	3.68	3.31	3.37			
	NT2RP2005748	1.86	1.86	5.94	3.8	3.72	2.95			
	NT2RP2005752	2.46	2.46	5.55	3.27	4.37	3.8			
	NT2RP2005753	8.45	8.45	14.76	11.12	11.69	14.45			
55	NT2RP2005763	3	3	8.03	4.22	4.77	5			
	NT2RP2005767	3.72	3.72	7.79	5.55	6.75	6.29			
	NT2RP2005773	8.11	8.11	10.02	10.6	11.59	13.37	*	+	
	NT2RP2005774	4.25	4.25	12.72	6.86	12.24	14.61			
	NT2RP2005775	3.75	3.75	7.2	3.35	4.83	5.63			
	NT2RP2005781	5.11	5.11	9.88	9.82	7.19	12.94			

EP 1 130 094 A2

	NT2RP2005784	5.41	5.41	11.51	7.68	12.12	14.06		
5	NT2RP2005789	3.98	3.98	11.24	7.89	9.52	8.86		
	NT2RP2005799	2.45	2.45	6.35	2.64	4.67	3.7		
	NT2RP2005804	9.01	9.01	25	27.85	27.32	30.57		
	NT2RP2005812	2.63	2.63	4.83	2.9	3.89	5.21		
	NT2RP2005815	2.48	2.48	3.15	2.38	3.21	5.2		
	NT2RP2005835	5.99	5.99	11.26	7.13	13.74	11.69		
10	NT2RP2005841	2.32	2.32	10.04	4.89	7.43	11.23		
	NT2RP2005853	1.29	1.29	4.44	2.71	4.6	4.96		
	NT2RP2005857	7.37	7.37	9.87	13.46	7.93	20.27		
	NT2RP2005859	2.76	2.76	5	2.91	6.14	4.78		
	NT2RP2005860	1.41	1.41	3.54	1.45	1.89	2.22		
15	NT2RP2005863	3.03	3.03	6.55	10.76	18.29	15.94	*	+
	NT2RP2005868	3.86	3.86	5.85	5.1	6.3	7.77		
	NT2RP2005876	5.7	5.7	12.31	7.84	8.29	8.2		
	NT2RP2005878	2.26	2.26	8.44	5.25	4.95	6.32		
	NT2RP2005883	13.54	13.54	21.06	23.75	9.57	28.09		
20	NT2RP2005886	7.18	7.18	50.05	51.13	62.09	50.14		
	NT2RP2005887	3.76	3.76	6.51	4.74	8.05	4.81		
	NT2RP2005890	4.17	4.17	9.77	11.87	17.13	12.15	*	+
	NT2RP2005901	3.19	3.19	5.69	3.91	6.18	5.14		
	NT2RP2005902	3.17	3.17	4.33	4.78	4.77	6.25		
25	NT2RP2005908	3.09	3.09	7.86	4.89	3.7	6.34		
	NT2RP2005927	1.77	1.77	2.66	2.25	4.36	3.07		
	NT2RP2005933	2.5	2.5	5.59	6.4	4.77	6.42		
	NT2RP2005941	2.09	2.09	5.2	3.31	4.41	3.9		
	NT2RP2005942	4	4	6.86	3.08	4.59	4.64		
30	NT2RP2005946	4.63	4.63	9.49	5.33	7.06	6.24		
	NT2RP2005970	5.44	5.44	14	16.16	22.05	18.9	*	+
	NT2RP2005980	3.71	3.71	5.25	2.69	3.46	2.37		
	NT2RP2005994	2.99	2.99	6.76	4.28	3.28	5.14		
	NT2RP2006004	1.31	1.31	2.89	2.07	6.09	2.58		
35	NT2RP2006013	1.38	1.38	4.91	3.1	5.07	4.92		
	NT2RP2006023	8.37	8.37	17.77	20	21.43	21.14	*	+
	NT2RP2006028	5.03	5.03	10.23	7.47	9.89	9.71		
	NT2RP2006038	4.67	4.67	5.86	2.79	5.4	1.09		
40	NT2RP2006042	8.3	8.3	7.22	6.63	5.89	6.3	*	-
	NT2RP2006043	5.65	5.65	7.59	7.6	10.99	8.29		
	NT2RP2006052	1.48	1.48	4.48	4.13	3.12	4.54		
	NT2RP2006057	3.73	3.73	6.23	5.69	3.83	4.95		
	NT2RP2006064	4.16	4.16	7.73	5.86	6.81	9.08		
45	NT2RP2006068	2.76	2.76	6.75	6.8	7.81	5.81		
	NT2RP2006069	1.46	1.46	4.94	3.56	3.95	3.3		
	NT2RP2006071	8.37	8.37	7.8	9.28	10.48	9.11	*	+
	NT2RP2006090	6.62	6.62	5.78	3.27	3.55	3.64	**	-
	NT2RP2006092	3.78	3.78	8.3	6.18	8.04	7.07		
50	NT2RP2006097	14.05	14.05	40.38	31.2	25.81	40.02		
	NT2RP2006098	1.94	1.94	4.27	4.52	4.61	7.65		
	NT2RP2006099	3.84	3.84	11.02	10.65	10.99	13.34		
	NT2RP2006100	2.87	2.87	5.78	3.63	7.31	5.19		
	NT2RP2006103	2.39	2.39	5.54	2.6	3.93	1.71		
55	NT2RP2006106	6.48	6.48	21.51	18.05	24.81	22.3		

EP 1 130 094 A2

	NT2RP2006127	3.17	3.17	4.92	1.62	1.26	1.21	*	-
5	NT2RP2006134	4.25	4.25	4.41	6.08	6.7	5.47	**	+
	NT2RP2006141	3.91	3.91	7.94	7.45	6.04	9.08		
	NT2RP2006166	3.1	3.1	10.65	9.01	8.94	7.85		
	NT2RP2006176	2.15	2.15	4.26	3.95	5.73	4.69		
10	NT2RP2006181	1.68	1.68	2.84	3.21	3.14	2.45		
	NT2RP2006184	8.85	8.85	17.16	20.8	19.95	17.1		
	NT2RP2006186	3.01	3.01	4.57	2.77	2.29	4.33		
	NT2RP2006196	5.24	5.24	7.21	5.25	5.23	4.16		
15	NT2RP2006199	5.06	5.06	4.38	3.81	3.65	3.64	**	-
	NT2RP2006200	0.87	0.87	3.43	4.37	4.52	2.17		
	NT2RP2006210	20.08	20.08	59.85	75.37	70.55	96.59	*	+
20	NT2RP2006219	2.88	2.88	6.26	5.97	5.11	7.36		
	NT2RP2006224	3.7	3.7	7.55	9	7.7	8.93		
	NT2RP2006237	1.97	1.97	4.79	3.45	2.74	4.14		
	NT2RP2006238	3.9	3.9	6.33	4.2	4.69	3.93		
25	NT2RP2006258	4.5	4.5	6.73	3.07	4.27	4.39		
	NT2RP2006261	7.32	7.32	3.98	2.04	3.19	7.69		
	NT2RP2006269	4.11	4.11	7.96	9.52	5.46	9.06		
	NT2RP2006275	3.67	3.67	30.36	23.46	35.36	25.14		
	NT2RP2006282	3.16	3.16	8.89	8.85	8.4	7.05		
30	NT2RP2006302	5.69	5.69	12.68	13.12	12.4	11.87		
	NT2RP2006312	4.88	4.88	8.22	8.47	9.13	9.8		
	NT2RP2006320	4.27	4.27	9.87	6.42	9.32	9.69		
	NT2RP2006321	3.27	3.27	4.23	2.79	4.99	4.13		
	NT2RP2006323	4.1	4.1	2.59	2.39	3.6	1.83		
35	NT2RP2006333	0.67	0.67	1.82	1.7	1.04	1.17		
	NT2RP2006334	2.24	2.24	4.02	4.57	2.72	3.54		
	NT2RP2006338	2.4	2.4	5.26	4.73	5.11	4.04		
	NT2RP2006339	2.24	2.24	2.94	2.47	1.93	2.06		
	NT2RP2006355	3.61	3.61	4.59	3.14	3.39	2.22		
40	NT2RP2006365	3.3	3.3	4.44	2.42	2.6	1.3	*	-
	NT2RP2006374	16.34	16.34	111.62	108.73	174.7	73.65		
	NT2RP2006393	4.93	4.93	7.68	7.38	8	6.95		
	NT2RP2006394	8.59	8.59	17.91	11.3	11.18	15.38		
	NT2RP2006400	2.25	2.25	4.51	2.08	3.58	1.95		
45	NT2RP2006411	27.71	27.71	42.11	23.61	17.25	37.31		
	NT2RP2006429	2.22	2.22	7.3	2.82	5.3	2.21		
	NT2RP2006435	1.46	1.46	5.29	1.76	2.65	1.98		
	NT2RP2006436	2.33	2.33	6.43	4.33	5.28	3.75		
	NT2RP2006441	4.69	4.69	8.19	7.76	8.89	8.37		
50	NT2RP2006447	2.41	2.41	4.78	3.18	2.63	3.87		
	NT2RP2006454	2.58	2.58	5.38	4.39	3.37	4.03		
	NT2RP2006455	3.79	3.79	7.14	2.91	4.62	9.23		
	NT2RP2006456	1.96	1.96	5.99	2.51	4.49	3.17		
	NT2RP2006464	5.44	5.44	8.28	4.47	8.85	7.9		
55	NT2RP2006467	4.17	4.17	10	8.56	12.47	12.58		
	NT2RP2006472	5.05	5.05	6.84	7.24	6.92	7.37		
	NT2RP2006474	4.69	4.69	16.3	18.19	32.31	21.3		
	NT2RP2006475	2.5	2.5	9.54	6.14	6.86	7.66		
	NT2RP2006476	5.34	5.34	14.94	7.62	13.82	17.24		
	NT2RP2006501	2.44	2.44	7.28	4.6	7.45	7.74		

EP 1 130 094 A2

	NT2RP2006512	10.25	10.25	19.79	16.72	7.89	29.01
5	NT2RP2006526	2.09	2.09	5.19	2.24	2.78	2.31
	NT2RP2006527	3.61	3.61	7.05	4.56	6.14	6.46
	NT2RP2006534	2.24	2.24	4.49	2.08	2.95	2.73
	NT2RP2006537	6.08	6.08	15.7	11.72	17.73	12.82
	NT2RP2006543	7.83	7.83	14.8	6.52	5.4	6.88
10	NT2RP2006554	1.33	1.33	3.71	1.79	3.76	2.2
	NT2RP2006565	3.78	3.78	8.91	5.79	8.42	7.55
	NT2RP2006571	1.38	1.38	3.88	2.77	4.01	2.29
	NT2RP2006573	2.1	2.1	4.02	3.05	3.6	2.41
	NT2RP2006598	2.25	2.25	7.04	4.34	6.56	4.78
15	NT2RP2006601	24.92	24.92	35.13	38.45	45.47	31.69
	NT2RP3000002	5.04	5.04	6.09	4.7	5.04	8.18
	NT2RP3000011	1.82	1.82	5.9	2.59	1.85	2.22
	NT2RP3000014	3.29	3.29	7.66	4.22	3.06	4.95
	NT2RP3000016	3.42	3.42	7	5.29	6.56	6.11
	NT2RP3000022	1.71	1.71	3.93	1.72	4.68	0.59
20	NT2RP3000024	3.74	3.74	7.03	4.31	4.92	4.06
	NT2RP3000031	4.66	4.66	8.66	4	6.75	4.86
	NT2RP3000034	3.76	3.76	6.24	4.44	7.13	3.23
	NT2RP3000037	2.76	2.76	6.5	9.41	13.44	11.06
	NT2RP3000040	2.04	2.04	5.96	3.21	3.46	3.56
25	NT2RP3000041	2.15	2.15	7.35	3.71	3.01	3.16
	NT2RP3000046	1.95	1.95	4.42	3.67	7.11	3.84
	NT2RP3000047	3.25	3.25	5.55	5.85	6.2	5.94
	NT2RP3000049	2.54	2.54	6.94	5.26	7.78	3.58
	NT2RP3000050	4.99	4.99	9.03	3.76	8.5	6.22
30	NT2RP3000051	5.99	5.99	10.69	8.51	11.19	9.72
	NT2RP3000054	4.31	4.31	6.5	4.38	5.35	3.22
	NT2RP3000055	1.98	1.98	4.76	3.81	2.67	3.96
	NT2RP3000056	2.87	2.87	7.09	5.59	3.32	3.91
	NT2RP3000059	2.54	2.54	5.1	1.89	4.07	1.6
35	NT2RP3000063	2.18	2.18	5.51	3.34	5.19	2.27
	NT2RP3000068	3.76	3.76	24.22	25.83	37.88	23.13
	NT2RP3000069	17.44	17.44	20.58	22	28.87	18.2
	NT2RP3000072	5.9	5.9	6.18	4.96	5.39	4.19
40	NT2RP3000080	4.38	4.38	6.72	3.78	5.28	3.93
	NT2RP3000085	1.9	1.9	4.84	5.13	4.66	5.5
	NT2RP3000087	3.77	3.77	9.1	6.22	5.61	6
	NT2RP3000092	1.92	1.92	3.6	2.72	3.2	2.52
	NT2RP3000109	1.74	1.74	5.05	5.63	7.94	4.24
45	NT2RP3000119	4.66	4.66	14.27	11.29	13.7	14.28
	NT2RP3000125	3.02	3.02	5.56	3.42	4.53	2
	NT2RP3000131	7.84	7.84	14.37	16.23	19.96	12.93
	NT2RP3000134	5.96	5.96	9.01	6.61	7.25	6.46
	NT2RP3000137	3.88	3.88	6.48	5.58	6.3	6.11
50	NT2RP3000142	2.87	2.87	7.77	7.28	5.03	5.31
	NT2RP3000148	1.84	1.84	6.28	4.9	5.04	5.34
	NT2RP3000149	2.51	2.51	6.97	6.14	7.77	8.24
	NT2RP3000163	2.16	2.16	6.17	3.27	3.9	2.5
	NT2RP3000168	5.53	5.53	14.55	12.8	11.65	11.73
55	NT2RP3000169	3.74	3.74	6.01	6.03	8.47	5.72

EP 1 130 094 A2

	NT2RP3000171	10.86	10.86	16.71	28.33	38.98	25.93	*	+
5	NT2RP3000172	0.86	0.86	1.53	1.66	1.2	1.46		
	NT2RP3000186	4.32	4.32	10.6	19.18	15.43	15.82	*	+
	NT2RP3000197	1.22	1.22	3.66	4.03	4.29	3.39		
10	NT2RP3000201	2.4	2.4	7.2	10.49	8.4	7.88		
	NT2RP3000204	2.16	2.16	4.44	3.88	4.1	4.25		
	NT2RP3000207	2.87	2.87	4.71	3	2.6	2.45		
15	NT2RP3000216	5.38	5.38	10.1	5.87	9.5	5.73		
	NT2RP3000220	5.14	5.14	5.66	3.68	5.69	2.92		
	NT2RP3000221	2.18	2.18	5.45	6.26	6.63	5.93		
	NT2RP3000232	2.7	2.7	8.01	7.1	5.52	5.92		
20	NT2RP3000233	1.55	1.55	6.01	6.9	5.91	4.06		
	NT2RP3000234	3.23	3.23	9.09	12.89	10.4	11.41	*	+
25	NT2RP3000235	1.57	1.57	3.3	2.35	2.92	1.38		
	NT2RP3000239	4.61	4.61	11.11	9.51	9.71	14.92		
	NT2RP3000247	3.25	3.25	5.82	2.92	4.04	1.96		
30	NT2RP3000251	6.11	6.11	6.52	5.22	5.82	3.25		
	NT2RP3000252	3.73	3.73	7.99	7.61	8.53	8.4		
	NT2RP3000255	2.18	2.18	2.96	3.26	3.13	1.97		
	NT2RP3000262	6.72	6.72	9.43	11.67	7.95	9.13		
	NT2RP3000266	6.47	6.47	15.5	13.38	10.83	12.64		
35	NT2RP3000267	2.71	2.71	4.04	2.9	2.64	3.03		
	NT2RP3000271	4.38	4.38	5.57	5.11	4.84	3.72		
	NT2RP3000278	7.84	7.84	56.85	48.55	82.07	42.57		
	NT2RP3000281	4.94	4.94	10.72	8.19	8.22	7.27		
	NT2RP3000292	5.63	5.63	14.1	9.17	6.77	6.93		
40	NT2RP3000299	2.31	2.31	4.92	3.73	4.89	4.98		
	NT2RP3000304	2.15	2.15	3.48	2.85	3.36	1.64		
	NT2RP3000310	7.24	7.24	24.22	18.94	23.07	19.88		
	NT2RP3000312	2.99	2.99	8.16	3.31	5.25	3.87		
45	NT2RP3000320	7.06	7.06	6.17	5.25	4.74	4.74	**	-
	NT2RP3000322	11.05	11.05	18.76	32.59	45.13	46.95	**	+
	NT2RP3000324	6.91	6.91	46.42	36.64	43.53	39.68		
	NT2RP3000326	1.95	1.95	6.17	4.02	5.75	3.53		
	NT2RP3000329	2.5	2.5	5.96	4.97	8.84	5.9		
	NT2RP3000330	4.1	4.1	6.18	4.62	5.53	6.12		
50	NT2RP3000333	3.23	3.23	7.45	4.36	5.28	4.52		
	NT2RP3000341	8.8	8.8	12.85	14.81	18.59	14.41	*	+
	NT2RP3000344	2.73	2.73	3.75	2.69	3.54	2.29		
	NT2RP3000345	3.09	3.09	3.57	1.65	1.97	2.66	*	-
55	NT2RP3000348	444.59	444.59	802.63	824.62	1016.01	909.68		
	NT2RP3000350	4.25	4.25	10.34	4.57	9.28	6.4		
	NT2RP3000359	9.53	9.53	24.44	8.54	11.36	16.62		
	NT2RP3000361	7.5	7.5	11.12	7.89	7.81	8.95		
	NT2RP3000366	7.38	7.38	14.27	9.52	11.84	16.13		
	NT2RP3000378	2.67	2.67	5.75	3.92	4.78	2.47		
	NT2RP3000384	5.42	5.42	10.88	9.52	13.1	9.28		
	NT2RP3000389	12.54	12.54	21.49	23.95	35.02	27.32	*	+
	NT2RP3000393	3.74	3.74	6.16	5.03	4.53	4.77		
	NT2RP3000395	110.27	110.27	212	108.33	38.18	148.45		
	NT2RP3000397	2.83	2.83	5.28	2.51	5.26	3.31		
	NT2RP3000398	3.39	3.39	10.12	11.46	11.18	12.26		

EP 1 130 094 A2

	NT2RP3000403	3.22	3.22	9.39	10.1	8.2	8.44
5	NT2RP3000418	3.4	3.4	10.22	7.12	11.08	13.42
	NT2RP3000424	2.86	2.86	9.43	6.25	9.52	6.86
	NT2RP3000427	4.65	4.65	9.05	11.55	13.43	12.35 * +
	NT2RP3000431	2.05	2.05	4.93	3.43	3.26	3.93
	NT2RP3000433	2.63	2.63	8.65	5.65	7.09	6.65
10	NT2RP3000436	11.39	11.39	20.93	18.76	9.35	18.86
	NT2RP3000439	1.4	1.4	3.61	2.54	3.56	2
	NT2RP3000441	3.88	3.88	7.4	7.56	7.92	6.39
	NT2RP3000444	3.31	3.31	7.29	2.36	3.25	2.2
	NT2RP3000448	4.45	4.45	10.15	4.05	6.54	3.93
15	NT2RP3000449	2.84	2.84	4.59	3.1	3.94	2.93
	NT2RP3000451	1.76	1.76	5.12	3.7	5	2.96
	NT2RP3000456	1.69	1.69	5.48	4.23	6.67	4.21
	NT2RP3000460	18.87	18.87	36.67	24.52	25.24	26.25
20	NT2RP3000471	3.14	3.14	6.49	2.74	4.98	5.84
	NT2RP3000477	19.96	19.96	23.67	28.98	17.78	32.78
	NT2RP3000478	5.86	5.86	8.95	5.21	8.98	2.6
	NT2RP3000481	5.48	5.48	5.76	2.76	3.61	1.52 ** -
	NT2RP3000484	3.51	3.51	4.26	2.32	2.55	1.76 * -
	NT2RP3000487	1.77	1.77	7.4	5.07	4.03	4.97
25	NT2RP3000512	3.29	3.29	17.7	15.17	15.9	14.52
	NT2RP3000523	13.05	13.05	30.74	31.75	27.83	34.4
	NT2RP3000526	3.07	3.07	7.38	5.18	6.31	4.64
	NT2RP3000527	2.83	2.83	6.5	3.76	7.25	5.03
	NT2RP3000531	2.9	2.9	7.71	5.11	5.51	4.69
30	NT2RP3000532	5.74	5.74	5.6	5.75	8.39	4.26
	NT2RP3000542	6.23	6.23	8.1	7.21	7.3	6.39
	NT2RP3000554	8.81	8.81	15.22	13.78	10.56	14.95
	NT2RP3000561	1.21	1.21	3.51	3.11	2.76	2.25
35	NT2RP3000562	1.84	1.84	3.5	3.7	3.87	3.23
	NT2RP3000578	1.56	1.56	2.54	2.54	3.37	2.36
	NT2RP3000582	1.26	1.26	4.66	2.24	2.52	0.41
	NT2RP3000584	2.82	2.82	6.52	3.2	2.5	2.02
	NT2RP3000586	4.08	4.08	4.59	3.28	3.9	2.87
	NT2RP3000590	5.69	5.69	4.61	3.78	4.35	2.57
40	NT2RP3000592	1.8	1.8	2.99	2.97	2.75	3.15
	NT2RP3000596	2.27	2.27	4.89	4.5	3.33	3.03
	NT2RP3000599	1.67	1.67	3.07	3.88	4.98	3.82 * +
	NT2RP3000603	6.09	6.09	39.25	40.43	44.88	35.89
45	NT2RP3000605	2.84	2.84	6.66	4.56	4.23	2.56
	NT2RP3000607	5.35	5.35	7.59	5.74	8.46	7.55
	NT2RP3000616	3.26	3.26	5.45	2.56	2.38	1.21
	NT2RP3000621	5.18	5.18	8.48	10.28	10.29	6.01
	NT2RP3000622	2.36	2.36	8.76	5.85	6.21	4.72
50	NT2RP3000624	1.53	1.53	3.19	3.97	3.06	2.78
	NT2RP3000628	2.44	2.44	8.04	10.27	7.85	5.58
	NT2RP3000631	4.71	4.71	14.95	22.82	16.45	14.2
	NT2RP3000632	2.35	2.35	5.5	7.78	8.91	5.91 * +
	NT2RP3000638	6.95	6.95	17.93	11.8	11.6	9.97
55	NT2RP3000644	25.72	25.72	48.41	57.98	72.01	52.49 * +
	NT2RP3000645	5.85	5.85	10.48	9.84	12.55	8.43

EP 1 130 094 A2

	NT2RP3000652	3.39	3.39	5.34	6.22	5.9	7.74	*	+
5	NT2RP3000658	2.26	2.26	5.01	6.16	4.24	4.86		
	NT2RP3000660	2.34	2.34	6.25	6.98	6.91	5.14		
	NT2RP3000661	1.98	1.98	4.49	4.06	3.87	3.1		
	NT2RP3000665	4.79	4.79	12.26	11.83	11.92	7		
10	NT2RP3000676	4.46	4.46	7.55	6.65	7.81	5.42		
	NT2RP3000677	2.87	2.87	4.13	2.44	3.07	1.54		
	NT2RP3000681	19.85	19.85	30.12	32.94	41.51	34.34	*	+
	NT2RP3000683	2.68	2.68	9.67	6.69	7.09	6.69		
	NT2RP3000685	1.7	1.7	2.5	3.63	2.36	3.44		
15	NT2RP3000690	2.77	2.77	3.29	3.82	3.75	2.72		
	NT2RP3000698	10	10	22.49	25.66	17.08	27.43		
	NT2RP3000708	3.45	3.45	5.5	8.17	9.22	8.56	**	+
20	NT2RP3000719	2.83	2.83	2.83	1.16	1.7	1.91	**	-
	NT2RP3000721	5.63	5.63	24.61	23.43	39.76	21.55		
	NT2RP3000728	3.33	3.33	2.57	1.4	1.64	1.05	**	-
	NT2RP3000730	2.06	2.06	5.04	2.76	4.23	1.86		
25	NT2RP3000733	2.87	2.87	6.32	3.48	4.47	4.25		
	NT2RP3000735	1.74	1.74	4.22	1.81	2.22	1.26		
	NT2RP3000736	2.71	2.71	6.35	3.29	5.05	3.65		
	NT2RP3000739	13.76	13.76	12.16	18.05	9.37	20.19		
	NT2RP3000742	3.89	3.89	10.06	4.54	4.97	4.43		
30	NT2RP3000753	2.29	2.29	3.9	2.17	2.65	6.3		
	NT2RP3000759	9.07	9.07	15.99	11.11	17.14	23.05		
	NT2RP3000789	1.58	1.58	5.76	4.89	4.23	3.69		
	NT2RP3000815	1.91	1.91	5.92	4.49	5.57	3.08		
35	NT2RP3000818	4.35	4.35	11.29	6.64	10.49	8.27		
	NT2RP3000820	9.01	9.01	18.49	18.58	20.1	16.9		
	NT2RP3000821	2.13	2.13	4.83	3.28	5.19	2.02		
	NT2RP3000825	1.87	1.87	4.94	1.92	1.47	2.27		
	NT2RP3000826	4.04	4.04	13.59	10.86	13.8	12.94		
	NT2RP3000836	5.33	5.33	11.61	11.55	14.11	13.3		
40	NT2RP3000838	319.2	319.2	741.74	710.2	743.55	1049.86		
	NT2RP3000839	2.35	2.35	6.67	4.53	6.38	4.36		
	NT2RP3000841	2.17	2.17	4.32	3.79	5.55	4.72		
	NT2RP3000845	3.96	3.96	8.89	5.76	6.71	7.85		
45	NT2RP3000847	3.7	3.7	7.94	4.48	5.94	5.28		
	NT2RP3000848	2.84	2.84	8.34	5.36	6.81	6.3		
	NT2RP3000850	5.67	5.67	7.04	6.58	11.29	7.47		
	NT2RP3000852	3.27	3.27	3.17	4.02	5.23	5.8	*	+
	NT2RP3000859	2.76	2.76	7.12	4.46	7.11	8.43		
	NT2RP3000861	2.58	2.58	10.51	6.13	10.36	6.43		
50	NT2RP3000862	15.29	15.29	24.16	16.36	9.81	23.13		
	NT2RP3000865	1.58	1.58	4.26	2.54	4.21	1.83		
	NT2RP3000866	2.08	2.08	5.03	2.37	3.59	5.22		
	NT2RP3000868	2.2	2.2	7.09	3.04	3.84	2.28		
	NT2RP3000869	3.54	3.54	11.36	9.61	15.76	7.9		
	NT2RP3000871	1.75	1.75	3.79	1.81	3.24	1.94		
	NT2RP3000875	0.99	0.99	4.25	2.57	2.71	3.64		
	NT2RP3000895	2.54	2.54	5.56	2.84	3.55	4.93		
	NT2RP3000900	6.01	6.01	11.86	11.3	7.7	14.58		
55	NT2RP3000901	3.67	3.67	7.03	4.11	6.39	5.3		

EP 1 130 094 A2

	NT2RP3000903	3.76	3.76	7.87	3.12	5.92	3.93		
5	NT2RP3000904	3.83	3.83	8.67	3.05	4.87	3.16		
	NT2RP3000907	5.66	5.66	10.03	8.94	10.67	10.14		
	NT2RP3000913	6.04	6.04	15.01	17.87	25.57	17.37	*	+
	NT2RP3000917	7.64	7.64	16.58	7.66	6.56	13.51		
	NT2RP3000919	1.99	1.99	5.15	3.5	4.3	2.68		
10	NT2RP3000921	2.26	2.26	7.67	4.88	4.07	6.51		
	NT2RP3000942	2.66	2.66	3.89	2.68	4.12	2.63		
	NT2RP3000968	70.24	70.24	87.55	105.89	110.05	115.38	**	+
	NT2RP3000974	5.36	5.36	9.06	3.21	4.48	2.64		
	NT2RP3000980	5.77	5.77	5.77	2.09	4.14	2.26	*	-
15	NT2RP3000984	3.17	3.17	7.65	6.33	6.68	4.58		
	NT2RP3000994	2.09	2.09	4.88	2.4	3.14	3.37		
	NT2RP3001001	1.46	1.46	3.45	3.75	4.14	1.31		
	NT2RP3001004	3.37	3.37	6.52	3.51	5.63	5.01		
	NT2RP3001007	4.46	4.46	9.87	10.02	10.62	6.81		
	NT2RP3001012	2.78	2.78	5.4	4.99	6.83	3.65		
20	NT2RP3001042	4.74	4.74	5.52	2.99	5.18	1.38		
	NT2RP3001044	6.26	6.26	7.12	7.16	6.76	4.92		
	NT2RP3001048	2.52	2.52	3.01	3.5	3.93	2.42		
	NT2RP3001050	1.79	1.79	4.99	4.68	5.94	4.7		
	NT2RP3001055	6.55	6.55	15.6	16.48	12.44	20.49		
25	NT2RP3001057	2.79	2.79	10.84	5.57	6.05	5.67		
	NT2RP3001061	3.18	3.18	6.57	5.03	7.85	5.42		
	NT2RP3001069	6.03	6.03	14.95	18.49	17.53	15.08		
	NT2RP3001074	4.2	4.2	7.22	8.72	10	6.64		
	NT2RP3001078	5.11	5.11	7.29	7.51	8.72	5.18		
30	NT2RP3001081	4	4	5.72	4.65	5.19	3.52		
	NT2RP3001084	2.7	2.7	7.92	6.85	6.71	6.23		
	NT2RP3001095	1.57	1.57	3.88	3.69	3.68	3.42		
	NT2RP3001096	2.52	2.52	7.33	16.78	8.08	18.7	*	+
35	NT2RP3001097	3.65	3.65	4.28	6.42	8.11	8.5	**	+
	NT2RP3001107	3.69	3.69	4.79	3.77	4.03	2.37		
	NT2RP3001109	3.2	3.2	5.5	6.01	9.56	7.26	*	+
	NT2RP3001111	4.58	4.58	4.19	3.41	3.51	2.29	*	-
	NT2RP3001112	12.61	12.61	18.48	25.73	29.85	24.61	**	+
40	NT2RP3001113	1.21	1.21	2.59	2.47	3.24	2.19		
	NT2RP3001115	1.51	1.51	3.32	2.57	3.77	2.19		
	NT2RP3001116	1.01	1.01	2.66	2.55	4.4	2.91		
	NT2RP3001119	3.69	3.69	6.75	9.07	6.67	5.44		
	NT2RP3001120	5.02	5.02	8.24	8.85	7.87	6.71		
45	NT2RP3001126	6.16	6.16	12.34	17.84	19.66	17.49	**	+
	NT2RP3001127	6.93	6.93	6.76	4.79	7.63	6.36		
	NT2RP3001133	3.95	3.95	4.95	3.95	4.16	3.62		
	NT2RP3001140	1.46	1.46	2.43	3.21	2.38	6.71		
	NT2RP3001147	3.16	3.16	6.96	16.08	14.49	13.84	**	+
50	NT2RP3001150	1.99	1.99	4.32	4.06	5.68	3.76		
	NT2RP3001152	1.7	1.7	3.29	3.15	3.62	2.51		
	NT2RP3001155	2.95	2.95	4.35	3.68	4.35	3.58		
	NT2RP3001156	4.38	4.38	6.57	2.91	5.72	5.67		
	NT2RP3001159	5.38	5.38	10.5	7.87	10.86	7.25		
55	NT2RP3001170	7.38	7.38	5.96	6.12	8.01	4.56		

EP 1 130 094 A2

	NT2RP3001176	3.49	3.49	10.75	6.27	8.23	9.49		
5	NT2RP3001195	2.35	2.35	4.81	6.79	5.79	6.22	*	+
	NT2RP3001209	3.47	3.47	5.98	5.96	4.64	5.22		
	NT2RP3001214	1.63	1.63	4.91	3.44	3.87	3.81		
10	NT2RP3001216	3.58	3.58	6.38	6.25	4.33	3.6		
	NT2RP3001221	3.33	3.33	4.27	3.07	3.06	1.79		
	NT2RP3001226	5.96	5.96	29.04	21.93	31.45	17.76		
	NT2RP3001230	3.17	3.17	2.41	3.09	3.14	1.56		
15	NT2RP3001232	1.8	1.8	4.72	2.36	3.7	2.85		
	NT2RP3001236	1.68	1.68	4.3	1.7	3.26	1.47		
	NT2RP3001239	1.58	1.58	5.21	2.81	4.31	2.01		
	NT2RP3001240	12.83	12.83	22.18	23.01	24.3	14.46		
20	NT2RP3001245	3.53	3.53	9.88	4.08	6.36	3.39		
	NT2RP3001253	2.79	2.79	4.87	3.34	4.53	5.21		
	NT2RP3001259	6.62	6.62	11.97	12.33	15.62	11.83		
	NT2RP3001260	3.74	3.74	5.15	3.45	5.44	3.97		
25	NT2RP3001264	2.2	2.2	10.29	5.99	6.92	6.38		
	NT2RP3001268	2.25	2.25	7.18	4.93	4.72	4.35		
	NT2RP3001271	7.06	7.06	16.29	13.07	12.27	14.24		
	NT2RP3001272	3.73	3.73	12.45	9.43	11.09	10.15		
	NT2RP3001274	6.08	6.08	8.09	6.72	6.35	5.11		
30	NT2RP3001275	9.78	9.78	11.58	21.56	26.84	22.59	**	+
	NT2RP3001280	3.39	3.39	5.5	3.58	5.24	4.18		
	NT2RP3001281	3.15	3.15	3.89	3.08	4.48	5.14		
	NT2RP3001288	49.31	49.31	103.24	124.07	142.92	164.41	*	+
	NT2RP3001297	6.39	6.39	42.01	37.04	42.75	41.14		
35	NT2RP3001300	5.23	5.23	15.92	16.78	17.41	17.76		
	NT2RP3001301	2.91	2.91	6.59	3.96	4.58	3.9		
	NT2RP3001307	1.76	1.76	7.67	2.07	2.81	2.06		
	NT2RP3001310	11.55	11.55	17.04	25.54	26.07	28.13	**	+
	NT2RP3001318	2.11	2.11	3.4	2.49	3.37	2.37		
40	NT2RP3001322	3.58	3.58	5.23	2.62	3.84	5.48		
	NT2RP3001325	2.7	2.7	8.39	5.82	6.82	5.58		
	NT2RP3001338	2.67	2.67	6.19	4.1	4.21	3.5		
	NT2RP3001339	2.53	2.53	5.64	3.08	4.89	2.91		
	NT2RP3001340	2.9	2.9	8.42	6.36	7.07	5.79		
45	NT2RP3001341	2.26	2.26	6.97	5.1	5.62	4.73		
	NT2RP3001354	3.22	3.22	9.77	4.28	6.93	9.35		
	NT2RP3001355	1.9	1.9	5.41	2.65	3.82	2.74		
	NT2RP3001356	2	2	5.34	2.59	3.2	3.55		
	NT2RP3001359	1.09	1.09	4.05	1.63	2.5	1.75		
50	NT2RP3001364	2.34	2.34	5.31	3.26	6.67	2.67		
	NT2RP3001373	1.12	1.12	3.22	2.1	3.74	1.71		
	NT2RP3001374	1.9	1.9	4.17	3.18	3.92	3.1		
	NT2RP3001383	3.84	3.84	8.96	3.92	6.65	3.85		
	NT2RP3001384	4.11	4.11	9.47	3.54	4.46	2.41		
55	NT2RP3001388	3.98	3.98	8.79	9.48	10.99	9.4		
	NT2RP3001392	4.61	4.61	6.19	3.91	6.14	3.23		
	NT2RP3001396	1.7	1.7	6.39	4.04	4.66	4.53		
	NT2RP3001398	2.51	2.51	6.55	3.85	7.05	2.94		
	NT2RP3001399	4.91	4.91	20.67	15.86	16.12	12.44		
	NT2RP3001402	6.46	6.46	36.36	33.37	41.61	39.66		

EP 1 130 094 A2

	NT2RP3001407	6.96	6.96	19.16	13.69	17.65	12.35			
5	NT2RP3001416	7.92	7.92	15.88	13.02	18.3	14.72			
	NT2RP3001420	5.33	5.33	6.4	3.27	3.64	1.8	*	-	
	NT2RP3001425	3.73	3.73	4.92	4.74	5.67	3.15			
	NT2RP3001426	2.39	2.39	6.08	5.45	4.45	5.11			
	NT2RP3001427	1.82	1.82	5.61	3.46	2.89	3.59			
10	NT2RP3001428	2.42	2.42	6.29	5.69	4.81	3.77			
	NT2RP3001429	3.08	3.08	5.91	4.15	7.37	4.73			
	NT2RP3001432	2.14	2.14	6.61	3.72	4.44	3.58			
	NT2RP3001439	4.14	4.14	6.39	5.87	7.27	4.41			
15	NT2RP3001441	6.45	6.45	12.63	11.13	14.61	11.2			
	NT2RP3001446	4.99	4.99	4.99	4.64	5.22	4.39			
	NT2RP3001447	2.72	2.72	5.21	6.64	5.14	6.33			
	NT2RP3001449	3.95	3.95	11.85	16.9	14.57	13.16	*	+	
	NT2RP3001453	1.84	1.84	3.66	3.5	4.4	2.81			
	NT2RP3001457	3.86	3.86	7.71	6.06	6.93	5.5			
20	NT2RP3001459	2.39	2.39	6.03	2.64	2.78	1.17			
	NT2RP3001463	2.77	2.77	6.74	5.93	5.94	3.98			
	NT2RP3001466	2.87	2.87	3.56	1.19	1.43	0.78	**	-	
	NT2RP3001472	5.74	5.74	4.02	3.7	4.85	4.32			
	NT2RP3001475	3.54	3.54	7.61	6.91	6.65	7.39			
25	NT2RP3001479	2.54	2.54	6.66	4.37	5.69	5.16			
	NT2RP3001490	3.18	3.18	9.26	4.4	6.02	5.21			
	NT2RP3001492	4.36	4.36	7.84	7.59	7.08	5.72			
	NT2RP3001495	4.14	4.14	3.85	2.75	2.92	1.76	*	-	
	NT2RP3001497	5.8	5.8	6.32	7.47	9.96	6.8			
30	NT2RP3001501	5.36	5.36	5.52	3.12	4.49	3.43	*	-	
	NT2RP3001527	4.89	4.89	6.71	4.9	5.14	3.52			
	NT2RP3001529	1.51	1.51	3.5	4.12	3.95	4.18	*	+	
	NT2RP3001538	1.78	1.78	6.2	6.93	7.81	6.23			
	NT2RP3001539	5.81	5.81	14.5	15.19	14.15	16.47			
35	NT2RP3001542	1.52	1.52	5.26	4.23	4.38	2.13			
	NT2RP3001549	4.75	4.75	11.12	14.57	11.37	13.44			
	NT2RP3001554	3.06	3.06	6.16	6.37	7.5	5.05			
	NT2RP3001560	4.96	4.96	5.73	4.67	6.35	2.36			
	NT2RP3001561	8.85	8.85	20.77	20.38	27.2	17.15			
40	NT2RP3001564	1.54	1.54	8.24	6.43	4.53	5.96			
	NT2RP3001568	2.1	2.1	7.68	11.84	10.29	8.49	*	+	
	NT2RP3001575	3.94	3.94	7.24	6.39	6.97	6.16			
	NT2RP3001580	1.78	1.78	4.49	4.35	3.8	3.11			
45	NT2RP3001587	4.38	4.38	8.74	10.75	10.04	7.77			
	NT2RP3001589	3.17	3.17	8.21	5.6	7.79	4.36			
	NT2RP3001592	4.52	4.52	21.6	19	32.62	14.54			
	NT2RP3001607	3.42	3.42	1.86	1.59	2.8	1			
	NT2RP3001608	1.05	1.05	3.59	2.41	1.73	2.31			
	NT2RP3001613	3.08	3.08	2.77	3.89	2.91	3.99			
50	NT2RP3001619	4.31	4.31	8.15	7.69	6.45	7.62			
	NT2RP3001621	1.18	1.18	2.69	2.39	2.28	2.02			
	NT2RP3001629	2.58	2.58	3.28	2.68	2.41	1.7			
	NT2RP3001630	3.39	3.39	4.56	1.67	2.02	1.17	**	-	
	NT2RP3001631	9.01	9.01	14.34	18.65	21.16	15.24	*	+	
55	NT2RP3001634	4	4	5.29	4.51	6.89	5.11			

EP 1 130 094 A2

	NT2RP3001642	3.71	3.71	7.45	5.77	4.41	5.09				
5	NT2RP3001646	1.56	1.56	3.7	0.89	2.79	0.95				
	NT2RP3001650	2.06	2.06	5.81	4.86	7.03	2.08				
	NT2RP3001667	4.66	4.66	11.91	6.93	9.95	5.13				
	NT2RP3001671	2.28	2.28	7.98	7.7	4.69	5.99				
	NT2RP3001672	1.33	1.33	4.55	1.66	1.47	1.72				
10	NT2RP3001676	2.18	2.18	5.02	2.35	3.14	2.24				
	NT2RP3001678	2.86	2.86	9.24	5.12	5.14	6.03				
	NT2RP3001679	6.12	6.12	9.19	6.74	4.73	6.91				
	NT2RP3001682	1.82	1.82	5.09	4.45	6.18	3.35				
	NT2RP3001685	3.02	3.02	6.74	3.52	6.53	3.01				
	NT2RP3001688	3.01	3.01	9.42	5.46	8.21	6.43				
15	NT2RP3001690	3.21	3.21	4.87	2.91	3.54	2.99				
	NT2RP3001693	5.69	5.69	10.93	16.59	18.34	16.12	**	+		
	NT2RP3001696	2.28	2.28	3.63	1.77	3.68	3.39				
	NT2RP3001698	35.35	35.35	79.65	85.09	91.88	105.32				
	NT2RP3001708	4.82	4.82	8.78	6.34	6.95	9.01				
20	NT2RP3001712	8.69	8.69	16.06	10.22	14.19	13				
	NT2RP3001716	1.44	1.44	5.45	2.14	3.42	2.31				
	NT2RP3001724	2.75	2.75	6	4.08	4.54	2.63				
	NT2RP3001727	11.73	11.73	38.73	39.17	49.36	31.26				
	NT2RP3001729	3.36	3.36	4.7	5.69	6.55	3.06				
25	NT2RP3001730	12.54	12.54	26.52	12.53	19.94	16.4				
	NT2RP3001733	1.46	1.46	3.04	2.09	3.7	1.62				
	NT2RP3001737	3.02	3.02	7.12	4.62	5.49	2.78				
	NT2RP3001738	1.59	1.59	8.22	3.38	6.01	3.03				
	NT2RP3001739	3.26	3.26	5.25	5.63	6.1	2.51				
30	NT2RP3001742	2.54	2.54	5.36	3.86	4.55	4.03				
	NT2RP3001751	3.61	3.61	11.54	9.94	12.82	8.76				
	NT2RP3001752	2.58	2.58	7.01	2.1	3.59	2.76				
	NT2RP3001753	5.73	5.73	9.48	10.83	15.3	13.69	*	+		
	NT2RP3001754	4.63	4.63	9.08	5.86	3.73	5.33				
35	NT2RP3001756	4.66	4.66	7.36	9.37	5.75	8.03				
	NT2RP3001764	2.1	2.1	3.76	2.54	4.25	2.49				
	NT2RP3001771	2.63	2.63	3.2	1.52	4.14	1.22				
	NT2RP3001777	2.59	2.59	5.99	3.25	5.19	3.26				
	NT2RP3001782	3.52	3.52	14.68	6.47	6.63	6.47				
40	NT2RP3001792	2.27	2.27	4.35	2.91	4.09	1.35				
	NT2RP3001799	1.76	1.76	5.18	5.71	6.36	5.68				
	NT2RP3001819	1.36	1.36	4.54	1.7	1.52	2.06				
	NT2RP3001829	21.63	21.63	43.14	35.64	17.14	24.87				
45	NT2RP3001836	7.31	7.31	10.67	15.24	7.26	11.37				
	NT2RP3001839	18.86	18.86	31.77	31.97	19.23	17.53				
	NT2RP3001844	4.15	4.15	11.37	8.33	9.59	8.54				
	NT2RP3001848	9.61	9.61	52.04	44.52	74.75	43.87				
	NT2RP3001854	6.41	6.41	11.29	12.86	16.75	13.26	*	+		
50	NT2RP3001855	2.27	2.27	3.94	1.87	1	1.74				
	NT2RP3001857	3.1	3.1	5.22	5.13	5.6	3.33				
	NT2RP3001858	1.53	1.53	4.45	4.41	6.04	2.97				
	NT2RP3001861	7.35	7.35	16.34	11.85	14.46	10.42				
	NT2RP3001866	4.35	4.35	9.63	5.52	10.42	7.93				
55	NT2RP3001871	4.82	4.82	6.34	5.55	6.38	4.55				

EP 1 130 094 A2

5	NT2RP3001874	6.8	6.8	9.73	7.72	11.19	6.14			
	NT2RP3001878	5.98	5.98	6.35	4.59	6.89	5.02			
	NT2RP3001885	3.21	3.21	5.3	5.65	5.25	4.42			
	NT2RP3001896	1.64	1.64	3.49	3.37	2.13	2.02			
	NT2RP3001898	9.03	9.03	17.69	14.71	8.69	11.94			
	NT2RP3001899	3.21	3.21	7.33	4.52	6.9	5.81			
	NT2RP3001901	4.58	4.58	9.18	8.19	9.44	9.21			
10	NT2RP3001915	4.84	4.84	11.12	14.09	15.67	14.04	*	+	
	NT2RP3001926	2.8	2.8	4.88	2.47	2.45	1.65			
	NT2RP3001929	3.74	3.74	4.06	2.56	3.38	0.86			
	NT2RP3001931	4.63	4.63	5.26	3.9	5.62	2.98			
	NT2RP3001938	2.27	2.27	5.53	4.93	3.93	4.75			
15	NT2RP3001943	3.27	3.27	5.36	5.77	6.5	5.56			
	NT2RP3001944	1.77	1.77	3.72	4.08	5.91	4.34			
	NT2RP3001945	4.25	4.25	12.2	11.86	11.78	6.11			
	NT2RP3001947	2.94	2.94	5.89	4.06	5.41	3.4			
	NT2RP3001949	4.21	4.21	8.9	10.49	11.08	8.08			
20	NT2RP3001952	23.54	23.54	43.64	48.59	88.56	41.86			
	NT2RP3001954	5.06	5.06	3.68	4.34	4.79	1.85			
	NT2RP3001956	4.97	4.97	9.44	7.76	8.22	6.29			
	NT2RP3001967	3.78	3.78	7.74	6.7	5.37	5.66			
	NT2RP3001969	1.71	1.71	2.91	4.05	4.39	3.62	*	+	
25	NT2RP3001976	2.25	2.25	4.67	6.22	6.25	4.84	*	+	
	NT2RP3001986	3.55	3.55	3.88	3.43	2.82	2.19			
	NT2RP3001989	3.76	3.76	5.23	2.86	3.58	2.54			
	NT2RP3002002	6.68	6.68	9.47	6.25	8.85	3.86			
	NT2RP3002004	5.02	5.02	6.23	3.79	5.74	3.55			
30	NT2RP3002007	1.29	1.29	2.3	3.46	4.05	1.69			
	NT2RP3002014	1.38	1.38	6.23	5.04	6.24	4.21			
	NT2RP3002015	3.61	3.61	10.33	14.17	9.94	8.85			
	NT2RP3002033	1.54	1.54	5.03	7.29	5.03	3.65			
	NT2RP3002045	1.89	1.89	5.29	4.67	4.36	2.5			
35	NT2RP3002054	5.26	5.26	8.12	6.27	9.17	5.42			
	NT2RP3002056	5.67	5.67	5.52	4.24	4.24	2.7	*	-	
	NT2RP3002057	4.35	4.35	3.5	2.87	2.41	0.81	*	-	
	NT2RP3002061	4.71	4.71	13.94	8.64	8.9	10.74			
	NT2RP3002062	0.8	0.8	2.42	3.58	3.26	1.11			
40	NT2RP3002063	5.61	5.61	10.31	9.29	9.3	7.31			
	NT2RP3002064	2.6	2.6	3.37	2.72	3.74	2.52			
	NT2RP3002071	1.6	1.6	3.91	1.99	3.29	1.45			
	NT2RP3002073	6.47	6.47	9.55	10.45	11.13	8.64			
	NT2RP3002074	4.2	4.2	7.25	6.33	7.82	4.24			
45	NT2RP3002075	7.58	7.58	11.93	21.64	30.17	18.15	*	+	
	NT2RP3002077	3.81	3.81	5.95	2.48	3.05	2.78			
	NT2RP3002081	4.25	4.25	7.55	13.22	12.62	11.13	**	+	
	NT2RP3002086	3.86	3.86	9.77	5.59	8.66	6.95			
50	NT2RP3002094	7.34	7.34	10.28	13.84	14.79	11.67	*	+	
	NT2RP3002096	1.98	1.98	4.53	1.28	3.12	1.73			
	NT2RP3002097	3.77	3.77	6.16	6.1	8.34	6.88			
	NT2RP3002098	1.61	1.61	4.3	1.04	1.8	1.46			
	NT2RP3002102	2	2	4.86	3.11	3.4	3.16			
55	NT2RP3002106	2.74	2.74	4.98	2.83	4.9	2.51			

EP 1 130 094 A2

	NT2RP3002108	3.69	3.69	7.8	3.11	3.39	3.15
5	NT2RP3002109	12.49	12.49	32.04	31.61	27.15	25.12
	NT2RP3002110	36.38	36.38	54.93	55.24	58.94	46.55
	NT2RP3002113	11.15	11.15	13.99	10.66	15.22	11.44
	NT2RP3002120	2.22	2.22	4.42	2.31	4.13	2.7
10	NT2RP3002121	5.93	5.93	14.39	13.38	14.39	15.06
	NT2RP3002126	34.03	34.03	108.96	121.18	130.55	142.49 * +
	NT2RP3002128	4.06	4.06	8.23	3.36	6.87	3.92
	NT2RP3002130	8.29	8.29	18.59	11.69	10.7	14.03
	NT2RP3002133	14.24	14.24	18.31	10.06	8.3	19.51
15	NT2RP3002136	10.32	10.32	15.42	12.49	17.64	17.49
	NT2RP3002140	3.13	3.13	6.35	6.15	3.9	4.16
	NT2RP3002142	16.86	16.86	50.85	56.54	81.25	62.65 * +
	NT2RP3002146	4	4	7.22	5.14	9.31	6.56
	NT2RP3002147	3.8	3.8	10.45	6.06	7.4	6.2
	NT2RP3002151	5.62	5.62	10.64	6.27	4.43	7.33
20	NT2RP3002155	1.62	1.62	3.27	2.01	4.98	0.8
	NT2RP3002156	3.15	3.15	4.82	2.55	4.08	2.42
	NT2RP3002160	1.57	1.57	3.43	1.36	3.43	1.56
	NT2RP3002163	20.86	20.86	55.1	35.13	44.03	32.6
	NT2RP3002165	4.17	4.17	3.67	6.21	8.31	4.86
	NT2RP3002166	4.04	4.04	10.53	7.76	8.79	5.58
25	NT2RP3002173	2.24	2.24	5.75	2.95	3.34	3.53
	NT2RP3002174	8.41	8.41	15.8	13.21	7.82	14.77
	NT2RP3002181	1.1	1.1	3.46	1.87	3.51	1.61
	NT2RP3002185	2.69	2.69	4.51	2.94	4.35	2.61
30	NT2RP3002193	5.51	5.51	13.38	16.39	15.35	11.36
	NT2RP3002204	5.66	5.66	12.49	17.04	24.14	18.95 * +
	NT2RP3002244	4.03	4.03	8.29	5.28	6.11	4.8
	NT2RP3002248	5.42	5.42	11.1	3.19	11.78	6.52
	NT2RP3002253	2.61	2.61	9.3	9.66	11.26	6.18
35	NT2RP3002255	11.07	11.07	26.56	22.78	11.53	20.93
	NT2RP3002264	3.06	3.06	5.54	5.88	7.37	4.07
	NT2RP3002267	1.26	1.26	4.33	3.1	4.65	1.82
	NT2RP3002273	7.51	7.51	12.98	10.15	13.8	12.11
	NT2RP3002276	5.22	5.22	7.89	3.08	7.68	3.48
40	NT2RP3002281	6.37	6.37	6.83	7.45	8.46	3.44
	NT2RP3002286	3	3	4.79	3.54	4.34	3.88
	NT2RP3002297	10.62	10.62	29.36	22.26	20.57	23.93
	NT2RP3002301	5.73	5.73	13.24	9.47	7.55	6.21
	NT2RP3002303	3.01	3.01	6.39	5.29	6.65	4.58
45	NT2RP3002304	2.66	2.66	7.17	6.3	7.3	4.91
	NT2RP3002309	2.3	2.3	7.18	9.26	13	4.39
	NT2RP3002311	4.54	4.54	6.67	3.17	4.02	1.83
	NT2RP3002315	15.27	15.27	20.91	25.82	33.13	21.82
50	NT2RP3002319	2.37	2.37	5.06	3.07	3.51	2.38
	NT2RP3002324	8.97	8.97	61.42	49.85	51.23	55.4
	NT2RP3002330	4.74	4.74	8.33	10.31	8.24	8.15
	NT2RP3002333	5.13	5.13	14.32	13.14	13.65	8.12
	NT2RP3002337	2.61	2.61	5.14	4.8	5.57	4.87
	NT2RP3002342	5.16	5.16	11.56	5.52	7.51	6.43
55	NT2RP3002343	3.38	3.38	7.29	5.8	7.03	4.13

EP 1 130 094 A2

	NT2RP3002351	4.32	4.32	4.55	4.38	3.9	2.55
5	NT2RP3002352	6.3	6.3	8.01	4.4	6.76	4.31
	NT2RP3002353	3	3	4.85	4.87	6.18	5.9
	NT2RP3002362	5	5	11.74	15.86	11.03	10.49
	NT2RP3002363	2.41	2.41	3.67	5.53	6.17	2.32
	NT2RP3002377	2.61	2.61	5.47	6.8	7.31	4.73
10	NT2RP3002377	4.47	4.47	7.73	11.4	5.31	7.09
	NT2RP3002394	5.58	5.58	7.35	7.82	10.17	4.46
	NT2RP3002397	3.77	3.77	4.81	2.7	3.12	1.68 * -
	NT2RP3002399	4.61	4.61	7.69	14.65	13.02	16.16 ** +
	NT2RP3002402	2.84	2.84	6.99	8.94	8.7	6.99
15	NT2RP3002404	2.88	2.88	5.6	3.12	3.73	1.83
	NT2RP3002410	4.85	4.85	15.65	17.05	14.13	10.65
	NT2RP3002411	2.98	2.98	5.68	3.7	5.29	2.85
	NT2RP3002414	5.62	5.62	9.35	10.28	6.81	7.92
	NT2RP3002430	5.11	5.11	14.63	18.24	19.29	14.51
20	NT2RP3002448	5.4	5.4	4.6	4.35	5.25	3.62
	NT2RP3002454	7.3	7.3	15.31	12.9	12.71	9.32
	NT2RP3002455	4.62	4.62	12.11	14.31	9.11	13.25
	NT2RP3002456	3.21	3.21	7.75	7.09	6.57	5.9
	NT2RP3002462	2.79	2.79	4.16	4.94	6.17	4.79 * +
25	NT2RP3002469	3.84	3.84	6.38	9.24	6.78	8.07 * +
	NT2RP3002470	6.7	6.7	14.71	17.86	16.99	13.48
	NT2RP3002484	4.01	4.01	6.86	6.81	8.01	4.59
	NT2RP3002491	3.62	3.62	4.1	2.05	2.51	1.46 ** -
	NT2RP3002494	79.24	79.24	131.02	118.47	163.2	105.2
30	NT2RP3002497	1.07	1.07	1.57	2.37	1.39	1.37
	NT2RP3002500	1.23	1.23	1.13	2.72	2.02	2.07 ** +
	NT2RP3002501	5.25	5.25	8.49	8.45	8.11	9.69
	NT2RP3002512	2.85	2.85	3.97	3.3	2.74	3.57
	NT2RP3002529	3.94	3.94	7.5	6.59	5.14	5.85
35	NT2RP3002533	7.95	7.95	10.26	9.79	10.51	8.18
	NT2RP3002539	4.39	4.39	4.32	5.66	6.61	2.85
	NT2RP3002540	5.24	5.24	5.5	3.48	4.76	3.65 * -
	NT2RP3002543	3.44	3.44	7.17	4.93	6.21	5.31
	NT2RP3002545	7.34	7.34	7.46	5.17	5.52	6.8 * -
40	NT2RP3002549	3.27	3.27	7.8	4.98	6.11	4.54
	NT2RP3002552	3.05	3.05	6.04	4.17	5.81	4.06
	NT2RP3002558	9.54	9.54	9.39	9.93	4.26	11.27
	NT2RP3002565	1.94	1.94	4.83	1.73	2.48	1.52
	NT2RP3002566	3.62	3.62	7.02	4.03	8.51	3.65
45	NT2RP3002571	2.53	2.53	4.85	3.77	5.41	3.74
	NT2RP3002572	2.98	2.98	5.28	4.75	4.74	5.21
	NT2RP3002573	4.31	4.31	11.38	7.06	9.48	7.06
	NT2RP3002577	1.57	1.57	4.61	2.71	2.32	1.9
	NT2RP3002579	3.92	3.92	6.41	4.03	7.75	11.16
50	NT2RP3002582	5.02	5.02	7.17	11.51	14.07	8.45 * +
	NT2RP3002587	1.9	1.9	3.13	2.68	3.04	1.97
	NT2RP3002590	3.16	3.16	5.65	9.06	10.39	8.06 ** +
	NT2RP3002602	3.02	3.02	4.24	3.95	5.85	3.77
	NT2RP3002603	71.53	71.53	214.41	268.41	257.84	298.26 * +
55	NT2RP3002621	1.95	1.95	3.42	2.13	5.13	1.85

EP 1 130 094 A2

	NT2RP3002622	2.63	2.63	7.38	3.7	7.36	4.67		
5	NT2RP3002624	2.29	2.29	7.4	4.04	4.9	3.64		
	NT2RP3002628	6.36	6.36	16.17	19.57	22.15	16.21		
	NT2RP3002629	8.96	8.96	13.58	15.4	18.26	15.57	*	+
	NT2RP3002631	1.95	1.95	1.67	0.91	1.65	1.69		
10	NT2RP3002647	4.04	4.04	4.01	5.44	7.16	4.6		
	NT2RP3002649	2.99	2.99	5.99	2.15	5.84	3.23		
	NT2RP3002650	3.32	3.32	11.62	4.98	8.53	6.88		
	NT2RP3002652	2.27	2.27	6.59	4.91	6.83	4.25		
	NT2RP3002654	3.05	3.05	7.5	5.58	5.4	4.2		
	NT2RP3002657	14.14	14.14	13.87	17.27	26.08	18.87		
15	NT2RP3002659	1.92	1.92	6.01	3.91	5.78	3.47		
	NT2RP3002660	3.09	3.09	4.84	3.77	7.72	3.52		
	NT2RP3002663	2.39	2.39	3.33	2.54	3.13	2.84		
	NT2RP3002664	2.74	2.74	7.28	3.65	2.56	2.13		
	NT2RP3002667	2.92	2.92	6.59	6.63	5.46	5.35		
	NT2RP3002671	2.37	2.37	5.02	3.91	5.52	4.11		
20	NT2RP3002682	6.34	6.34	20.62	14.37	17.64	21.7		
	NT2RP3002684	4	4	6.34	3.32	6.16	3.18		
	NT2RP3002687	3.25	3.25	6.22	2.7	3.87	6.41		
	NT2RP3002688	3.22	3.22	4.98	2.63	3.91	2.61		
	NT2RP3002698	2.2	2.2	3.99	3.07	4.28	2.38		
25	NT2RP3002701	2.93	2.93	6.73	3.45	3.07	3.6		
	NT2RP3002705	2.17	2.17	8.01	4.36	8.76	4.72		
	NT2RP3002708	3.69	3.69	9.88	5.64	7.34	4.9		
	NT2RP3002711	6.67	6.67	7.85	7.77	7.56	6.69		
	NT2RP3002712	55.99	55.99	75.28	146.74	168.42	130.64	**	+
30	NT2RP3002713	4.31	4.31	7.06	2.66	2.19	1.87	*	-
	NT2RP3002721	5.77	5.77	10.06	11.06	16.94	8.96		
	NT2RP3002722	7.11	7.11	10.08	7.8	6.45	6.62		
	NT2RP3002723	42.31	42.31	75.85	60.39	46.74	58.76		
	NT2RP3002737	8.35	8.35	18.1	10.97	11.6	9.37		
35	NT2RP3002738	1.9	1.9	6.13	3.09	5.23	3.54		
	NT2RP3002742	14.11	14.11	23.22	30.39	28.27	27.66	*	+
	NT2RP3002744	4.09	4.09	5.24	3.92	4.92	1.71		
	NT2RP3002756	5.8	5.8	5.8	3.19	2.68	1.55	**	-
	NT2RP3002757	12	12	17.79	19.76	24.24	19.75	*	+
40	NT2RP3002758	21.11	21.11	42.35	44.47	63.91	36.38		
	NT2RP3002762	5.07	5.07	8.82	7.21	7.43	7.76		
	NT2RP3002763	1.62	1.62	4.86	3.76	4.99	2.18		
	NT2RP3002770	1.78	1.78	5.14	3.46	3.7	2.93		
	NT2RP3002771	17.04	17.04	39.53	24.93	40.21	34.4		
45	NT2RP3002785	2.42	2.42	5.45	3.36	4.09	2.66		
	NT2RP3002790	4.65	4.65	4.22	3.16	3.57	2.33	*	-
	NT2RP3002799	4.73	4.73	6.33	3.42	2.7	1.43	*	-
	NT2RP3002801	4.14	4.14	3.59	3.6	3.22	2.49		
50	NT2RP3002802	2.31	2.31	6.3	6.78	5.43	4.4		
	NT2RP3002810	2.98	2.98	5.41	7.44	12.32	13.27	*	+
	NT2RP3002818	1.5	1.5	2.44	2.18	4.16	2.47		
	NT2RP3002821	12.8	12.8	33.14	26.1	35.81	23.02		
	NT2RP3002823	3.85	3.85	8.98	4.65	5.92	3.87		
55	NT2RP3002825	5.47	5.47	13.04	13.47	19.19	7.12		

EP 1 130 094 A2

	NT2RP3002829	5.37	5.37	6.25	4.75	4.89	3.8		
5	NT2RP3002831	4.01	4.01	6.13	9.07	8.77	5.19		
	NT2RP3002836	7.33	7.33	19.42	11.56	16.91	20.66		
	NT2RP3002845	4.17	4.17	6.63	7.87	8.6	8.45	*	+
10	NT2RP3002852	3.37	3.37	7.57	7.8	8.72	8.21		
	NT2RP3002861	3.82	3.82	6.4	7.34	7.35	4.63		
	NT2RP3002869	3.66	3.66	3.26	2.49	1.86	0.49	*	-
	NT2RP3002874	11.25	11.25	21.44	25.33	31.95	25.54	*	+
15	NT2RP3002876	6.98	6.98	11.06	12.8	14.93	14.39	*	+
	NT2RP3002877	4.7	4.7	5.96	3.3	5.24	2.53		
	NT2RP3002887	0.47	0.47	3.42	2.81	3.53	3.91		
	NT2RP3002900	6.46	6.46	19.64	21.86	21.54	22.3		
20	NT2RP3002902	4.01	4.01	10.25	11.72	8.52	8.06		
	NT2RP3002909	2.61	2.61	6.19	6.67	5.38	3.93		
	NT2RP3002911	3.05	3.05	3.68	3.09	3.73	2.24		
	NT2RP3002948	4.09	4.09	4.81	2.73	4.44	2.07		
	NT2RP3002953	3.85	3.85	3.6	2.27	2.52	0.84	*	-
25	NT2RP3002955	6.55	6.55	3.78	1.93	2.47	0.86	*	-
	NT2RP3002958	5.85	5.85	11.4	16.5	10.57	16.64		
	NT2RP3002969	4.28	4.28	8.27	12.91	7.49	7.33		
	NT2RP3002972	3.55	3.55	4.82	4.41	6.18	2.29		
	NT2RP3002978	1.48	1.48	2.99	2.61	3.7	1.49		
30	NT2RP3002983	2.89	2.89	4.69	4.46	6.12	4.37		
	NT2RP3002985	4.23	4.23	17.87	13.64	20.26	11.12		
	NT2RP3002988	3.97	3.97	4.6	4.12	5.64	4.13		
	NT2RP3003000	3.11	3.11	3.46	2.46	3.2	1.51		
	NT2RP3003008	3.26	3.26	5.87	3.95	4.55	2.96		
35	NT2RP3003012	3.43	3.43	6.06	3.9	4.96	2.79		
	NT2RP3003015	1.35	1.35	4.9	1.5	2.5	0.54		
	NT2RP3003018	2.15	2.15	6.09	3.45	7.24	2.59		
	NT2RP3003028	3.53	3.53	7.23	3.5	5.05	4.01		
	NT2RP3003029	111.75	111.75	149.73	175.13	159.77	181.4	*	+
40	NT2RP3003032	7.06	7.06	9.05	11.87	18.84	9.94		
	NT2RP3003041	2.07	2.07	1.88	1.61	1.41	0.69		
	NT2RP3003044	3.06	3.06	7.45	5.72	6.11	7.57		
	NT2RP3003047	3.09	3.09	5.16	2.4	4.67	2.06		
45	NT2RP3003050	5.96	5.96	12.03	6.74	10.3	8.42		
	NT2RP3003053	7.46	7.46	18	14.42	17.14	13.72		
	NT2RP3003059	1.93	1.93	4.76	2.88	4.41	3.06		
	NT2RP3003061	2.8	2.8	8.59	5.49	5.68	5.16		
	NT2RP3003068	5.99	5.99	11.77	9.41	8.75	10.04		
50	NT2RP3003071	7.22	7.22	10.77	10.39	14.52	10.39		
	NT2RP3003076	2.67	2.67	9.49	5.57	6.57	4.01		
	NT2RP3003078	1.5	1.5	4.12	2.09	4.52	2.43		
	NT2RP3003081	6.21	6.21	10.54	9.94	9.6	9.97		
	NT2RP3003090	1.49	1.49	5.95	3.28	3.57	3.25		
55	NT2RP3003097	2.42	2.42	7.15	2.71	3.72	2.93		
	NT2RP3003098	2.75	2.75	4.22	2.73	3.43	1.73		
	NT2RP3003101	5.56	5.56	7.24	7.73	10.35	7.18		
	NT2RP3003109	16.11	16.11	27.38	27.36	41.03	21.91		
	NT2RP3003121	3.39	3.39	11.03	4.61	8	2.44		
	NT2RP3003133	2.09	2.09	5.78	4.93	8.58	3.96		

EP 1 130 094 A2

	NT2RP3003137	3.42	3.42	5.74	6.32	7.59	5.29
5	NT2RP3003138	2.36	2.36	5.27	5.26	5.7	3.74
	NT2RP3003139	2.53	2.53	7.8	3.15	5.74	2.7
	NT2RP3003145	5.08	5.08	32.56	25.8	29.74	19.72
	NT2RP3003150	2.03	2.03	5.17	3.56	3.76	1.97
	NT2RP3003157	2.52	2.52	8.34	6.4	10.1	4.94
10	NT2RP3003185	1.77	1.77	3.88	1.91	3.34	2.62
	NT2RP3003193	2.62	2.62	5.75	6.03	4.59	2.65
	NT2RP3003197	2.38	2.38	3.8	3.11	4.02	2.2
	NT2RP3003203	11.82	11.82	14.35	16.85	10.17	15.27
	NT2RP3003204	3.76	3.76	7.93	4.04	6.17	3.79
15	NT2RP3003210	14.48	14.48	75.3	58.97	84.6	68.66
	NT2RP3003212	5.15	5.15	9.44	9.21	10.67	7.36
	NT2RP3003213	4.16	4.16	5.68	5.15	7.02	5.44
	NT2RP3003224	1.7	1.7	4.75	2.43	2.11	2.64
	NT2RP3003226	3.25	3.25	5.68	6.57	5.94	3.63
	NT2RP3003230	7.79	7.79	11.47	12.39	8.89	6.72
20	NT2RP3003235	7.61	7.61	10.79	7.77	7.73	6.89
	NT2RP3003242	12.17	12.17	23.49	26.68	32.03	19.25
	NT2RP3003251	5.61	5.61	9.47	3.73	4.95	4.08
	NT2RP3003252	3.95	3.95	5.95	2.19	3.7	2.42
25	NT2RP3003258	4.92	4.92	7.89	19.94	24.95	15.47 ** +
	NT2RP3003260	4.54	4.54	12.34	13.46	11.52	12.68
	NT2RP3003264	1.64	1.64	5.99	3.18	4.32	1.86
	NT2RP3003273	2.18	2.18	4.93	4.57	3.58	1.72
	NT2RP3003278	1.33	1.33	4	1.31	5.12	0.63
30	NT2RP3003280	9.85	9.85	23.11	18.18	19.52	18.19
	NT2RP3003282	5.29	5.29	6.25	3.62	3.97	3.48 ** -
	NT2RP3003290	6.64	6.64	9.09	4.8	5.38	3.78 * -
	NT2RP3003301	4.01	4.01	5.73	4.31	4.59	3.23
	NT2RP3003302	1.45	1.45	2.31	2.91	2.64	1.91
35	NT2RP3003311	2.45	2.45	6.76	15.72	13.09	11.55 ** +
	NT2RP3003312	1.81	1.81	3.35	3.73	3.87	2.41
	NT2RP3003313	1.61	1.61	4.2	2.91	5.4	2.87
	NT2RP3003327	1.62	1.62	6.24	4.81	4.95	3.34
	NT2RP3003330	5.13	5.13	8.01	15.68	16.13	12.78 ** +
40	NT2RP3003344	3.36	3.36	4.14	2.92	3.74	2.6
	NT2RP3003346	3.81	3.81	4.83	4.38	4.05	1.24
	NT2RP3003349	4.04	4.04	6.93	9.96	9.41	9.65 ** +
	NT2RP3003353	1.95	1.95	3.24	4.06	5.37	2.45
	NT2RP3003354	5.09	5.09	13.72	16.29	12.02	13.5
45	NT2RP3003368	3.03	3.03	4.73	4.04	4.08	2.63
	NT2RP3003375	4.1	4.1	7.4	7.41	9.67	6.62
	NT2RP3003377	4.16	4.16	3.98	2.57	3.58	1.65
	NT2RP3003384	5.77	5.77	4.55	2.83	3.43	2.56 ** -
50	NT2RP3003385	4.55	4.55	3.12	1.9	2.36	1.47 * -
	NT2RP3003396	3.93	3.93	13.63	16.4	8.38	12.32
	NT2RP3003403	1.62	1.62	2.54	3.24	4.73	1.92
	NT2RP3003409	1.18	1.18	2.97	3.3	4.48	3.03
	NT2RP3003411	4.59	4.59	15.42	14.11	15.42	10.96
	NT2RP3003420	3.79	3.79	4.36	3.68	2.13	1.85
55	NT2RP3003425	3.25	3.25	6.71	5.85	7.25	5.49

EP 1 130 094 A2

	NT2RP3003426	9.11	9.11	16.3	10.88	11.12	17.45
5	NT2RP3003427	5.95	5.95	10.09	9.15	13.58	8.03
	NT2RP3003433	2.55	2.55	6.26	8.42	9.57	4.87
	NT2RP3003437	22.12	22.12	49.85	51.81	44	38.77
	NT2RP3003448	1.88	1.88	4.24	3.5	3.83	2.63
	NT2RP3003455	5.23	5.23	12.16	11.8	9.96	8.44
10	NT2RP3003462	4.96	4.96	10.07	10.76	8.25	7.08
	NT2RP3003464	3.79	3.79	5.03	3.01	4.76	1.2
	NT2RP3003469	4.1	4.1	7.77	6.62	7.56	5.07
	NT2RP3003473	22.06	22.06	36.6	54.82	69.25	56.46 ** +
	NT2RP3003474	8.26	8.26	23.04	13.23	12.04	13.52
15	NT2RP3003475	2.84	2.84	4.04	4.55	4.45	3.28
	NT2RP3003490	2.7	2.7	5.81	4.21	4.43	3.12
	NT2RP3003491	2.26	2.26	3	2.14	2.75	1.26
	NT2RP3003493	11.75	11.75	30.77	34.59	28.9	34.45
	NT2RP3003500	4.93	4.93	5.26	4.99	7.46	3.65
20	NT2RP3003527	2.73	2.73	3.09	2.42	2.92	1.72
	NT2RP3003532	2.7	2.7	1.81	2.14	3.33	2.13
	NT2RP3003535	3.14	3.14	4.37	1.92	3.4	2.19
	NT2RP3003536	3.04	3.04	5.95	3.45	5.2	4.97
	NT2RP3003543	2.61	2.61	6.24	3.21	4.81	3.83
25	NT2RP3003549	1.43	1.43	6.66	2.18	4.07	1.55
	NT2RP3003552	1.8	1.8	5.76	0.64	0.84	1.58
	NT2RP3003555	4.4	4.4	14.14	12.16	17.43	16.23
	NT2RP3003559	2.81	2.81	6.7	3.88	5.11	5.49
	NT2RP3003564	3.11	3.11	5.9	2.24	4.6	5.25
30	NT2RP3003572	2.1	2.1	4.21	1.88	3.02	2.32
	NT2RP3003576	5.88	5.88	10.15	11.32	8.98	9.22
	NT2RP3003587	7.39	7.39	12.41	10.01	12.71	12.75
	NT2RP3003589	15.33	15.33	22.45	23.89	23.75	26.58
	NT2RP3003592	7.77	7.77	10.4	8.42	14.48	9.74
35	NT2RP3003593	8.16	8.16	13.62	13.47	13.84	110.49
	NT2RP3003614	2.66	2.66	8.18	3.11	4.48	7.09
	NT2RP3003621	1.64	1.64	3.91	2.1	3.68	2.96
	NT2RP3003625	1.54	1.54	6.94	3.79	5.09	4.96
	NT2RP3003627	6.73	6.73	20.05	16.23	13.97	25.71
40	NT2RP3003636	3.3	3.3	7.74	5.99	3.79	10.4
	NT2RP3003642	7.12	7.12	12.2	12.85	13.15	15.83
	NT2RP3003645	2.91	2.91	6.07	2.23	2.42	3.53
	NT2RP3003648	2.88	2.88	3.71	2.17	2.44	3.13
45	NT2RP3003649	2.7	2.7	9.28	6.36	5.11	12.04
	NT2RP3003650	2.65	2.65	4.25	4.38	3.16	4.09
	NT2RP3003656	1.69	1.69	3.23	1.94	4.12	3
	NT2RP3003659	2.76	2.76	4.56	2.14	4.8	4.88
	NT2RP3003662	31.39	31.39	53.28	34.35	14.68	34.64
50	NT2RP3003664	3.56	3.56	6.5	6.18	5.45	6.55
	NT2RP3003665	1.89	1.89	4.83	2.07	2.8	4.96
	NT2RP3003671	2.88	2.88	4.33	3.03	2.6	4.29
	NT2RP3003672	4.78	4.78	9.8	10.69	14.73	16.35 * +
	NT2RP3003673	4.98	4.98	9.42	5.35	3.05	4.12
55	NT2RP3003679	40.1	40.1	95.75	69.92	23.86	83.88
	NT2RP3003680	3.13	3.13	5.38	3.96	4.58	5.88

EP 1 130 094 A2

	NT2RP3003686	2.22	2.22	4.43	2.84	4.85	2.25				
5	NT2RP3003689	4.05	4.05	9.69	5.94	5.63	8.27				
	NT2RP3003697	13.79	13.79	120.74	108.93	77.49	68.74				
	NT2RP3003701	2.7	2.7	5.17	2.58	3.05	2.57				
10	NT2RP3003704	2.99	2.99	6.96	7.09	7.61	6.96				
	NT2RP3003714	1.39	1.39	4.25	1.68	0.89	1.14				
	NT2RP3003716	2.05	2.05	4.23	3	2.29	2.24				
15	NT2RP3003721	1.83	1.83	3.27	1.85	3.45	2.18				
	NT2RP3003722	3.45	3.45	8.18	8.08	7.79	5.45				
	NT2RP3003726	3.5	3.5	4.9	2.77	4.51	2.32				
	NT2RP3003729	4.1	4.1	8.53	4.22	5.44	4.6				
20	NT2RP3003731	5.06	5.06	6.98	4.19	3.54	7.45				
	NT2RP3003740	2.58	2.58	5.08	2.42	2.48	2.94				
	NT2RP3003746	3.63	3.63	8.14	6.7	5.94	6.59				
	NT2RP3003749	0.67	0.67	2.58	1.55	2.08	1.73				
	NT2RP3003754	3.32	3.32	7.31	4.66	5.87	5.81				
25	NT2RP3003759	1.16	1.16	4.44	2.49	4.41	1.43				
	NT2RP3003764	3.97	3.97	7.08	6.85	7.41	5.06				
	NT2RP3003766	6.93	6.93	7.84	3.3	5.87	3.79	*	-		
	NT2RP3003767	11.19	11.19	16.8	14.83	21.08	16.97				
	NT2RP3003778	3.36	3.36	4.89	4.46	5.55	4.27				
	NT2RP3003779	4.05	4.05	15.26	13.02	8.74	10.52				
30	NT2RP3003783	9.25	9.25	21.72	22.42	13.65	18.76				
	NT2RP3003787	2.15	2.15	4.65	4.41	4.74	6.37				
	NT2RP3003789	5.12	5.12	10.16	11.63	12.19	14.96	*	+		
	NT2RP3003795	1.48	1.48	6.48	4.09	2.82	2.24				
35	NT2RP3003799	2.67	2.67	5.5	3.08	2.38	1.75				
	NT2RP3003800	4.36	4.36	5.92	4.14	4.57	6.91				
	NT2RP3003805	8.15	8.15	6.78	8.4	5.48	5.89				
	NT2RP3003809	1.94	1.94	7.2	5.83	5.4	4.82				
	NT2RP3003819	3.39	3.39	6.07	7.3	5.97	6.35				
40	NT2RP3003824	5.69	5.69	10.69	14.08	14.85	13.32	*	+		
	NT2RP3003825	9.06	9.06	16.31	12.87	16.88	16.75				
	NT2RP3003828	4.7	4.7	14.38	13.36	15.69	14.55				
	NT2RP3003831	4.01	4.01	6.38	5.77	6.54	7.23				
45	NT2RP3003833	5.12	5.12	7.5	6.44	8.88	6.96				
	NT2RP3003836	6.37	6.37	5.05	5.74	6.47	4.31				
	NT2RP3003842	2.7	2.7	9.08	6.84	6.51	7.09				
	NT2RP3003843	9.26	9.26	26.77	16.67	12.71	16.2				
	NT2RP3003844	20.38	20.38	46.56	42.84	27.94	44.32				
50	NT2RP3003846	4.04	4.04	8.45	8.94	7.18	8.05				
	NT2RP3003849	2.27	2.27	2.68	2.67	2.73	1.68				
	NT2RP3003862	28.91	28.91	45.63	32	37.58	44.88				
	NT2RP3003870	4.76	4.76	4.81	2.54	2.93	2.05	**	-		
55	NT2RP3003874	21.46	21.46	20.88	33.11	47.25	36.44	*	+		
	NT2RP3003876	1.62	1.62	8.08	5.45	7.49	6.81				
	NT2RP3003880	1.74	1.74	4.63	5.31	4.66	4.73				
	NT2RP3003889	1.69	1.69	3.04	3.41	3.53	9.53				
	NT2RP3003891	1.88	1.88	2.98	2.56	3.19	1.37				
	NT2RP3003914	3.1	3.1	7.35	6.88	5.15	7.39				
	NT2RP3003915	5.03	5.03	8.44	9.52	11.35	8.6				
	NT2RP3003918	6.79	6.79	10.39	10.04	13.71	12.42				

EP 1 130 094 A2

	NT2RP3003920	6.9	6.9	9.13	8.31	10.22	8.96
5	NT2RP3003924	2.25	2.25	9.57	6.49	5.34	6.91
	NT2RP3003932	1.41	1.41	3.85	5.17	5.26	3.85
	NT2RP3003939	3.48	3.48	11.88	9.86	14.05	11.09
	NT2RP3003940	11.34	11.34	27.33	23.54	20.59	23.06
10	NT2RP3003943	2.6	2.6	2.83	2.85	2.78	3.88
	NT2RP3003959	3.52	3.52	6.96	6.54	5.93	5.49
	NT2RP3003963	4.83	4.83	7.59	4.01	4.61	2.52
	NT2RP3003965	11.14	11.14	13.85	18.75	20.67	17.22
	NT2RP3003972	26.1	26.1	40.32	22.13	17.98	38.48
15	NT2RP3003973	2.85	2.85	4.33	1.96	3.6	3.96
	NT2RP3003979	5.89	5.89	12.53	6.92	8.49	8.84
	NT2RP3003980	3.52	3.52	9.41	9.34	8.89	7.92
	NT2RP3003982	4.2	4.2	4.63	2.44	1.6	4.61
	NT2RP3003989	6.24	6.24	4.69	9.61	5.62	16.05
	NT2RP3003992	2.13	2.13	4.89	2.47	5.12	4.8
20	NT2RP3004000	2.81	2.81	6	1.72	3.22	2.62
	NT2RP3004001	11.38	11.38	19.94	11.62	11.37	21.11
	NT2RP3004005	2.89	2.89	7.79	4.7	4.48	6.84
	NT2RP3004013	2.23	2.23	7.2	2.66	4.87	3.57
	NT2RP3004016	1.5	1.5	7.1	2.22	3.14	2.88
25	NT2RP3004025	4.02	4.02	7.69	7.48	12.19	9.01
	NT2RP3004030	7.05	7.05	12.64	13.97	15.8	17.66
	NT2RP3004041	5.65	5.65	11.38	10.48	9.57	19.81
	NT2RP3004042	15.22	15.22	102.33	97.27	103.6	99.67
	NT2RP3004044	2.13	2.13	6.51	5.14	7.21	4.22
30	NT2RP3004051	2.6	2.6	5.79	2.23	5.51	4.69
	NT2RP3004052	7.1	7.1	11.22	5.63	4.98	9.78
	NT2RP3004053	15.87	15.87	35.04	23.12	40.67	40.17
	NT2RP3004055	2.38	2.38	5.33	2.98	3.3	4.47
	NT2RP3004059	4.05	4.05	8.8	8.15	7.03	11
35	NT2RP3004063	5.13	5.13	11.23	8.78	11.27	12.33
	NT2RP3004067	4.24	4.24	8.4	6.62	6.42	4.47
	NT2RP3004070	3.58	3.58	9.92	6.26	4.4	5.47
	NT2RP3004075	4.16	4.16	11.23	12.62	11.88	13.3
40	NT2RP3004078	2.6	2.6	5.25	4.94	4.19	2.79
	NT2RP3004083	2.93	2.93	6.23	4.57	6.8	11.37
	NT2RP3004084	4.65	4.65	20.29	6.18	8.56	5.32
	NT2RP3004087	4.2	4.2	7.86	7.14	10.81	9.03
	NT2RP3004090	4.11	4.11	6.42	9	8.19	8.61
45	NT2RP3004093	2.38	2.38	7.49	4.07	3.51	4.47
	NT2RP3004095	5.02	5.02	13.11	11.57	10.17	18.55
	NT2RP3004102	3.32	3.32	5.59	5.25	4.27	3.21
	NT2RP3004110	12.74	12.74	18.66	22.12	14.31	19.97
	NT2RP3004119	3.3	3.3	7.71	3.91	4.08	3.73
50	NT2RP3004125	5.55	5.55	12.05	8.13	10.88	8.38
	NT2RP3004129	4.62	4.62	7.38	3.36	2.95	6.08
	NT2RP3004130	11.81	11.81	28.12	21.92	31.13	21.05
	NT2RP3004133	4.51	4.51	12.95	14.62	8.94	16.81
	NT2RP3004145	1.43	1.43	4.17	2.62	4.87	3.59
55	NT2RP3004148	2.67	2.67	7.07	5.26	6.24	4.5
	NT2RP3004155	2.37	2.37	4.82	4.7	4.57	6.59

EP 1 130 094 A2

	NT2RP3004165	17.94	17.94	29.96	29.58	31.82	39.18			
5	NT2RP3004179	7.34	7.34	6.72	2.71	5.41	3.3	*	-	
	NT2RP3004185	5.2	5.2	5.53	2.76	2.76	1.95	**	-	
	NT2RP3004188	4.77	4.77	10.82	7.74	11.35	7			
	NT2RP3004189	4.23	4.23	5.91	4.97	4.82	6.28			
	NT2RP3004190	2.6	2.6	5.57	5.84	4.36	5.26			
10	NT2RP3004191	14.09	14.09	23.4	31.41	29.45	30.09	*	+	
	NT2RP3004202	2.04	2.04	4.56	4.16	4.42	2.3			
	NT2RP3004205	8.75	8.75	21.54	21.27	25.35	20.28			
	NT2RP3004206	4.5	4.5	9.74	5.14	6.37	9			
	NT2RP3004207	5.19	5.19	4.99	3.09	3.25	1.77	**	-	
15	NT2RP3004209	4.74	4.74	7.74	8.2	11.23	9.08	*	+	
	NT2RP3004215	1.86	1.86	6.7	3.96	2.41	4.55			
	NT2RP3004219	5.15	5.15	11.25	10.04	8.81	13.65			
	NT2RP3004242	4.65	4.65	10.36	9.8	10.19	14.56			
	NT2RP3004246	4.5	4.5	9.39	9.18	10.95	3.8			
20	NT2RP3004253	1.89	1.89	4.85	3.64	4.99	2.8			
	NT2RP3004258	5.45	5.45	10.89	12.77	11.07	11.39			
	NT2RP3004262	4.26	4.26	5.71	2.63	2.99	2.01	*	-	
	NT2RP3004275	5.59	5.59	3.43	1.4	2.97	2.34	*	-	
	NT2RP3004282	5.45	5.45	68.08	51.29	52.72	53.57			
25	NT2RP3004289	1.79	1.79	2.95	1.9	2.18	3.99			
	NT2RP3004294	2.74	2.74	6.02	6.95	6.93	7.24	*	+	
	NT2RP3004298	8.76	8.76	48.63	46.33	60.89	50.83			
	NT2RP3004309	3.3	3.3	6.46	5.2	5.22	5.31			
30	NT2RP3004321	3.71	3.71	6.11	3.29	3.74	3.34			
	NT2RP3004322	5.61	5.61	6.86	6.06	6.43	6.56			
	NT2RP3004332	11.69	11.69	100.11	78.54	102.41	76.72			
	NT2RP3004334	1.49	1.49	6.97	8.56	6.06	9.06			
	NT2RP3004336	2.11	2.11	6.24	6.02	4.44	5.63			
	NT2RP3004338	3.09	3.09	8.41	10.22	9.52	16.47			
35	NT2RP3004341	1.81	1.81	4.56	6.13	5.17	9.13			
	NT2RP3004345	4.1	4.1	8.68	9.3	9.63	8.48			
	NT2RP3004348	5.06	5.06	11.25	13.04	10.79	12.54			
	NT2RP3004349	5	5	7.5	4.89	7.75	5.76			
	NT2RP3004355	5.57	5.57	7.09	7.55	7.07	7.18			
40	NT2RP3004356	5.76	5.76	21.51	11.29	15.14	15.56			
	NT2RP3004360	3.4	3.4	5.26	6.01	5.32	7.85			
	NT2RP3004361	2.6	2.6	6.26	7.67	7.3	8.87	*	+	
	NT2RP3004374	3.06	3.06	10.09	8.8	6.6	5.75			
45	NT2RP3004378	10.48	10.48	18.57	28.26	24.09	34.81	*	+	
	NT2RP3004399	3.88	3.88	5.77	3.53	3.17	9.06			
	NT2RP3004405	4.07	4.07	6.77	3.03	5.52	3.93			
	NT2RP3004406	5.36	5.36	6.23	5.19	6.03	6.12			
	NT2RP3004411	5.93	5.93	13.28	8.08	6.39	9.51			
50	NT2RP3004424	1.53	1.53	2.43	3.27	1.81	2.83			
	NT2RP3004428	3.03	3.03	5.36	5.07	3.82	4.09			
	NT2RP3004432	3.3	3.3	3.52	3.61	3.11	4.38			
	NT2RP3004434	3.42	3.42	8.41	7.28	9.09	7.99			
	NT2RP3004446	3.29	3.29	4.6	3.29	4.1	2.63			
55	NT2RP3004451	3.2	3.2	6.01	3.89	3.38	2.48			
	NT2RP3004454	2.96	2.96	4.16	2.69	3.5	2.5			

EP 1 130 094 A2

	NT2RP3004466	3.5	3.5	7.89	5.25	3.85	5.61	
5	NT2RP3004470	7.42	7.42	24.53	18.4	16.35	24.72	
	NT2RP3004472	2.49	2.49	4.4	3.97	3.84	3.88	
	NT2RP3004475	1.71	1.71	5.52	2.72	5.93	3.9	
	NT2RP3004480	14.12	14.12	17.04	18.94	10.5	18.82	
	NT2RP3004481	5.42	5.42	11.37	5.04	7.37	12.39	
	NT2RP3004490	2.66	2.66	8.45	3.92	7.03	8.25	
10	NT2RP3004496	4.8	4.8	14.38	7.22	9.3	11.08	
	NT2RP3004498	6.39	6.39	21.39	16.86	15.11	18.92	
	NT2RP3004503	2.78	2.78	9.34	4.85	6.23	5.88	
	NT2RP3004504	3.91	3.91	11.09	6.05	10.67	11.52	
	NT2RP3004505	17.38	17.38	28.56	37.35	26.72	37.82	
15	NT2RP3004507	1.57	1.57	6.6	2.52	5.52	1.68	
	NT2RP3004519	4.9	4.9	7.73	4.93	8.36	8.75	
	NT2RP3004524	10.04	10.04	29.21	26.88	26.43	29.62	
	NT2RP3004527	3.03	3.03	3.22	1.29	2.23	2.08	*
20	NT2RP3004534	3.08	3.08	10.44	5.58	12	7.38	
	NT2RP3004539	4.45	4.45	12.17	9.8	8.97	12	
	NT2RP3004541	2.65	2.65	11.06	5.48	9.44	8.25	
	NT2RP3004544	3.54	3.54	8.89	6.62	5.24	9.48	
	NT2RP3004551	3.46	3.46	6.75	6.6	6.6	6.98	
25	NT2RP3004552	2.76	2.76	4.33	2.84	3.22	4.98	
	NT2RP3004557	5.68	5.68	8.73	9.74	15.44	13.16	* +
	NT2RP3004561	1.96	1.96	3.77	2.55	4.46	4.1	
	NT2RP3004566	3.09	3.09	11.55	7.2	10.05	8.79	
	NT2RP3004569	2.21	2.21	7.09	4.63	5.36	6.91	
30	NT2RP3004572	4.37	4.37	6.83	7.08	5.55	7.07	
	NT2RP3004578	2.35	2.35	5.38	4.15	4.27	3.24	
	NT2RP3004584	4.76	4.76	28.36	34.99	37.13	30.29	
	NT2RP3004588	2.38	2.38	4.89	1.6	3.7	3.28	
	NT2RP3004594	2.25	2.25	5.9	5.67	6.49	8.94	
35	NT2RP3004603	34.16	34.16	99.64	80.2	102.6	97.27	
	NT2RP3004612	4.71	4.71	12.17	5.3	3.36	5.34	
	NT2RP3004617	1.09	1.09	2.32	2.49	3.3	2.39	
	NT2RP3004618	4.61	4.61	5.9	2.49	5.21	5.9	
	NT2RP3004625	3.97	3.97	8.17	4.55	6.92	7.1	
40	NT2RP3004635	4.76	4.76	7.83	1.52	2.86	3.47	
	NT2RP3004640	10.61	10.61	62.15	59.33	67.97	48.32	
	NT2RP3004642	8.04	8.04	29.31	22.82	26.12	25.12	
	NT2RP3004647	3.5	3.5	5.65	5.89	7.35	6.88	* +
45	NT2RP3004652	1.76	1.76	10.37	4.2	3.71	4.34	
	NT2RP3004669	2.01	2.01	5.36	4.01	5.33	3.46	
	NT2RP3004670	5.04	5.04	10.58	12.4	9.19	14.23	
	NT2RP4000008	45.17	45.17	71.24	49.77	32.43	48.77	
	NT2RP4000018	11.64	11.64	14.61	11.69	14.8	14.87	
50	NT2RP4000023	6.96	6.96	8.91	4.86	7.38	5.98	
	NT2RP4000025	16.2	16.2	22.16	26.22	29.89	24.7	* +
	NT2RP4000035	6.3	6.3	12.01	11.28	15.33	11.01	
	NT2RP4000041	14.46	14.46	34.8	22.01	17.41	23.68	
	NT2RP4000049	2.64	2.64	6.34	6.59	6.88	5.3	
	NT2RP4000050	2.24	2.24	6.87	3.54	4.48	4.05	
55	NT2RP4000051	4.66	4.66	10.5	10.58	10.02	8.96	

EP 1 130 094 A2

	NT2RP4000063	20.51	20.51	33.5	26.77	31	18.33		
5	NT2RP4000065	7.54	7.54	9.24	11.85	15.01	11.47	*	+
	NT2RP4000070	6.63	6.63	5.29	3.79	4.54	3.84	*	-
	NT2RP4000074	6.55	6.55	13.63	10.29	15.39	9.52		
	NT2RP4000078	3.41	3.41	9.55	12.2	11.66	12.56	*	+
	NT2RP4000080	3.52	3.52	7.01	5.06	6.84	6.81		
10	NT2RP4000099	128.86	128.86	236.22	149.44	161.1	211.56		
	NT2RP4000102	3.55	3.55	6.48	5.27	4.97	5.54		
	NT2RP4000103	2	2	5.47	2.57	2.85	3.96		
	NT2RP4000108	4.66	4.66	7.91	9.33	10.73	10.61	*	+
	NT2RP4000109	18.89	18.89	22.84	19.87	24.15	16.14		
15	NT2RP4000111	4.56	4.56	6.38	4.87	5.27	4.85		
	NT2RP4000112	5.62	5.62	10.14	12.45	8.7	11.81		
	NT2RP4000115	2.94	2.94	3.62	4.95	7.82	10.93		
	NT2RP4000129	2.18	2.18	4.58	3.02	5.04	5.03		
	NT2RP4000137	3.36	3.36	10.05	5.34	8.72	11.4		
20	NT2RP4000138	7.21	7.21	10.91	17.75	20.19	19.17	**	+
	NT2RP4000141	3.25	3.25	6.1	5.22	4.9	3.57		
	NT2RP4000147	6.21	6.21	4.49	4.27	5.2	3.47		
	NT2RP4000150	5.96	5.96	6.93	7.33	10.41	7.06		
	NT2RP4000151	2.82	2.82	7.82	5.69	6.24	5.05		
25	NT2RP4000157	73.27	73.27	222.87	169.53	97.5	173.8		
	NT2RP4000159	2.02	2.02	5.03	3.38	5.03	2.92		
	NT2RP4000163	5.21	5.21	8.74	10.89	9.18	6.63		
	NT2RP4000167	3.26	3.26	4.35	4.32	3.22	3.69		
	NT2RP4000171	5.72	5.72	7	5.72	7.45	5.03		
30	NT2RP4000175	62.48	62.48	94.56	144.06	214.73	147.88	*	+
	NT2RP4000180	17.17	17.17	106.15	88.61	123.6	81.8		
	NT2RP4000185	7.64	7.64	31.76	31.82	23.23	34.01		
	NT2RP4000192	1.04	1.04	4.78	4.19	3.6	3.05		
	NT2RP4000194	3.13	3.13	7.53	7.58	4.98	6.36		
35	NT2RP4000196	6.81	6.81	43.94	35.57	46.56	41.91		
	NT2RP4000210	5.63	5.63	9.71	9.96	8.35	9.27		
	NT2RP4000212	5.59	5.59	8.88	8.57	8.41	9.08		
	NT2RP4000214	5.53	5.53	10.21	5.72	6.68	11.29		
	NT2RP4000216	8.89	8.89	7.36	7	12.63	10.08		
40	NT2RP4000218	3.45	3.45	9.78	7.25	6.07	5.77		
	NT2RP4000223	21.18	21.18	177.28	121.8	125.75	125.3		
	NT2RP4000243	16.52	16.52	54.51	42.94	41.61	51.74		
	NT2RP4000246	17.75	17.75	37.97	26.43	11.42	27.5		
	NT2RP4000250	16.86	16.86	31.23	24.92	23.85	26.39		
45	NT2RP4000256	4.38	4.38	8.45	4.99	6.44	4.67		
	NT2RP4000257	32.45	32.45	44.22	48.67	57.52	39.19		
	NT2RP4000259	7.07	7.07	6.96	8.48	13.07	9.08		
	NT2RP4000261	4.18	4.18	8.13	4.07	4.55	6.48		
	NT2RP4000262	8.36	8.36	11.02	7.11	10.05	7.64		
50	NT2RP4000263	2.6	2.6	5.14	3.47	3.67	3.78		
	NT2RP4000280	5.84	5.84	11.62	9.05	11.58	14.23		
	NT2RP4000286	4.73	4.73	10.16	4.38	6.77	11.94		
	NT2RP4000290	5.77	5.77	5.42	3.18	3.19	5.5		
	NT2RP4000291	42.53	42.53	73.59	62.12	70.23	70.61		
55	NT2RP4000301	3.31	3.31	20.59	22.93	34.62	26.63	*	+

EP 1 130 094 A2

	NT2RP4000312	7.76	7.76	45.27	39.01	43.59	45.92
5	NT2RP4000321	3.73	3.73	8.16	7.88	7.14	9.75
	NT2RP4000323	1.44	1.44	4.26	2.27	2.55	2.12
	NT2RP4000324	7.77	7.77	16.76	8.33	10.2	11.08
	NT2RP4000334	20.97	20.97	77.78	63.81	71.76	68.24
	NT2RP4000343	2.48	2.48	5.54	1.57	3.16	2.38
10	NT2RP4000348	3.4	3.4	10.81	8.38	6.75	13.2
	NT2RP4000349	1.78	1.78	0.83	0.37	0.72	2.48
	NT2RP4000355	3.98	3.98	14.84	7.18	9.13	9.04
	NT2RP4000356	8.3	8.3	22.64	9.22	11.44	21.13
	NT2RP4000360	3.04	3.04	6.98	5.06	5.43	4.73
15	NT2RP4000367	2.18	2.18	3.72	2.04	2.58	2.83
	NT2RP4000370	4.21	4.21	7.51	3.62	7.12	5.99
	NT2RP4000373	3.33	3.33	5.18	3.19	5.23	2.95
	NT2RP4000376	4.2	4.2	5.5	4.85	5.53	6.5
	NT2RP4000381	1.97	1.97	6.46	4.31	7.01	5.59
20	NT2RP4000388	85.82	85.82	204.63	128.93	93.38	116.03
	NT2RP4000390	12.16	12.16	94.1	78.97	76.6	82.02
	NT2RP4000393	8.66	8.66	9.77	9.09	5.99	10.79
	NT2RP4000398	5.51	5.51	26.52	22.08	28.3	26.61
	NT2RP4000406	6.68	6.68	15.61	12.95	15.02	10.08
25	NT2RP4000407	6.17	6.17	11.52	9.41	14.74	9.13
	NT2RP4000413	1.79	1.79	3.63	1.15	2.35	2.12
	NT2RP4000415	7.59	7.59	26.11	18.6	21.68	21.68
	NT2RP4000417	7.76	7.76	26.64	14.47	12.79	19.19
	NT2RP4000423	3.52	3.52	7.56	7	6.98	6.46
30	NT2RP4000424	2.51	2.51	7.2	3.07	5.03	3.27
	NT2RP4000447	10.3	10.3	64.21	64.91	71.82	68.48
	NT2RP4000448	5.59	5.59	6.67	4.32	3.56	6.27
	NT2RP4000449	5.67	5.67	20.48	14.2	19.45	14.67
	NT2RP4000453	3.53	3.53	6.32	9.02	10.32	10.12
35		**	+				
	NT2RP4000455	2.64	2.64	3.98	1.81	1.75	2.4
	NT2RP4000456	12.57	12.57	21.7	14.7	9.86	13.58
	NT2RP4000457	1.54	1.54	7.12	3.9	7.55	2.98
	NT2RP4000461	5.7	5.7	9.84	7.65	6.41	4.6
40	NT2RP4000462	11.76	11.76	15.32	11.86	11.53	17.37
	NT2RP4000463	10.2	10.2	52.59	50.66	69.3	48.36
	NT2RP4000471	6.36	6.36	10.74	5.74	6.23	4.98
	NT2RP4000472	3.97	3.97	4.41	1.27	1.27	1.66
	NT2RP4000476	27.14	27.14	52.56	74.95	94.93	65.35
		*	+				
45	NT2RP4000480	11.56	11.56	29.27	19.08	9.95	26.66
	NT2RP4000481	2.29	2.29	4.76	3.73	4.16	4.33
	NT2RP4000483	1.38	1.38	7.59	7.58	7.85	6.26
	NT2RP4000487	1.54	1.54	4.9	2.26	3.17	0.91
	NT2RP4000496	2.16	2.16	4.98	2.95	4.07	3.65
50	NT2RP4000497	17.15	17.15	22.33	34.9	44.46	29.9
		*	+				
	NT2RP4000498	10.46	10.46	21.39	20.15	30.33	24.49
	NT2RP4000500	2.43	2.43	3.21	2.03	1.49	1.39
		*	-				
	NT2RP4000507	5.63	5.63	9.02	12.49	10.62	17.51
		*	+				
	NT2RP4000515	12.85	12.85	88.89	90.3	101.29	96.12
55	NT2RP4000516	8.77	8.77	26.09	19.63	21.76	21.82
	NT2RP4000517	3.22	3.22	5.73	4.69	5.89	4.79

EP 1 130 094 A2

	NT2RP4000518	3.42	3.42	7.4	4.47	6.05	3.82				
5	NT2RP4000519	2.9	2.9	5.76	2.18	2.22	1.77				
	NT2RP4000524	4.2	4.2	3.44	2.05	1.72	1.3	**	-		
	NT2RP4000528	3.67	3.67	3.06	3.01	3.27	8.01				
	NT2RP4000537	35.4	35.4	62.6	36.23	30.93	44.52				
	NT2RP4000541	2.04	2.04	2.45	3.34	4.33	3.09	*	+		
10	NT2RP4000543	2.93	2.93	8.94	7.96	9.72	8.75				
	NT2RP4000545	4.03	4.03	6.38	4.99	6.43	4.78				
	NT2RP4000546	3.34	3.34	5.93	5.53	4.9	6.03				
	NT2RP4000549	23.81	23.81	56.43	41.6	51.57	38.82				
	NT2RP4000556	7.36	7.36	13.04	14.69	15.54	12.07				
15	NT2RP4000557	6.1	6.1	4.53	1.82	3.97	6.27				
	NT2RP4000558	30.12	30.12	94.23	68.16	57.01	73.2				
	NT2RP4000560	14.8	14.8	52.31	49.75	58.69	56.12				
	NT2RP4000568	1.72	1.72	3.83	5.6	6.08	4.46	*	+		
	NT2RP4000583	11.61	11.61	20.2	23.65	14.97	20.56				
20	NT2RP4000585	3.04	3.04	4.14	3.12	2.55	3.24				
	NT2RP4000588	8.65	8.65	12.77	14.58	16.96	13.55	*	+		
	NT2RP4000590	24.89	24.89	41.97	41.86	50.81	32.65				
	NT2RP4000599	4.29	4.29	3.24	2.44	2.23	3.59				
	NT2RP4000603	14.08	14.08	33.32	31.06	21.01	29.12				
25	NT2RP4000607	2.41	2.41	10.04	4.45	7.87	15.35				
	NT2RP4000614	6.14	6.14	15.21	15.57	12.53	15.19				
	NT2RP4000634	6.61	6.61	11	7.78	9.84	10.31				
	NT2RP4000638	3.59	3.59	7.77	8.45	5.8	4.73				
	NT2RP4000648	3.13	3.13	4.26	2.54	2.69	2.19				
30	NT2RP4000657	9.94	9.94	15.38	15.95	18.93	14.49				
	NT2RP4000691	5.76	5.76	5.82	4.92	7.47	7.73				
	NT2RP4000697	3.74	3.74	8.5	5.55	6.56	6.12				
	NT2RP4000704	8.91	8.91	47.2	44.17	54.81	38.14				
	NT2RP4000710	40.22	40.22	98.85	90.4	59.28	83.71				
35	NT2RP4000713	4.35	4.35	19.92	16.67	20.85	15.52				
	NT2RP4000724	6.29	6.29	12.5	8.19	9.81	7.83				
	NT2RP4000725	3.61	3.61	4	1.88	1.74	2.33	**	-		
	NT2RP4000728	10.13	10.13	41.12	43.53	66.46	39.83				
	NT2RP4000737	4.07	4.07	2.15	3.63	3.09	3.28				
40	NT2RP4000739	5.07	5.07	7.71	4.61	3.63	5.84				
	NT2RP4000749	2.4	2.4	5.29	2.59	3.97	1.68				
	NT2RP4000769	4.93	4.93	10.12	4.67	6.27	6.2				
	NT2RP4000774	3.34	3.34	8.87	5.12	6.63	4.27				
	NT2RP4000781	2.15	2.15	5.12	2.06	2.26	1.55				
45	NT2RP4000783	6.81	6.81	15.16	13.48	15.44	12.67				
	NT2RP4000787	1.45	1.45	2.27	0.31	0.51	0.54	*	-		
	NT2RP4000788	3.58	3.58	23.26	16	18.3	18.73				
	NT2RP4000792	3.68	3.68	5.64	5.5	5.8	9.45				
	NT2RP4000809	43.7	43.7	56.09	46.75	50.47	81.62				
50	NT2RP4000817	3.65	3.65	7.83	7.92	7.25	5.82				
	NT2RP4000821	31.34	31.34	38.66	28.32	33.11	25.22				
	NT2RP4000822	2.46	2.46	5.91	4.29	6.19	2.6				
	NT2RP4000823	697.74	697.74	741.12	747.48	923.16	1026.8	947.85			
55	NT2RP4000831	9.98	9.98	61.97	44.37	68.47	50.69				
	NT2RP4000833	3.19	3.19	11.26	6.73	7.19	11.91				

EP 1 130 094 A2

	NT2RP4000837	1.41	1.41	4.03	1.56	3.65	2.29		
5	NT2RP4000839	12.23	12.23	97.13	79.71	85.74	86.06		
	NT2RP4000846	3.8	3.8	10.13	4.65	3.46	6.65		
	NT2RP4000848	4.63	4.63	10.74	8.65	8.58	6.07		
	NT2RP4000855	2.91	2.91	4.7	4	3.85	3.43		
	NT2RP4000863	3.08	3.08	4.33	3.11	5.3	3.78		
10	NT2RP4000865	6.43	6.43	25.36	20.09	39.64	21.24		
	NT2RP4000873	9.64	9.64	88.25	63.22	69.65	71.33		
	NT2RP4000874	1.76	1.76	3.98	2.37	3.67	2.03		
	NT2RP4000875	3.31	3.31	9.24	6.88	6.52	7.19		
	NT2RP4000878	24.17	24.17	42.53	28.01	16.35	29.04		
15	NT2RP4000879	2.56	2.56	5.1	2.95	5.29	2.62		
	NT2RP4000880	5.17	5.17	21.59	20.97	27.22	16.8		
	NT2RP4000891	81.07	81.07	192.57	252.29	351.53	221.08	*	+
	NT2RP4000894	5.16	5.16	9.81	8.53	4.8	6.97		
	NT2RP4000898	0.86	0.86	2.74	1.88	2.14	1.64		
20	NT2RP4000899	9.63	9.63	29.48	24.01	20.85	23.95		
	NT2RP4000907	2.14	2.14	3.58	1.74	4.04	0.81		
	NT2RP4000908	4.62	4.62	9.67	7.51	5.9	5.87		
	NT2RP4000910	14.4	14.4	104.68	124.04	197.74	160.9	*	+
	NT2RP4000918	2.85	2.85	4.76	4.73	4.26	5.35		
25	NT2RP4000925	3.9	3.9	5.53	2.81	3.15	1.86		
	NT2RP4000927	1.99	1.99	2.5	0.46	1.08	0.6	**	-
	NT2RP4000928	3.11	3.11	6.8	4.48	4.22	5.18		
	NT2RP4000929	1.44	1.44	3.68	1.94	2.86	0.84		
	NT2RP4000946	0.92	0.92	3.41	1.78	3.22	1.47		
30	NT2RP4000947	1.71	1.71	3.51	1.94	3.31	1.79		
	NT2RP4000949	4.94	4.94	7.84	3.88	5.48	2.38		
	NT2RP4000955	4.17	4.17	6.34	2.07	2.86	0.54	*	-
	NT2RP4000959	20.55	20.55	28.14	36.21	42.82	36.14	*	+
35	NT2RP4000962	3.4	3.4	4.24	8.33	10.09	4.53		
	NT2RP4000973	8.6	8.6	16.04	10.31	8.92	9.03		
	NT2RP4000975	2.18	2.18	5.84	3.29	3.05	2.62		
	NT2RP4000979	3.83	3.83	8.67	5.55	8.13	7.1		
	NT2RP4000984	1.61	1.61	4.31	3.15	3.93	1.85		
40	NT2RP4000986	7.32	7.32	13.27	12.66	12.35	2.52		
	NT2RP4000988	5.74	5.74	8.37	4	5.2	2.63		
	NT2RP4000989	6.24	6.24	6.55	4.05	3.48	2.89	**	-
	NT2RP4000990	3.16	3.16	4	1.92	1.69	2.16	**	-
	NT2RP4000994	4.04	4.04	7.67	16.48	10.13	15.95	*	+
45	NT2RP4000996	3.54	3.54	7.49	6.77	6.52	7.38		
	NT2RP4000997	21.59	21.59	36.81	28.52	15.18	34.38		
	NT2RP4001001	5.53	5.53	9.17	16.66	18.38	15.09	**	+
	NT2RP4001004	1.71	1.71	4.88	2.84	3.09	1.37		
	NT2RP4001006	3.46	3.46	8.12	6.85	6.52	6.13		
50	NT2RP4001009	9.3	9.3	10.45	15.44	20.46	8.25		
	NT2RP4001010	7.33	7.33	9.13	7.38	9.75	6.68		
	NT2RP4001013	23.29	23.29	50.16	30.87	28.1	30.91		
	NT2RP4001029	2.49	2.49	5.95	4.05	2.84	3.63		
	NT2RP4001036	7.55	7.55	13.55	9.11	11.51	13.16		
55	NT2RP4001041	6.57	6.57	14.4	9.89	12.3	6.35		
	NT2RP4001042	4.34	4.34	8.11	9.44	12.5	8.79		

EP 1 130 094 A2

	NT2RP4001046	6.98	6.98	9.95	13.24	16.28	15.36	**	+
5	NT2RP4001050	5.28	5.28	4.81	3.79	4.64	3.35	*	-
	NT2RP4001051	6.48	6.48	8.44	5.43	6.82	5.26		
	NT2RP4001057	0.76	0.76	2.19	2.34	2.43	1.87		
	NT2RP4001063	1.48	1.48	4.39	3.34	3.53	1.8		
10	NT2RP4001064	3.51	3.51	9.18	12.02	9.13	11.57		
	NT2RP4001067	4.42	4.42	9.77	10.96	9.63	6.6		
	NT2RP4001078	2.12	2.12	3.43	2.67	2.53	1.82		
	NT2RP4001079	5.3	5.3	9.35	8.51	8.02	8.98		
15	NT2RP4001080	4.1	4.1	5.27	3.52	4.52	2.3		
	NT2RP4001086	5.08	5.08	4.19	3.93	6.64	2.85		
	NT2RP4001095	2.49	2.49	7.25	7.96	6.49	6.85		
	NT2RP4001098	0.92	0.92	3.38	3.87	2.95	3.41		
20	NT2RP4001100	6.47	6.47	24.34	20.89	20.64	16.99		
	NT2RP4001105	3.13	3.13	7.23	6.51	5.58	4.61		
	NT2RP4001110	1.75	1.75	3.5	7.07	8.35	5.29	*	+
	NT2RP4001115	9.95	9.95	17.68	20.6	18.48	15.31		
25	NT2RP4001117	19.81	19.81	30.49	35.35	42.53	27.5		
	NT2RP4001122	6.06	6.06	6.09	5.17	6.25	3.27		
	NT2RP4001123	3.62	3.62	7.76	7.95	5.96	6.27		
	NT2RP4001126	4.36	4.36	11.28	10.87	9.09	8.04		
	NT2RP4001127	3.25	3.25	4.59	3.39	3.08	2.17		
30	NT2RP4001138	2.46	2.46	5.8	3.41	2.56	1.62		
	NT2RP4001143	2.73	2.73	5.98	6.44	6.54	5.66		
	NT2RP4001148	3.72	3.72	6.76	3.77	3.03	2.05		
	NT2RP4001149	5.07	5.07	7.28	6.76	9.03	6.37		
	NT2RP4001150	3.8	3.8	3.17	3.15	3.7	2.88		
35	NT2RP4001159	7.08	7.08	11.61	7.69	5.58	10.46		
	NT2RP4001162	3.77	3.77	6.14	4.07	6.06	3.41		
	NT2RP4001170	1.15	1.15	4.53	1.28	3.2	2.15		
	NT2RP4001174	4.16	4.16	12.27	7.91	11.95	5.02		
	NT2RP4001175	9.65	9.65	19.14	15.72	21.29	13.28		
40	NT2RP4001176	99.19	99.19	161.51	174.03	241.92	194	*	+
	NT2RP4001184	4.83	4.83	27.1	25.76	32.51	22.85		
	NT2RP4001198	21.66	21.66	48.22	29.54	29.17	38.54		
	NT2RP4001199	2.52	2.52	6.45	2.59	4.74	3.71		
	NT2RP4001206	8.25	8.25	33.2	25.92	32.07	25.48		
45	NT2RP4001207	2.38	2.38	5.15	2.21	3.11	4.01		
	NT2RP4001210	2.73	2.73	5.2	3.62	4.26	2.64		
	NT2RP4001213	3.42	3.42	5.11	3.99	4.23	3.63		
	NT2RP4001214	3.34	3.34	4.3	3.51	3.76	2.16		
	NT2RP4001219	7.4	7.4	12.05	14.35	19.28	13.39	*	+
50	NT2RP4001228	5.26	5.26	9.63	12.15	15.74	20.07	*	+
	NT2RP4001235	2.42	2.42	7.45	3.46	6.02	4.48		
	NT2RP4001256	2.11	2.11	4.24	1.66	3.41	2.66		
	NT2RP4001257	2.48	2.48	7.27	4.05	4.35	4.05		
	NT2RP4001260	3.16	3.16	5.79	2.52	3.86	2.92		
	NT2RP4001261	3.84	3.84	6.63	8.42	6.47	5		
	NT2RP4001274	22.92	22.92	38.08	25.02	31.56	21.25		
	NT2RP4001276	5.24	5.24	10.03	11.38	15.97	11.63	*	+
	NT2RP4001283	20.72	20.72	122.55	87.44	93.43	86.47		
55	NT2RP4001299	9.62	9.62	15.14	14.95	10.52	15.18		

EP 1 130 094 A2

5	NT2RP4001313	1.45	1.45	3.26	1.72	2.96	0.97
	NT2RP4001315	6.06	6.06	11.14	7.45	9.92	7.74
	NT2RP4001320	14.6	14.6	42.74	32.02	38.13	29.24
	NT2RP4001325	32.53	32.53	146.14	142.88	178.36	128.89
	NT2RP4001336	6.69	6.69	40.75	38.55	46.66	32.11
	NT2RP4001339	4.12	4.12	5.6	3.35	5.56	2.76
10	NT2RP4001343	10.46	10.46	83.37	54.71	61.01	60.06
	NT2RP4001344	6.7	6.7	60.08	49.79	55.21	42.62
	NT2RP4001345	1.65	1.65	6.68	5.64	5.7	3.87
	NT2RP4001351	4.1	4.1	15.97	10.01	20.05	11.42
	NT2RP4001353	2.8	2.8	5.91	1.63	2.94	1.86
15	NT2RP4001355	2.57	2.57	8.67	1.83	3.12	2.08
	NT2RP4001367	10.64	10.64	17.66	11.92	17.06	13.16
	NT2RP4001372	2.26	2.26	3.82	2.1	2.06	2.07
	NT2RP4001373	8.86	8.86	16.4	10.99	8.59	11.48
	NT2RP4001375	2.71	2.71	6.06	4.91	7.42	2.94
20	NT2RP4001379	1.74	1.74	3.52	2.34	4.67	1.38
	NT2RP4001381	5.6	5.6	12.51	12.8	12.66	8.27
	NT2RP4001386	6.39	6.39	14.52	14.77	20.11	12.32
	NT2RP4001389	7.28	7.28	8.66	5.43	9.25	4.09
	NT2RP4001396	5.76	5.76	6.42	2.83	4.61	2.12
25	NT2RP4001407	2.92	2.92	2.98	3.07	2.04	1.76
	NT2RP4001409	13.6	13.6	28.28	8.87	5.85	8.84
	NT2RP4001410	33.56	33.56	61.26	40.57	18.92	37.8
	NT2RP4001414	16.59	16.59	37.89	14.29	21.3	16.8
	NT2RP4001424	3.55	3.55	8.85	7.99	10.45	7.41
30	NT2RP4001433	3.85	3.85	6	8.39	9.79	3.38
	NT2RP4001438	9.95	9.95	27.94	46.22	53.63	30.76
	NT2RP4001442	4.33	4.33	4.97	3.3	3.41	2.64
	NT2RP4001447	4.42	4.42	4.69	5.08	5.51	3.41
35	NT2RP4001466	3.74	3.74	5.45	7.38	3.23	5.57
	NT2RP4001467	21.67	21.67	58.89	54.18	44.07	55.8
	NT2RP4001472	8.05	8.05	12.19	11.7	11.76	11.97
	NT2RP4001474	2.83	2.83	4.81	3.2	5.73	1.98
	NT2RP4001483	1.48	1.48	4.33	2.61	3.7	1.19
40	NT2RP4001488	21.03	21.03	32.41	39.07	46.9	33.42
	NT2RP4001492	4.18	4.18	6.73	3.21	3.81	1.91
	NT2RP4001498	4.3	4.3	2.43	2.95	3.52	2.13
	NT2RP4001502	28.2	28.2	57.38	27.65	34.81	41.83
	NT2RP4001503	3.83	3.83	6.74	5.51	4.1	3.37
45	NT2RP4001507	2.39	2.39	3.69	5.03	5.95	5.18
	NT2RP4001510	1.74	1.74	4.63	5.64	5.05	3.02
	NT2RP4001516	3.54	3.54	4.16	2.52	1.9	1.27
	NT2RP4001520	25.33	25.33	70.64	73.93	107.21	85.05
	NT2RP4001523	5.57	5.57	9.99	8.4	7.79	6.19
50	NT2RP4001524	6.1	6.1	10.17	8.92	11.45	5.98
	NT2RP4001529	29.8	29.8	74.89	59.39	60.69	55.29
	NT2RP4001531	2.88	2.88	10.96	8.63	11.05	7.81
	NT2RP4001546	143.48	143.48	388.31	316.63	215.6	309.45
	NT2RP4001547	9.05	9.05	26.31	28.76	23.06	18.81
55	NT2RP4001551	2.27	2.27	3.93	3.87	4.08	2.02
	NT2RP4001555	2.95	2.95	5.8	4.14	3.58	1.74

EP 1 130 094 A2

	NT2RP4001567	6.54	6.54	6.88	5.82	7.12	5.68
5	NT2RP4001568	7.58	7.58	11.65	10.02	19.33	12.97
	NT2RP4001569	15.49	15.49	41.42	32.56	40.11	27.18
	NT2RP4001571	5.75	5.75	13.28	9.06	7.43	8.13
	NT2RP4001574	8.5	8.5	19.03	15.54	17.52	15.29
	NT2RP4001575	2.46	2.46	5.86	5.71	5.53	4.24
10	NT2RP4001578	17.21	17.21	45.64	52.76	53.63	40.92
	NT2RP4001592	9.76	9.76	13.68	14.13	19.64	11.68
	NT2RP4001593	9.4	9.4	18.11	22.12	27.3	18.04
	NT2RP4001605	5.97	5.97	4.78	4.1	7.77	4.66
	NT2RP4001606	2.9	2.9	8.34	6.01	3.51	6.75
15	NT2RP4001607	2.04	2.04	5.24	4.57	3.26	3.78
	NT2RP4001610	1.74	1.74	2.42	2.6	2.48	1.7
	NT2RP4001614	2.17	2.17	7.19	5.38	4.34	6.86
	NT2RP4001623	2.38	2.38	5.26	2.43	2.65	2.02
	NT2RP4001626	9.48	9.48	11.67	18.67	23.9	19.44
	NT2RP4001634	2.74	2.74	4.93	3.67	5.24	4.26
20	NT2RP4001638	3.41	3.41	3.03	2.36	2.11	1.87
	NT2RP4001644	7.86	7.86	33.73	24.36	26.04	24.99
	NT2RP4001646	11.61	11.61	15.02	7.42	10.74	11.21
	NT2RP4001656	3.75	3.75	5.23	2.89	4.51	2.07
	NT2RP4001666	1.99	1.99	4.68	3.26	6.25	2.02
25	NT2RP4001670	11.74	11.74	15.51	12.45	7.09	8.31
	NT2RP4001677	28.27	28.27	42.75	42.01	45.48	47.53
	NT2RP4001679	8.82	8.82	33.83	33.23	51.5	29.78
	NT2RP4001695	7.71	7.71	12.76	15.66	20.35	12.87
30	NT2RP4001696	2.64	2.64	5.45	3.13	3.92	3.72
	NT2RP4001699	3.58	3.58	8.03	3.18	4.12	4.42
	NT2RP4001717	2.79	2.79	7.03	3.29	5.84	4.15
	NT2RP4001719	3.59	3.59	9.11	7.6	9.27	6.28
	NT2RP4001725	2.27	2.27	4.79	2.28	5.07	1.43
35	NT2RP4001726	7.07	7.07	11.18	5.85	6.91	4.98
	NT2RP4001730	3.11	3.11	12.82	11.96	19.81	16.3
	NT2RP4001739	2.83	2.83	5.83	5.79	6.55	4.98
	NT2RP4001741	7.25	7.25	15.93	9.28	12.42	10.97
	NT2RP4001753	3.04	3.04	8.4	4.39	4.64	6.64
40	NT2RP4001760	4.32	4.32	6.6	7.79	7.73	12.96
	NT2RP4001787	67.61	67.61	173.05	169.17	187.1	193.22
	NT2RP4001790	2	2	5.29	3.42	2.97	2.58
	NT2RP4001795	9.31	9.31	12.31	14.38	19.76	12.34
	NT2RP4001803	3.35	3.35	3.6	3.94	4.78	3.67
45	NT2RP4001805	2.64	2.64	3.57	3.64	2.47	2.95
	NT2RP4001809	4.84	4.84	26.35	18.18	23.17	11.33
	NT2RP4001817	11.55	11.55	19.09	9.5	10.78	12.71
	NT2RP4001822	2.09	2.09	5.36	3.73	5.11	3.33
	NT2RP4001823	1.91	1.91	3.95	1.14	3.34	1.24
50	NT2RP4001827	14.88	14.88	25.96	35.78	40.37	29.5
	NT2RP4001828	9.76	9.76	34.37	27.78	34.21	26.3
	NT2RP4001836	7.74	7.74	33.26	27.19	39.14	26.78
	NT2RP4001838	1.59	1.59	7.49	2.09	4.5	2.71
	NT2RP4001841	8.75	8.75	80.37	61.67	50.27	56.46
55	NT2RP4001849	1.9	1.9	4.55	2.51	5.08	1.58

EP 1 130 094 A2

	NT2RP4001861	7.27	7.27	34.6	36.09	41.9	34.39		
5	NT2RP4001877	6.59	6.59	8.44	12.87	9.04	14.1	*	+
	NT2RP4001879	9.64	9.64	15.47	11.58	14.24	10.73		
	NT2RP4001889	5.09	5.09	10.66	6.68	11.25	8.91		
	NT2RP4001893	3.97	3.97	7.34	3.19	6.11	2.72		
10	NT2RP4001896	3.18	3.18	6.86	5.38	7.87	4.92		
	NT2RP4001898	7.83	7.83	26.41	22.98	20.13	20.15		
	NT2RP4001901	1.73	1.73	4.69	4.08	5.87	2.69		
	NT2RP4001910	39.51	39.51	58.21	53.45	33.59	45.93		
	NT2RP4001925	4.1	4.1	10.21	6.69	6.32	6.12		
	NT2RP4001926	6.41	6.41	7.22	7.1	9.54	5.52		
15	NT2RP4001927	6.26	6.26	9.97	5.83	8.13	2.82		
	NT2RP4001931	8.64	8.64	14.16	15.49	17.54	11.89		
	NT2RP4001933	38.49	38.49	87.13	96.81	133.51	91.22		
	NT2RP4001938	2.93	2.93	4.53	4.27	3.31	3.55		
	NT2RP4001942	13.44	13.44	27.12	31.34	24.8	18.71		
20	NT2RP4001945	1.41	1.41	4	1.55	3.67	1.77		
	NT2RP4001946	1.97	1.97	5.67	3.04	3.96	1.66		
	NT2RP4001947	4.42	4.42	8.93	5.92	9.81	5.16		
	NT2RP4001950	4.13	4.13	5	2.25	2.84	1.34	*	-
	NT2RP4001953	10.44	10.44	14.15	13.81	19.4	14.36		
25	NT2RP4001966	2.44	2.44	2.41	2.51	4.26	1.52		
	NT2RP4001970	2.26	2.26	5.32	3.91	3.4	2.88		
	NT2RP4001975	8.56	8.56	20.03	18.32	13.05	12.02		
	NT2RP4001988	6.72	6.72	18.78	22.92	24.78	29.44	*	+
	NT2RP4001996	5.27	5.27	12.83	10.65	16.35	12.42		
30	NT2RP4002014	3.4	3.4	8.14	43.19	37.87	33.17	**	+
	NT2RP4002018	6.19	6.19	13.71	10.47	11.39	10.36		
	NT2RP4002035	5.35	5.35	5.95	5.4	4.17	2.54		
	NT2RP4002043	7.1	7.1	10.8	9.64	12.2	6.5		
	NT2RP4002046	9.74	9.74	20.08	21.94	15.28	17.11		
35	NT2RP4002047	8.37	8.37	19.18	22.28	24.07	28.83	*	+
	NT2RP4002052	5.78	5.78	10.36	9.02	9.36	9.37		
	NT2RP4002056	32.58	32.58	71.49	58.09	76.58	49.75		
	NT2RP4002057	6.37	6.37	11.06	12.13	13.58	7.41		
	NT2RP4002058	3.85	3.85	6.6	4.1	4.2	3.22		
40	NT2RP4002064	5.93	5.93	4.39	2.6	4.16	2.07	*	-
	NT2RP4002071	6.67	6.67	7.07	6.95	10.06	6.27		
	NT2RP4002075	1.16	1.16	2.11	2.27	2.35	1.27		
	NT2RP4002078	2.25	2.25	8.63	6.86	8.24	4.97		
	NT2RP4002081	8.11	8.11	26.15	18.73	18.78	19.42		
45	NT2RP4002083	1.39	1.39	5.25	3.36	3.16	1.88		
	NT2RP4002099	3.26	3.26	4.73	2.84	3.56	2.51		
	NT2RP4002106	10.35	10.35	20.34	22.36	25.93	20.55		
	NT2RP4002111	11.7	11.7	12.37	19.77	30.44	17.72		
50	NT2RP4002112	6.15	6.15	10.97	8.9	8.34	3.22		
	NT2RP4002116	12.6	12.6	47.19	37.43	41.25	28.65		
	NT2RP4002122	5.34	5.34	9.29	14.84	14.86	12.67	**	+
	NT2RP4002126	6.42	6.42	14.44	16.82	14.35	10.42		
	NT2RP4002133	7.56	7.56	20.82	29.17	26.14	21		
	NT2RP4002136	3.63	3.63	5.74	4.89	5.38	2.69		
55	NT2RP4002139	26.89	26.89	31.12	60.65	61.92	32.88		

EP 1 130 094 A2

	NT2RP4002174	139.27	139.27	232.64	240.71	275.01	193.19
5	NT2RP4002185	7.77	7.77	13.2	12.36	19.06	11.58
	NT2RP4002186	4.5	4.5	9.83	7.82	4.72	6.78
	NT2RP4002187	15.42	15.42	32.13	26.94	19.84	21.17
	NT2RP4002188	3.01	3.01	8.34	8.3	7.75	6.41
	NT2RP4002199	1.85	1.85	3.73	2.6	2.91	3.78
10	NT2RP4002206	2.08	2.08	3.39	2.48	2.34	1.29
	NT2RP4002210	3.13	3.13	4.75	2.02	2.86	0.98
	NT2RP4002222	4.2	4.2	6.63	5.56	6.28	4.16
	NT2RP4002241	7.97	7.97	8.24	10.82	11.75	7.19
	NT2RP4002248	5.08	5.08	16.69	10.74	8.9	8.13
15	NT2RP4002250	1.54	1.54	3.22	0.73	1.69	0.56
	NT2RP4002259	4.86	4.86	9.82	3.21	4.85	1.75
	NT2RP4002268	16.62	16.62	29.54	28.9	28.18	25.68
	NT2RP4002288	6.42	6.42	12.57	13.29	14.36	11.97
	NT2RP4002290	7.55	7.55	7.61	7.96	7.67	5.87
	NT2RP4002298	3.92	3.92	4.18	5.54	5.03	4.18
20	NT2RP4002306	2.38	2.38	5.79	2.97	5.77	2.64
	NT2RP4002308	2.04	2.04	6.03	5.31	5.23	4.1
	NT2RP4002336	2.71	2.71	6.33	3.71	4.19	4.63
	NT2RP4002340	1.09	1.09	3.96	1.28	2.75	0.49
25	NT2RP4002361	2.77	2.77	5.78	3.73	4.03	2.48
	NT2RP4002367	2.27	2.27	5.84	3.23	2.48	2.77
	NT2RP4002368	9.87	9.87	17.2	18.26	19.27	16
	NT2RP4002377	3.3	3.3	23.8	25.46	30.75	23.93
	NT2RP4002408	2.22	2.22	3.87	3.75	6.37	4.11
30	NT2RP4002425	2.84	2.84	5.81	8.24	7.98	5.23
	NT2RP4002432	12.33	12.33	85.4	61.06	72.53	67.82
	NT2RP4002447	2.97	2.97	7.68	3.96	5.4	4.59
	NT2RP4002451	5.48	5.48	6.2	5.84	5.85	6.83
	NT2RP4002461	9.8	9.8	32.09	32.76	38.91	29.04
35	NT2RP4002486	3.5	3.5	6.71	2.47	4.15	2.87
	NT2RP4002517	3.65	3.65	9.11	7.02	8.53	7.18
	NT2RP4002556	4.29	4.29	3.91	5.68	10.03	6.41
	NT2RP4002569	3.36	3.36	7.36	4.93	5.29	3.42
	NT2RP4002587	2.26	2.26	4.19	2.8	3.4	2.02
40	NT2RP4002591	2.21	2.21	4.89	2.89	4.5	3.08
	NT2RP4002607	1.43	1.43	3.34	2.87	4.63	1.58
	NT2RP4002627	17.83	17.83	61.9	55.9	76.17	65.3
	NT2RP4002628	7.28	7.28	15.48	14.53	23.95	12.54
45	NT2RP4002630	4.19	4.19	5.25	6.72	9.4	7.16 * +
	NT2RP4002639	9.43	9.43	70.25	52.38	77.24	57.28
	NT2RP4002641	1.58	1.58	9.03	3.94	4.07	4.1
	NT2RP4002658	114.62	114.62	166.93	76.49	34.96	109.83
	NT2RP4002669	3.5	3.5	5.67	5.4	5.33	4.68
50	NT2RP4002677	6.24	6.24	9.41	10.14	7.99	13.62
	NT2RP4002715	8.42	8.42	34.92	40.1	48.46	32.3
	NT2RP4002750	2.6	2.6	8.29	1.68	2.04	1.33
	NT2RP4002784	3.71	3.71	9.51	9.44	11.22	7.06
	NT2RP4002791	4.91	4.91	9.44	4.88	9.76	5.33
55	NT2RP4002811	1.63	1.63	6.38	3.17	2.95	3.43
	NT2RP4002830	4.26	4.26	7.45	3.9	5.9	5.46

EP 1 130 094 A2

5	NT2RP4002832	2.12	2.12	3.13	2.38	5.59	2.54
	NT2RP4002850	5.07	5.07	12.04	14.36	12.63	8.06
	NT2RP4002874	5.17	5.17	6.67	3.41	5.14	1.96
	NT2RP4002884	28.81	28.81	49.75	43.57	74.75	52.87
	NT2RP4002888	5.55	5.55	4.83	3.67	4.32	3.08 *
	NT2RP4002891	5.48	5.48	15.79	13.16	19.42	11.91
10	NT2RP4002894	12.04	12.04	24.47	18.44	12.76	16.4
	NT2RP4002896	5.54	5.54	12.2	8.96	6.18	7.78
	NT2RP4002905	1.71	1.71	4.27	2.32	3.58	1.28
	NT2RP4002907	5.11	5.11	7.62	6.94	10.72	1.41
15	NT2RP5003459	68.11	68.11	133.25	154.61	146.15	164.37 * +
	NT2RP5003461	7.34	7.34	10.14	10.85	14.36	8
	NT2RP5003471	106.6	106.6	168.71	124.4	148.85	112.14
	NT2RP5003477	2.71	2.71	2.62	2.59	2.33	1.9
	NT2RP5003487	157.44	157.44	424.89	292.71	256.56	354.93
20	NT2RP5003492	3.1	3.1	4.91	5.25	6.17	5.91 * +
	NT2RP5003500	1.5	1.5	3.28	2.38	2.54	2.59
	NT2RP5003506	4.96	4.96	9.3	7.83	10.37	9.04
	NT2RP5003512	2.21	2.21	4.35	2.63	3.46	2.15
	NT2RP5003522	4.1	4.1	5.97	4.62	4.19	2.34
	NT2RP5003524	4.38	4.38	3.86	1.61	1.54	0.84 ** -
25	NT2RP5003527	24.72	24.72	71.27	76.81	87.24	60.59
	NT2RP5003531	7.16	7.16	17.2	15.58	14.06	14.11
	NT2RP5003534	2.68	2.68	5.49	5.54	6.82	4.55
	NT2RP6000020	8.69	8.69	19.96	14.65	15.13	16.29
30	NT2RP6000022	3.19	3.19	4.05	4.06	3.96	2.44
	NT2RP6000050	3.95	3.95	3.99	4.98	5.82	2.88
	NT2RP6000063	3.91	3.91	6.04	3.61	2.52	2.56
	NT2RP6000074	5.38	5.38	4.88	3.41	3.27	2.17 ** -
	NT2RP6000083	7.76	7.76	11.18	11.49	16	9.91
35	NT2RP6000100	2.49	2.49	4.58	4.04	4.71	3.3
	NT2RP6000123	1.94	1.94	3.29	5.1	4.26	4.22 * +
	NT2RP6000129	1.9	1.9	4.47	4.06	4.27	2.74
	NT2RP6000147	3.75	3.75	11.74	10.8	11.03	7.48
40	NT2RP6000163	2.62	2.62	4.23	2.28	1.95	1.71
	NT2RP6000181	8.03	8.03	12.4	9.44	13.25	9.01
	NT2RP6000182	5.44	5.44	6.42	4.82	5.56	3.88
	OVARC1000001	4.97	4.97	5.24	6.04	7.48	2.35
	OVARC1000003	3.21	3.21	8.31	8.51	7.66	7.05
	OVARC1000004	9.87	9.87	116.19	88.04	109.99	85.44
45	OVARC1000006	3.57	3.57	6.58	9.04	7.88	4.73
	OVARC1000013	6.51	6.51	9.19	7.32	8.36	8.33
	OVARC1000014	3.39	3.39	5.02	4.23	5.02	4.17
	OVARC1000017	3.11	3.11	6.81	4.2	4.45	2.72
	OVARC1000026	24.79	24.79	32.1	56.82	69.34	44.53 * +
50	OVARC1000035	11.11	11.11	20.26	20.41	23.65	15.36
	OVARC1000037	8.73	8.73	19.12	15.64	9.13	15.9
	OVARC1000058	6.06	6.06	11.69	13.84	7.56	10.6
	OVARC1000060	1.89	1.89	6.28	5.98	5.24	5.13
	OVARC1000068	2.38	2.38	5.33	5.31	3.56	2.42
55	OVARC1000069	74.66	74.66	101.53	75.95	84.36	86.42
	OVARC1000071	4.4	4.4	4.77	6.47	5.35	4.04

EP 1 130 094 A2

	OVARC1000075	55.43	55.43	125.63	120.89	150.97	117.03		
5	OVARC1000083	9.58	9.58	9.24	13.12	12.7	10.64	*	+
	OVARC1000085	106.6	90.9	156.14	214.2	177.05	273.14	*	+
	OVARC1000086	3.98	6.82	9.23	11.98	11.3	14.09	*	+
	OVARC1000087	1.51	2.83	1.79	4.03	3.57	3.35	*	+
	OVARC1000090	1.48	4.1	6.14	10.88	9.58	8.79	*	+
10	OVARC1000091	4.88	8.33	8.01	7.99	7.76	6.82		
	OVARC1000092	2.83	6.81	4.18	4.68	6.25	4.85		
	OVARC1000105	9.73	14.86	17.21	26.29	25.62	22.88	*	+
	OVARC1000106	26.02	23.03	46.38	66.36	50.1	53.01	*	+
	OVARC1000109	9.12	13.08	18.04	16.72	12.91	17.46		
15	OVARC1000113	4.12	6.25	6.53	6.83	8.19	7.65		
	OVARC1000114	2.14	3.44	5.77	5.94	5.86	4.98		
	OVARC1000133	2.53	4.96	6.36	4.05	4.97	2.95		
	OVARC1000137	6.14	10.05	13.51	13.3	18.59	14.39		
	OVARC1000139	14.75	20.77	83.44	71.14	98.1	69.29		
20	OVARC1000145	0.72	6.64	2.89	1.78	2.42	2		
	OVARC1000148	5.09	4.98	7.88	4.91	5.32	7.91		
	OVARC1000151	1.41	2.11	2.4	3.58	4.08	3.58	**	+
	OVARC1000157	10.99	14.16	17.51	21.21	25.06	22.76	*	+
	OVARC1000162	1.22	4.4	2.5	2.93	2.49	2.59		
	OVARC1000168	1.98	8.46	6.2	8.01	9.61	9.96		
25	OVARC1000169	32.03	45.07	49.48	70.63	69.6	89.08	*	+
	OVARC1000178	0.84	5.08	2.53	3.37	3.18	2.78		
	OVARC1000182	0.8	3.3	1.42	2.02	1.95	1.78		
	OVARC1000186	2.51	3.72	3.23	5.95	3.27	4.77		
30	OVARC1000188	1.04	2.67	2.33	2.48	2.87	1.9		
	OVARC1000191	1.01	3.8	2.63	3.12	2.85	2.54		
	OVARC1000198	2.09	3.59	4.32	5.62	5.12	5.06	*	+
	OVARC1000208	6.49	10.37	22.5	17.79	24.54	22.02		
	OVARC1000209	7.99	13.69	22.32	23.42	27.81	29.16		
35	OVARC1000212	2.47	5.63	3.59	4.76	5.03	4.88		
	OVARC1000216	1.72	4.96	4.35	15.43	11.3	12.54	**	+
	OVARC1000240	2.98	3.53	8.13	5.39	5.46	4.87		
	OVARC1000241	1.29	2.47	3.18	2.65	3.17	1.4		
	OVARC1000249	4.14	5.43	8.17	5.46	5	6.13		
40	OVARC1000254	33.15	39.39	100.99	100.41	131.42	100.89		
	OVARC1000255	0.85	4.83	2.51	2.98	2.45	1.95		
	OVARC1000267	2.37	6.41	6.71	6.66	7.16	7.31		
	OVARC1000275	79.02	93.7	161.08	199.43	240.76	175.96	*	+
	OVARC1000287	226.67	224.66	236.08	433.91	512.76	470.31	**	+
45	OVARC1000288	3.2	4.25	7.38	6.23	5.32	4.47		
	OVARC1000298	8.96	10.09	19.62	13.37	7.19	9.6		
	OVARC1000302	1.12	2.14	2.13	2.47	1.85	2		
	OVARC1000304	1.09	2.68	3.23	5.02	3.41	6		
	OVARC1000307	2.95	6.19	4.74	7.59	4.7	6.29		
50	OVARC1000309	1.18	7.16	3.22	3.24	2.85	2.4		
	OVARC1000312	2.83	11.64	6.03	4.17	5.4	2.46		
	OVARC1000313	10.48	19.25	14.81	9.39	17.54	22.17		
	OVARC1000321	31.6	24.05	47.79	30.5	31.37	15.43		
	OVARC1000326	1.52	2.3	3.9	3.84	3.17	2.79		
55	OVARC1000327	1.52	3.28	4.24	3.13	1.49	2.46		

EP 1 130 094 A2

	OVARC1000331	2.22	4.72	2.41	4.33	4.45	4.58
5	OVARC1000335	2.3	5.84	4.02	2.72	5.16	4.75
	OVARC1000347	1.83	8.18	6.24	7.35	9.24	8.44
	OVARC1000348	1.61	10.62	3.73	2.84	4.59	3.05
	OVARC1000363	3.7	9.61	6.51	7.31	11.52	6.83
	OVARC1000377	1.07	2.09	2.43	2.28	2.51	2.45
10	OVARC1000382	3.34	3.39	4.33	5.07	2.52	1.03
	OVARC1000384	4.2	5.42	8.35	5.32	4.4	6.04
	OVARC1000401	0.62	3.63	2.09	3.35	4.08	3.64
	OVARC1000406	18.98	23.3	49.12	57.09	74.48	54.63 * +
	OVARC1000407	1.99	6.28	3.99	4.11	6.42	3.16
15	OVARC1000408	27.5	38.45	70.39	74.84	111.17	71.25
	OVARC1000410	6.83	12.72	10.41	4.78	6.65	5.01
	OVARC1000411	0.91	1.5	2.6	3.49	3	2.22
	OVARC1000414	1.31	2.22	3.7	4.5	3.78	3.71
	OVARC1000420	1.44	2.76	3.29	3.3	2.59	2.1
20	OVARC1000421	1.42	2.65	3.33	3.96	4.21	4.99 * +
	OVARC1000427	25.78	27.02	130.06	156.9	215.67	142.19
	OVARC1000431	10.51	17.6	19.12	33.66	31.78	25.78 * +
	OVARC1000437	3.14	6.37	7.31	5.97	7.63	6.36
	OVARC1000439	5.81	10.95	13.82	21.81	23.01	21.52 ** +
25	OVARC1000440	2.56	3.74	5.01	7.47	9.31	7.08 * +
	OVARC1000442	2.34	2.38	6.81	6.66	9.5	8.12
	OVARC1000443	2.09	2.2	2.88	3.29	3.41	2.62
	OVARC1000461	1.11	2.84	2.2	2.55	1.12	2.14
	OVARC1000465	3.27	5.01	3.51	3.94	4.62	3.95
30	OVARC1000466	1.94	5.47	5.9	6.54	10.13	6.76
	OVARC1000467	1.01	5.08	2.41	3.65	2.98	3.78
	OVARC1000470	1.13	5.81	3.03	3.18	4.02	3.78
	OVARC1000473	1.81	1.95	2.65	2.44	4.16	1.39
	OVARC1000479	5.67	5.88	9.88	10.35	14.26	6.88
35	OVARC1000484	3.99	5.74	6.54	8.66	9.93	6.87
	OVARC1000486	3.17	4.71	4.49	5.74	4.93	4.28
	OVARC1000496	0.93	3.55	0.66	0.31	1.07	0.62
	OVARC1000520	0.84	5.89	1.18	1.32	2.27	2
	OVARC1000522	4.1	7.19	12	13.85	14.03	10.34
40	OVARC1000526	1.96	7.04	3.75	5.93	5.48	4.69
	OVARC1000529	2.38	2.57	4.44	3.66	4.16	3.08
	OVARC1000533	3.3	4.66	7.95	8.89	12.29	7.83
	OVARC1000543	0.84	2.44	2.06	2.57	3.08	2.72
	OVARC1000550	0.75	3.68	2.32	2.82	4.04	2.34
45	OVARC1000553	2.1	5.63	7.02	7.72	7.69	6.95
	OVARC1000556	5.77	15.21	11.77	8.95	13.91	8.96
	OVARC1000557	0.83	5.12	1.4	1.61	2.29	1.88
	OVARC1000561	3.48	7.38	9.26	13	17.66	15.09 * +
	OVARC1000564	8.89	9.02	10.44	17.84	11.31	16.69 * +
50	OVARC1000573	1.87	3.68	4.86	5.75	5.32	3.83
	OVARC1000576	24.12	29.23	124.94	83.09	93.83	98.58
	OVARC1000578	2.43	4.6	5.53	8.64	4.46	3.93
	OVARC1000581	0.34	3.28	1.15	1.75	1.27	1.23
	OVARC1000586	22.54	28.9	41.17	34.58	43.39	40.93
55	OVARC1000588	0.74	5.23	2.03	2.75	3.72	2.05

EP 1 130 094 A2

	OVARC1000605	1.98	2.62	2.88	4.47	4.23	3.87	**	+
5	OVARC1000622	3.86	4.59	11.57	12.7	11.13	11.6		
	OVARC1000636	1.64	3.79	4.58	4.19	4.03	5.09		
	OVARC1000640	1.97	4.72	3.93	4.21	3.67	3.09		
	OVARC1000649	9.69	14.8	53.54	53.32	64.51	52.67		
	OVARC1000661	1.14	9.33	2.99	5.34	5.24	5.24		
10	OVARC1000677	8.53	10.16	14.87	11.77	10.98	15.47		
	OVARC1000678	1.21	4.49	2.71	3.28	4.17	3.26		
	OVARC1000679	2.86	3.25	4.09	5.29	5.16	6.25	*	+
	OVARC1000681	1.47	1.55	3.2	2.41	2.22	1.71		
	OVARC1000682	10.09	11.33	50.91	33.79	47.49	44.31		
15	OVARC1000689	3.81	7.1	19.94	20.18	22.12	21.83		
	OVARC1000700	1.8	10.37	3.18	4.98	4.37	5.14		
	OVARC1000703	1.74	7.18	5.35	6.4	6.64	7.77		
	OVARC1000722	10.59	11.92	47.93	43.41	60.06	39.34		
	OVARC1000726	1.44	3.48	4.62	4.88	5.89	3.58		
	OVARC1000727	1.93	2.09	4.13	3.78	3.79	3.89		
20	OVARC1000730	5.95	5.86	9.01	4.07	4.16	5.62		
	OVARC1000741	4.85	6.13	8.74	15.19	10.58	13.71	*	+
	OVARC1000746	0.89	3.61	2.43	2.06	2.9	2.84		
	OVARC1000764	1.76	4.93	4.77	5.35	7.01	5.44		
	OVARC1000769	1.13	4.3	3.6	3.76	4.42	5.2		
25	OVARC1000771	2.42	6.28	2.3	4.02	4.81	3.71		
	OVARC1000773	19.09	24.7	31.93	44.69	56.24	46.24	*	+
	OVARC1000775	11.67	8.94	16.44	12.16	8.7	4.26		
	OVARC1000778	2.37	3.89	5.69	4.59	6.23	4.92		
	OVARC1000779	0.8	2.02	1.85	2.23	2.45	1.46		
30	OVARC1000781	1.67	5.05	4.16	6.37	3.45	5.07		
	OVARC1000787	1.64	4.79	4.22	2.97	5.44	3.25		
	OVARC1000789	7.62	14.23	16.39	24.95	29.69	25.94	**	+
	OVARC1000800	2.91	10.72	5.72	6.41	10.65	6.2		
	OVARC1000802	1.55	8.77	2.97	2.99	5.34	2.76		
35	OVARC1000810	3.37	3.54	8.29	6.66	7.99	7.21		
	OVARC1000811	2.41	2.73	7.5	4.88	3.67	4.95		
	OVARC1000814	3.44	4.55	9.03	7.92	11.3	9.05		
	OVARC1000816	7.64	10.41	12.41	10.99	10.58	14.11		
40	OVARC1000817	1.18	3.38	1.27	1.71	2.14	1.55		
	OVARC1000834	2.46	8.3	3.39	4.84	5.81	4.01		
	OVARC1000846	2.23	10.02	5.35	7.38	9.66	7.72		
	OVARC1000850	1.74	8.37	3.38	3.39	2.51	3.1		
	OVARC1000853	23.21	24.23	43.4	30.67	37.81	18.39		
45	OVARC1000862	2.28	2.66	4.91	3.05	1.61	1.49		
	OVARC1000873	2.56	2.98	4.14	4.4	3.79	3.85		
	OVARC1000875	1.47	3.07	1.79	2.35	3.09	1.87		
	OVARC1000876	3.71	5.67	4.46	5.11	6.06	5.45		
	OVARC1000883	6.06	9.53	9.18	12.43	15.42	13.05	*	+
50	OVARC1000885	2.84	9.95	3.38	3.74	5.66	4.11		
	OVARC1000886	4.31	8.19	4.29	3.74	5.15	4.39		
	OVARC1000890	17.47	18.3	91.22	70.97	78.71	51.68		
	OVARC1000891	1.28	1.44	3.03	2.85	2.19	3.22		
	OVARC1000897	0.48	1.74	1.29	1.21	1.33	0.5		
55	OVARC1000912	2.06	3.22	4.33	5.21	6.1	5.86	*	+

EP 1 130 094 A2

	OVARC1000914	1.48	6.18	1.61	3.68	3.02	2.18		
5	OVARC1000915	1.71	6.64	4.14	4.87	3.54	4.76		
	OVARC1000916	1.91	5.19	2.56	4.05	4.32	3.88		
	OVARC1000924	1.45	5.5	3.09	3.28	3.85	3.48		
	OVARC1000928	6.05	5.46	8.78	4.22	5.83	5.35		
	OVARC1000936	1.37	1.39	2.17	2.04	3.25	2.49		
10	OVARC1000937	1.69	3.01	1.94	4.17	3.26	3.24		
	OVARC1000945	1.55	3.67	3.62	3.83	3.22	2.28		
	OVARC1000948	1.57	3.85	2.66	3.15	3.68	1.99		
	OVARC1000956	1.41	5.08	4.36	7.56	7.26	5.51		
	OVARC1000959	1.8	4.87	3.39	4.88	3.02	3.9		
15	OVARC1000960	2.64	7.53	9.55	11.64	13.89	12.86	*	+
	OVARC1000964	19.89	17.19	103.98	118.41	165.46	96.14		
	OVARC1000971	0.42	1.58	1.4	2.53	2.27	2.28	*	+
	OVARC1000975	5.93	8.3	36.1	31.27	51.54	30.22		
	OVARC1000976	0.65	2.12	1.27	2.17	1.46	1.5		
20	OVARC1000981	4.06	7.18	4.94	7.97	12.1	8.53		
	OVARC1000982	2.83	5.41	2.23	3.13	3.02	3.54		
	OVARC1000984	1.78	5.43	3.32	3.01	3.08	2.16		
	OVARC1000995	2.94	6.59	4.5	5.98	6.19	6.72		
	OVARC1000996	1.68	1.87	4.29	3.58	4.15	4.56		
25	OVARC1000999	6.02	5.65	15.29	15.61	13.18	13.29		
	OVARC1001000	1.96	4.5	6.2	6.26	7.09	6.86		
	OVARC1001004	0.51	3.4	1.45	2.05	3.3	1.47		
	OVARC1001010	1.35	3.99	1.66	3.04	1.4	1.54		
	OVARC1001011	1.46	5.57	1.13	2.39	3.27	2.45		
30	OVARC1001030	96.19	101.41	143.98	119.24	154.26	133		
	OVARC1001032	1.42	5.34	1.89	1.83	2.82	1.92		
	OVARC1001034	4.44	5.58	6.51	3.29	5.21	3.77		
	OVARC1001038	3.62	5.03	7.4	10.3	10.88	8.61	*	+
	OVARC1001040	2.63	3.77	6.93	5.25	6.51	4.25		
35	OVARC1001041	4.54	8.03	12.87	8.57	12.25	9.4		
	OVARC1001044	1.05	2.92	1.83	1.96	2.43	1.84		
	OVARC1001049	3.78	8.78	10.67	10.65	11.87	10.26		
	OVARC1001051	40.95	55.97	80.66	66.89	109.71	87.49		
	OVARC1001054	1.22	4.06	3.22	2.86	4.19	1.93		
40	OVARC1001055	2.13	3.38	3.82	4.32	5.61	5.22	*	+
	OVARC1001062	5.8	6.15	12.54	8.04	9.94	9.57		
	OVARC1001065	8.85	13.63	51.33	51.41	60.3	56.97		
	OVARC1001068	2.82	5.62	4.76	4.72	4.02	5.52		
	OVARC1001072	0.73	4.18	4.41	3.2	3.71	3.07		
45	OVARC1001073	0.92	5.7	2.65	2.91	2.54	1.79		
	OVARC1001074	0.81	4.66	3.31	1.87	2.95	2.04		
	OVARC1001078	2	5.12	2.79	3.57	3.08	2.83		
	OVARC1001085	2.41	2.83	3.66	5.54	5.02	6.36	**	+
	OVARC1001086	1.97	3.17	2.85	3.98	2.83	4.13		
50	OVARC1001091	16.24	19.32	92.73	76.48	96.74	77.99		
	OVARC1001092	4.62	5.35	7.22	9.69	7.84	6.05		
	OVARC1001104	1.05	4.37	2.66	3.16	2.58	2.03		
	OVARC1001107	11.59	15.6	40.28	31.21	49.49	42.22		
	OVARC1001113	1.04	5.81	1.59	2.46	3.05	2.39		
55	OVARC1001117	2.71	6.63	4.31	4.67	5.74	2.67		

EP 1 130 094 A2

	OVARC1001118	2.38	3.69	7.08	7.36	6.91	8.28		
5	OVARC1001125	2.02	2.9	3	5.92	4.97	5.9	**	+
	OVARC1001129	2.61	4.58	3.19	8.46	9.43	11	**	+
	OVARC1001132	1.7	6.48	2.66	3.69	4.26	4.66		
	OVARC1001138	9.52	15.82	23.8	48.95	45.16	44.97	**	+
10	OVARC1001141	1.68	4.97	3.48	3.77	3.68	3.84		
	OVARC1001154	18.31	29.49	68.39	60.43	83.49	65.64		
	OVARC1001161	2.49	5.55	6.15	7.03	6.69	5.89		
15	OVARC1001162	2.2	3.13	5.34	5.09	4.86	5.26		
	OVARC1001163	0.69	3.59	2.77	2.2	3.98	2.54		
	OVARC1001167	3.03	4.57	7.69	10.19	12.95	9.3	*	+
	OVARC1001169	0.74	4.87	2.68	2.47	1.91	2.06		
20	OVARC1001170	7.81	15.04	17.59	14.61	19.45	14.99		
	OVARC1001171	15.57	17.71	24.31	16.12	23.34	22.51		
	OVARC1001173	2.09	5.08	5.1	4.32	6.75	5.49		
	OVARC1001176	22.57	21.48	89.96	76.74	102.3	70.7		
25	OVARC1001180	3.01	4.58	12.7	11.81	10.77	9.56		
	OVARC1001188	2.66	3.7	3.95	3.62	3.44	4.16		
	OVARC1001200	1.52	4.56	3.62	3.47	2.9	2.96		
	OVARC1001202	3.75	6.65	6.53	9.26	7.79	10.23	*	+
	OVARC1001206	1.52	5.52	1.15	1.59	1.13	1.9		
	OVARC1001209	4.89	8.92	27.46	24.69	30.38	24.27		
30	OVARC1001219	1.81	6.36	4.71	5.33	3.95	3.62		
	OVARC1001222	2.5	8.36	5.01	3.2	4.34	5.63		
	OVARC1001232	2.91	4.18	7.74	6.75	6.02	5.65		
	OVARC1001240	2.05	3.27	6.84	5.55	5.06	5.4		
	OVARC1001243	0.94	2.59	1.76	3.64	2.64	1.86		
35	OVARC1001244	9.07	12.05	18	21.61	18.57	26.62		
	OVARC1001246	30.48	50.95	48.51	80.54	100.83	101.88	**	+
	OVARC1001247	3.64	9.86	7.7	6.57	7.02	4.49		
	OVARC1001260	1.05	9.07	1.85	2.62	2.65	1.85		
	OVARC1001261	4.23	10.5	6.99	3.46	2.08	2.94		
40	OVARC1001268	24.4	19.69	52.37	32.58	35.32	14.16		
	OVARC1001270	14.46	15.1	20.83	9.69	9.8	8.65	*	-
	OVARC1001271	2.62	3.62	3.88	3.95	7.02	4.26		
	OVARC1001282	0.88	3.02	3.09	1.37	1.59	2		
	OVARC1001296	3.02	8.06	2.3	3.04	4.11	5.41		
45	OVARC1001306	1.48	8.27	2.4	2.04	2.29	3.82		
	OVARC1001314	0.49	8.47	1.57	1.06	1.79	1.32		
	OVARC1001316	2.77	7.17	4.81	5.48	8.11	5.36		
	OVARC1001329	6.12	6.18	21.11	17.09	19.29	16.22		
50	OVARC1001330	0.2	1.89	1.38	1.22	1.35	1.42		
	OVARC1001336	1.92	3.7	3.59	5.67	4.09	4.02		
	OVARC1001338	0.26	2.87	0.86	2.49	1.71	1.07		
	OVARC1001339	12.07	18.29	22.73	33.65	32.72	37.29	**	+
	OVARC1001340	0.72	4.83	1.23	1.33	2.44	1.3		
	OVARC1001341	4.35	9.25	6.77	7.94	11.38	9.69		
55	OVARC1001342	90.37	98.53	136.12	129.68	163.22	127.78		
	OVARC1001344	2.1	2.51	6.27	6.52	6.89	6.2		
	OVARC1001357	5.61	8.93	16.02	15.52	11.34	11.69		
	OVARC1001359	8.96	12.4	16.15	21.66	13.84	10.6		
	OVARC1001360	0.44	2.52	0.99	1.97	2.6	1.62		

EP 1 130 094 A2

	OVARC1001369	1.56	5.66	1.89	3.41	1.88	3.1
5	OVARC1001372	0.96	4.23	3.33	1.52	2.77	1.95
	OVARC1001376	1.82	5.1	3.62	5.79	5.79	4.18
	OVARC1001381	4.51	6.44	9.94	10.95	12.91	11.21
	OVARC1001391	0.5	1.62	1.44	1.88	1.27	1.26
10	OVARC1001392	2.12	4.69	6.14	11.96	12.7	7.79 * +
	OVARC1001399	0.98	3.59	2.16	1.77	2.54	1.1
	OVARC1001417	1.01	3.07	1.76	2.39	3.61	2.81
	OVARC1001419	2.47	5.4	3.06	4.39	4.03	3.16
	OVARC1001425	2.29	5.58	5.15	8.76	8.5	8.07 * +
15	OVARC1001436	1.37	5.85	2.54	2.9	3.57	3.18
	OVARC1001442	0.64	4.84	1.39	2.27	1.52	0.69
	OVARC1001451	3.09	2	3.89	5.18	5.98	4.75 * +
	OVARC1001452	1.35	2.41	2.87	2.96	4.69	3.13
	OVARC1001453	1.21	2.84	1.88	2.3	1.82	1.57
	OVARC1001476	10.67	14.38	16.52	17.22	12.9	13.09
20	OVARC1001480	0.93	4.73	1.5	3.1	2.98	2.21
	OVARC1001489	0.97	6.89	2.51	3.01	2.83	2.09
	OVARC1001493	2.09	6.59	3.75	7.38	8.78	10.48 * +
	OVARC1001496	4.65	9.58	8.63	10.74	7.37	11.03
	OVARC1001499	1.24	1.18	2.6	3.47	2.68	2.84
25	OVARC1001506	2.9	2.7	5.31	5.33	6.73	5.48
	OVARC1001509	1.73	3.89	3.69	4.07	4.59	3.07
	OVARC1001510	0.16	3.69	1.42	1.94	1.73	0.86
	OVARC1001516	2.57	5.78	3.85	6.04	4.97	4.39
	OVARC1001525	0.53	4.76	2.12	1.94	2.01	1.81
30	OVARC1001542	8.8	12.86	13.01	15.91	13.63	17.23
	OVARC1001544	2.14	6.6	6.72	7.54	8.33	6.22
	OVARC1001546	4.08	4.32	4.6	6.12	5.31	7.23 * +
	OVARC1001547	1.29	2.53	1.68	2.44	1.85	2.22
	OVARC1001555	10.39	16.51	68.77	48.66	65.39	56.39
35	OVARC1001560	3.35	4.91	5.52	5.36	4.93	5.34
	OVARC1001569	1.63	4.75	4.79	5.92	5.19	5.1
	OVARC1001570	3.96	7.9	6.93	7.72	10.7	8.55
	OVARC1001577	1.68	5.89	5.41	8.61	6.9	10.2
	OVARC1001578	0.25	3.47	-0.19	-0.47	0.24	0.15
40	OVARC1001596	12.13	11.65	14.23	13.51	14.82	27.15
	OVARC1001600	1.13	2.9	1.48	2.81	2.67	3.67
	OVARC1001607	6.22	7.72	10.91	13.42	14.01	13.45 * +
	OVARC1001610	1.81	5.25	2.84	4.25	2.66	2.7
	OVARC1001611	0.13	5.11	1.24	1.48	2.89	1.79
45	OVARC1001615	0.58	5.42	1.93	1.54	2.56	1.74
	OVARC1001636	1.09	3.75	1.05	2.39	2.05	2.15
	OVARC1001668	3.77	6.75	10.04	10.5	11.4	10.48
	OVARC1001702	1.18	2.21	2.42	3.86	2.07	2.25
	OVARC1001703	2.82	3.18	2.97	2.64	4.71	4.65
50	OVARC1001710	3.58	7.03	8.67	8.01	6.28	9.55
	OVARC1001711	1.96	7.3	3.36	5.01	4.15	5.4
	OVARC1001713	9.17	11.54	44.65	36.47	51.48	43.79
	OVARC1001725	1.01	5.45	6.11	2.56	3.77	4.01
	OVARC1001726	1.64	4.48	3.23	4.97	5.6	5.18
55	OVARC1001727	1.4	2.41	1.52	1.43	2.35	1.14

EP 1 130 094 A2

	OVARC1001731	120.62	110.86	255.43	140.73	139.03	74.2		
5	OVARC1001735	1.29	3.44	3.54	3.75	3.25	2.89		
	OVARC1001741	3.3	4.73	15.28	13.09	12.93	13.17		
	OVARC1001745	2.72	5.39	6.83	9.17	10.23	8.89	*	+
	OVARC1001759	3.31	9.01	6.31	7.61	7.61	11.95		
10	OVARC1001762	3.96	7.78	6.38	10.3	11.01	13.4	*	+
	OVARC1001766	5.33	7.8	11.99	15.56	16.86	15.33	*	+
	OVARC1001767	0.94	3.76	1.18	1.97	1.96	2.41		
	OVARC1001768	3.31	3.86	3.76	5.35	4.59	3.54		
15	OVARC1001770	3.04	6.58	9.98	11.46	9.08	9.46		
	OVARC1001776	2.11	4.7	3.5	4.72	3.64	2.92		
	OVARC1001791	1.13	4.77	3.54	3.07	3.12	3.42		
20	OVARC1001795	0.89	6.19	1.24	2.31	2.87	2.11		
	OVARC1001798	2.81	12.11	7.57	9.72	11.93	9.04		
	OVARC1001802	1.73	11.64	4.9	5.6	5.93	4.01		
	OVARC1001805	1.92	6.96	2.58	3.62	4.59	3.51		
	OVARC1001807	1.9	2.53	4.18	3.06	3.12	2.46		
25	OVARC1001809	12.38	14.06	76.32	55.87	81.41	52.83		
	OVARC1001812	1.44	3.39	3.15	3.23	4.63	3.71		
	OVARC1001813	1.61	4.29	2.33	2.93	3.98	2.51		
	OVARC1001820	1.67	7.15	3.21	3.47	3.76	3.22		
	OVARC1001828	0.78	6.85	2.36	1.91	3.23	2.2		
30	OVARC1001833	1.07	8.12	2.02	2.4	2.1	1.92		
	OVARC1001839	1.56	8.43	2.98	2.91	3.59	1.15		
	OVARC1001846	1.91	1.38	2.9	2.15	2.11	1.8		
	OVARC1001849	1.21	2.52	2.42	5.79	3.69	4.03	*	+
35	OVARC1001861	1.46	3.56	2.73	2.78	2.5	2.09		
	OVARC1001873	3.09	3.78	4.63	5.47	4.42	4.73		
	OVARC1001879	1.44	6.08	3.48	2.35	2.93	2.22		
	OVARC1001880	0.91	7.84	2.94	3.63	5.78	3.8		
	OVARC1001883	0.99	7.61	3.12	2.61	3.42	2.52		
40	OVARC1001900	1.11	7.07	4.03	2.57	3.61	2.89		
	OVARC1001901	0.54	1.84	1.21	2.42	1.37	2.43		
	OVARC1001911	0.59	1.57	1.66	1.51	1.39	1.55		
	OVARC1001916	1.86	3.13	3.35	4.16	4.61	3.51		
	OVARC1001928	1.45	3.53	1.55	1.58	1.62	1.72		
45	OVARC1001937	5.12	11.69	8.13	17.41	11.63	15.16		
	OVARC1001940	1.1	4.51	3.13	3.72	3.14	2.78		
	OVARC1001942	3.85	7.4	8.03	11.47	13.91	12.77	*	+
	OVARC1001943	7.16	10.07	11.08	9.62	13.85	11.87		
	OVARC1001949	1.69	3.34	4.15	5.35	4.01	5.55		
50	OVARC1001950	1.53	2.41	3.79	6.3	4.35	3.98		
	OVARC1001952	11.3	11.38	53.57	52.33	78.84	38.05		
	OVARC1001954	1.12	2.99	2.2	3.09	2.67	2.05		
	OVARC1001963	1	4.91	2.89	4.5	3.39	3.21		
	OVARC1001983	3.62	14.16	14.25	20.96	19.21	21.67		
55	OVARC1001987	3.12	6.54	5.94	6.08	8.39	8.02		
	OVARC1001989	1.41	5.2	4.96	4.54	5.59	5.26		
	OVARC1001991	1.74	3.27	4.08	4.57	3.86	3.27		
	OVARC1002005	4.14	3.55	7.66	10.01	9.06	8.2	*	+
	OVARC1002044	3.73	3.94	6.17	6.57	8.32	6.99	*	+
	OVARC1002046	10.28	16.21	20.07	29.4	37.78	37.02	**	+

EP 1 130 094 A2

	OVARC1002050	1.7	5.6	2.43	3.96	3.82	2.53
5	OVARC1002058	4.23	6.11	4.02	4.69	5.55	5.43
	OVARC1002066	11.47	13.5	25.49	26.02	28.69	22.63
	OVARC1002082	3.6	8.55	8.81	9.6	8.89	6.49
	OVARC1002091	3.17	5.67	8.37	9.49	5.49	7.64
10	OVARC1002092	1.38	2.72	2.2	4	3.97	1.88
	OVARC1002093	1.79	3.1	4.51	5.01	4.44	3.88
	OVARC1002094	1.55	6.24	4.17	36.42	27.25	28.35 ** +
	OVARC1002107	1.42	4.63	2.69	4.86	5.48	3.6
15	OVARC1002112	6.17	11.59	8.5	13.47	17.48	11.92
	OVARC1002126	2.66	6.35	6.68	7.95	6.44	8.79
	OVARC1002127	0.73	5.04	1.86	1.92	2.61	1.52
	OVARC1002138	1.4	1.79	1.86	3.16	4.82	2.75 * +
20	OVARC1002143	0.73	1.51	1.55	1.29	3.03	2.09
	OVARC1002156	2.42	3.87	4.19	4.43	3.9	3.65
	OVARC1002158	0.88	2.63	1.6	2.36	1.57	1.51
25	OVARC1002165	4.85	6.3	9.83	10.73	14.03	10.87
	OVARC1002176	0.86	5.08	3.59	2.01	3.46	2.64
	OVARC1002178	0.83	5.35	3.12	3.8	5.02	4.25
	OVARC1002182	1.29	2.89	3.77	2.45	4.64	3.12
	OVARC1002185	11.45	13.19	62.79	43.91	53.43	55.56
30	PLACE1000004	1.42	3.23	2.35	3.87	4.25	4.05 * +
	PLACE1000005	1.18	3.06	3.3	5.27	5.31	4.83 * +
	PLACE1000006	2.01	8.33	3.23	4.2	5.44	4.67
	PLACE1000007	0.97	5.13	2.89	3.03	2.47	2.56
	PLACE1000014	2.9	8.06	6.26	6.67	8.18	6.55
35	PLACE1000031	0.88	4.81	0.45	2.61	2.71	2.79
	PLACE1000033	1.23	2.15	2.75	2.42	3.17	2.56
	PLACE1000040	3.08	4.43	6.18	7.11	5.54	7.37
	PLACE1000048	1.83	3.24	2.14	3.32	3.96	3.74
	PLACE1000050	2.12	5.36	9.1	9	6.55	8.25
40	PLACE1000061	138.29	147.36	249.77	165.55	233.98	230.37
	PLACE1000066	14.23	15	19.46	15.86	15.62	18.52
	PLACE1000075	3.03	6.24	9.08	4.98	6.93	7.11
45	PLACE1000078	2.1	5.75	5	6.07	6.93	5.19
	PLACE1000081	1.08	1.88	1.52	1.13	1.89	1.27
	PLACE1000086	4.97	6.55	11.25	8.1	9.16	7.75
	PLACE1000094	0.7	4.18	1.72	1	3.44	2.96
50	PLACE1000101	4.67	8.44	7.7	11.69	10.38	13.65 * +
	PLACE1000121	0.87	6.29	2.02	1.95	2.85	2.39
	PLACE1000133	6.65	11.93	17.66	15.19	17.59	21.71
	PLACE1000142	1.79	6.03	5.66	2.64	4.77	4.24
55	PLACE1000146	1.95	4.51	2.89	3.71	5.02	2.82
	PLACE1000163	4.52	5.99	10.71	16.27	10.95	13.78
	PLACE1000172	1.12	2.63	1.48	1.81	3.21	2.29
	PLACE1000181	1.06	3	2.98	2.63	3.75	2.86
	PLACE1000184	1.17	3.08	1.48	1.87	3.28	2.27
	PLACE1000185	2.99	6.52	8.47	9.53	9.99	12.03
	PLACE1000198	0.78	4.09	2.49	2.19	2.17	1.93
	PLACE1000213	3.3	5.87	7.36	4.35	5.38	8.09
	PLACE1000214	1.37	4.29	4.54	5.22	6.72	4.22
	PLACE1000220	9.61	7.84	16.78	7.48	5.77	4.1

EP 1 130 094 A2

	PLACE1000231	2.48	4.1	4.92	4.57	4.65	3.91		
5	PLACE1000236	0.66	3.33	2.43	2.8	3.63	2.37		
	PLACE1000245	2.92	5.88	6.34	9.34	11.24	10.55	*	+
	PLACE1000246	5.15	8.27	9.95	3.29	2.55	2.86	*	-
	PLACE1000258	5.4	12.61	13.52	14.88	16.7	14.95		
10	PLACE1000288	1.68	7.22	2.96	2.83	4.02	2.48		
	PLACE1000292	3.72	9.02	8.85	10.23	20.58	9.21		
	PLACE1000302	0.56	1.01	1.39	1.07	0.92	0.62		
15	PLACE1000304	1.13	3.26	3.17	3.75	2.32	3.05		
	PLACE1000308	2.54	4.35	4.17	4.42	3.87	1.34		
	PLACE1000309	2.29	4.02	4	6.72	5.23	7.88	*	+
	PLACE1000312	1.33	3.44	2.48	2.74	3.99	2.5		
20	PLACE1000330	0.46	5.76	3.02	1.32	1.93	1.35		
	PLACE1000332	1.02	8.82	2.01	3.01	3.78	1.68		
	PLACE1000347	2.3	9.48	3.89	2.59	5.81	3.22		
	PLACE1000351	1.2	1.5	2.87	2.2	2.4	2		
25	PLACE1000374	2.01	3.03	7.02	8.89	6.55	6.85		
	PLACE1000380	2.39	4.27	3.95	4.9	2.12	2.38		
	PLACE1000383	1.03	2.62	1.9	2.53	3.64	2.4		
	PLACE1000397	0.63	4.06	1.89	2.82	3.34	3.47		
	PLACE1000401	1.22	6.39	2.24	2.23	3.05	2.36		
30	PLACE1000406	1.08	8.76	3.4	3.72	4.08	3.64		
	PLACE1000412	1.61	6.38	1.56	1.62	3.45	1.46		
	PLACE1000420	2.59	3.51	4.6	8.95	7.28	5.6	*	+
	PLACE1000421	0.99	1.3	2.32	2.97	2	1.7		
	PLACE1000423	16.6	23.29	32.85	10.67	8.02	8.09	*	-
35	PLACE1000424	1.36	3.09	2.12	3.35	2.65	1.97		
	PLACE1000430	0.77	4.36	1.95	3.51	2.94	3.77		
	PLACE1000433	1.06	5.9	1.65	1.89	2.6	1.8		
	PLACE1000435	1.39	7.21	4.77	6.22	6.29	4.22		
	PLACE1000437	6.06	10.65	10.14	17.29	20.07	18.79	**	+
40	PLACE1000442	3.75	3.85	6.27	7.81	5.7	6.7		
	PLACE1000444	2.14	3.94	8.96	11.14	11.55	9.8		
	PLACE1000453	5.57	11.03	14.16	10.42	7.4	2.99		
	PLACE1000456	1.25	2.21	1.97	1.33	2.18	1.07		
45	PLACE1000465	2.09	5.63	6.62	12.97	11.8	10.69	**	+
	PLACE1000481	2.32	8.1	3.73	6.89	6.64	6.45		
	PLACE1000492	1.15	4.45	2.95	3.27	3.06	2.81		
	PLACE1000508	1.36	4.64	4	3.91	4.24	3.71		
	PLACE1000512	4.91	4.29	6.39	8.12	7.8	4.6		
50	PLACE1000540	5.18	3.93	7.84	5.44	6.9	5.57		
	PLACE1000541	13.59	15.07	48.84	60.62	81.24	41.96		
	PLACE1000546	0.86	3.61	2.82	4.72	4.63	2.5		
	PLACE1000547	2.16	4.61	3.83	6.31	5.64	5.92	*	+
	PLACE1000560	2.08	5.97	2.1	1.62	2.8	1.72		
55	PLACE1000562	2.8	6.23	6.04	8.86	11.26	8.61	*	+
	PLACE1000564	1.54	6.4	3.07	3.16	4.41	3.43		
	PLACE1000583	3.75	3.28	6.32	6.78	11.53	6.8		
	PLACE1000587	8.52	9.32	12.99	13.64	14.69	9.43		
	PLACE1000588	1.92	4.36	3.99	8.79	8.15	4.48		
	PLACE1000596	1.99	5.34	4.39	7.8	6.74	4.51		
	PLACE1000599	2.39	5.51	7.05	7.92	7.79	6.46		

EP 1 130 094 A2

	PLACE1000605	5.12	11.43	7.06	14.2	15.1	12.67	*	+
5	PLACE1000610	2.01	6.08	3.54	5.26	4.48	2.94		
	PLACE1000611	13.18	19.13	24.68	16.45	20.37	22.79		
	PLACE1000626	3.19	4.04	8.04	5.71	9.93	8.12		
10	PLACE1000633	1.32	2.12	3.95	4.8	6.06	3.59		
	PLACE1000636	1.15	2.54	1.43	2.72	4.25	2.94		
	PLACE1000653	5.07	8.56	9.29	11.07	11.87	14.08	*	+
15	PLACE1000656	4.2	12.9	25.22	16.66	16.71	12.92		
	PLACE1000663	2	6.43	3.59	2.39	6.61	4.03		
	PLACE1000706	2	6.3	5.04	5.37	7.27	6.26		
	PLACE1000712	3.9	9.52	10.82	10.49	10.07	9.11		
20	PLACE1000716	0.98	2.75	3.44	2.44	3.2	2.82		
	PLACE1000740	2.74	5.28	6.24	8.83	8.13	9.69	*	+
	PLACE1000748	3.35	3.51	6.81	3.12	5.02	4.23		
	PLACE1000749	3.49	6.35	5.94	4.61	4.65	6.02		
25	PLACE1000751	2.71	5.34	4.07	7.81	8.32	8.36	**	+
	PLACE1000755	1.39	6.14	1.93	2.55	5.1	2.96		
	PLACE1000769	2.29	6.8	3.45	3.33	4.58	2.6		
	PLACE1000778	0.87	1.48	1.99	2.05	2.94	2.38		
	PLACE1000785	9.56	12.21	27.18	28	24.34	29.54		
	PLACE1000786	2.68	4.22	3.63	3.09	3.77	3.7		
30	PLACE1000793	4.05	7.21	6.7	6.06	7.6	9.1		
	PLACE1000795	2.15	5.5	3.99	4.44	5.29	4.31		
	PLACE1000798	0.88	8.44	3.24	3.13	3.8	3.72		
	PLACE1000812	2.13	5.08	4.46	5.06	5.16	6.03		
	PLACE1000823	1.71	5.2	4.89	5.67	7.28	4.84		
35	PLACE1000825	1.6	2.86	2.02	3.77	3.96	3.76	*	+
	PLACE1000838	16	15.77	23.73	13.88	15.6	15.65		
	PLACE1000841	1.22	3.78	3.31	3.97	10.65	3.77		
	PLACE1000843	2.14	6.2	5.68	5.79	7.7	5.38		
	PLACE1000849	2.79	8.82	6.72	7.24	6.78	10.02		
40	PLACE1000856	2.01	5.3	3.59	3.42	4.79	4.19		
	PLACE1000863	5.2	7.58	9.56	8.97	12.34	11.53		
	PLACE1000876	3.65	7.6	6.02	6.7	9.95	9.06		
	PLACE1000899	1.36	2.24	3.12	4.12	5.14	4.22	*	+
45	PLACE1000907	4.82	5.53	9.59	6.77	8.44	5.83		
	PLACE1000909	1.18	3.31	2.45	3.65	3.88	3.44		
	PLACE1000912	0.42	4.55	1.77	1.76	2.72	1.46		
	PLACE1000914	1.05	4.41	3.5	3	6.09	4.22		
	PLACE1000918	0.54	4.49	1.61	1.82	3.13	1.98		
	PLACE1000927	10.48	12.41	16.9	20.91	23.21	25.47	*	+
50	PLACE1000931	0.69	3.44	2.12	2.44	3.94	3.3		
	PLACE1000944	2.55	2.24	4.78	3.84	3.32	2.09		
	PLACE1000948	0.52	2.31	2.96	2.21	2.72	1.72		
	PLACE1000958	0.12	2.2	1.73	1.11	1.77	2.27		
55	PLACE1000972	1.01	3.43	2.89	4.49	5.33	3.75		
	PLACE1000977	2.33	5.67	4.42	2.71	5.33	5.25		
	PLACE1000979	1.63	8.01	3.93	4.24	5.92	4.57		
	PLACE1000986	3.37	16.51	6.63	6.97	8.75	7.69		
	PLACE1000987	1.76	10.13	4.79	4.17	4.74	5.11		
	PLACE1001000	4.85	4.62	7.76	6.02	4.25	3.02		
	PLACE1001007	7	6.94	14.66	5.39	3.76	3.47		

EP 1 130 094 A2

	PLACE1001010	0.61	2.04	2.45	2.56	2.73	2.84		
5	PLACE1001015	0.88	2.55	1.84	2.36	1.72	2.42		
	PLACE1001016	1.79	4.54	4.29	6.37	9	6.57	*	+
	PLACE1001022	0.68	6.5	2.45	1.9	2.39	1.29		
10	PLACE1001024	1.05	8.89	1.83	1.34	2.49	2.35		
	PLACE1001036	2.63	10.55	5.42	3.62	5.49	5.43		
	PLACE1001038	50.16	49.81	118.83	82.67	64.83	52.8		
15	PLACE1001048	1.07	1.82	0.92	2.39	2.09	1.21		
	PLACE1001054	9.95	10.74	63.88	62.96	79.44	66.71		
	PLACE1001062	1.45	4.19	3.71	3.12	4.17	3.05		
	PLACE1001063	1.35	3.74	2.2	4.06	3.65	2.74		
20	PLACE1001076	0.46	6.48	1	1.86	2.18	1.62		
	PLACE1001081	1.53	7.95	3.33	3.65	5.24	4.8		
	PLACE1001088	1.32	5.24	1.22	1.42	2.81	1.37		
	PLACE1001092	2.31	2.47	4.68	5.8	4.18	3.9		
25	PLACE1001098	0.93	2.62	4.53	5.49	4.05	3.17		
	PLACE1001100	1.31	2.58	2.48	4.27	4.17	3.37	*	+
	PLACE1001104	1.95	4.09	4.54	3.39	3.42	4.47		
	PLACE1001114	1.56	6.54	4.33	5.17	3.78	3.27		
	PLACE1001118	2.52	5.77	6.12	6.21	6.14	5.1		
	PLACE1001123	2.86	5.3	7.53	7.08	8.51	7.63		
30	PLACE1001136	1.58	4.39	5.13	5.29	5.95	5.85		
	PLACE1001144	6.27	5.67	13.43	10.34	11	10.08		
	PLACE1001147	2.11	2.98	6.03	6.13	5.15	4.83		
	PLACE1001148	1.72	1.31	1.89	1.76	2.39	2.31		
	PLACE1001159	0.86	2.37	2.05	2.27	3.73	1.43		
35	PLACE1001168	8.87	14.52	15.09	25.46	23.18	30.79	*	+
	PLACE1001171	0.69	3.89	1.23	2.53	1.42	1.53		
	PLACE1001183	0.24	3.61	1.81	1.57	2.78	1.38		
	PLACE1001185	3.13	7.43	3.76	5	6.4	5.64		
40	PLACE1001201	1.77	2.8	3.29	6.32	6.94	6.32	**	+
	PLACE1001229	7.51	8.56	12.64	15.24	11.45	10.42		
	PLACE1001231	1.83	2.73	3.07	4.09	5.1	2.3		
	PLACE1001238	1.52	4.35	3.74	3.65	4.52	4.57		
	PLACE1001241	1.63	5.58	2.92	5.73	8.13	7.04		
45	PLACE1001242	22.28	29.54	30.28	46.43	48.89	62.65	*	+
	PLACE1001247	2.43	7.02	4.07	5.03	5.91	4.52		
	PLACE1001250	1.01	5.36	3.61	4.68	4.39	4.81		
	PLACE1001257	2.99	3.06	7.06	7.89	9.21	7.69		
	PLACE1001272	3.19	4.27	5.68	7.13	6.43	5.14		
50	PLACE1001279	0.96	3.12	2.74	3.08	3.81	3.29		
	PLACE1001280	1.08	4.75	2.68	4.98	4.45	2.86		
	PLACE1001294	1.91	7.23	6.91	4.88	5.57	6.18		
	PLACE1001295	4.16	9.94	7.53	8.55	11.85	8.43		
	PLACE1001300	2.46	7.9	4.31	4.65	14.73	4.95		
55	PLACE1001304	3	8.27	10.47	8.57	10.81	10.64		
	PLACE1001311	3.95	3.34	5.67	6.85	9.14	7.6	*	+
	PLACE1001323	2.17	2.95	5.12	5.66	8.43	5.5		
	PLACE1001325	0.88	1.95	3.71	2.84	3.56	3.27		
	PLACE1001340	5.18	6.99	9.8	8.69	12.02	10.48		
	PLACE1001344	1.52	3.49	1.77	2.34	2.06	1.75		
	PLACE1001351	3.23	6.39	8.39	6.4	8.62	6.1		

EP 1 130 094 A2

	PLACE1001366	1	4.49	4.02	4.19	4.6	3.72		
5	PLACE1001377	3.02	4.97	5.1	7.91	7.28	5.83	*	+
	PLACE1001383	2.31	4.13	3.53	2.62	5.5	5.72		
	PLACE1001384	1.81	3.23	2.89	2.05	3.43	3.15		
	PLACE1001387	1.65	3.64	3.7	3.03	4.83	3		
	PLACE1001395	3.72	6.64	6.54	7.01	7.61	7.73		
10	PLACE1001399	3.71	6.58	9.31	7.37	8.61	9.22		
	PLACE1001401	0.83	5.25	2.33	1.55	1.76	0.87		
	PLACE1001407	11.65	21.8	24.47	22.63	18.09	26.24		
	PLACE1001412	1.6	4.98	4.53	4.08	4.42	3.83		
	PLACE1001414	2.3	3.02	5.86	7.57	5.13	6.83		
15	PLACE1001416	2.99	4.71	3.29	5.62	4.04	7.08		
	PLACE1001433	33.62	33.05	51.64	49.1	58.33	55.88		
	PLACE1001440	1.95	3.99	3.96	3.6	3.53	2.1		
	PLACE1001456	1.64	5.5	4.26	4.15	4.87	4.49		
	PLACE1001464	32.76	28.05	47.41	53.22	68.42	61.32	*	+
20	PLACE1001468	0.85	5.04	1.17	1.56	2.55	2.27		
	PLACE1001484	1.31	4.85	2.96	4.25	5.8	3.04		
	PLACE1001500	0.92	2.22	2.14	2.72	3.34	3.26	*	+
	PLACE1001502	1.36	3.6	3.9	3.54	5.9	4.54		
	PLACE1001503	1.7	4.58	6.72	7.47	8.2	8.05		
25	PLACE1001505	6.34	14.13	16.16	39.97	27.14	46.65	*	+
	PLACE1001513	4.09	10.82	8.17	5.87	8.53	14.61		
	PLACE1001516	0.61	4.33	1.33	1.71	3.49	1.99		
	PLACE1001517	5.56	8.58	14.77	14.14	14.96	14.28		
	PLACE1001523	12.83	14.09	20.42	22.79	19.74	32.9		
30	PLACE1001526	5.12	4.89	8.42	9.51	9.11	6.89		
	PLACE1001534	2.12	5.12	3.58	3.62	5.55	3.99		
	PLACE1001536	0.61	2.5	1.52	2.11	3.2	1.9		
	PLACE1001545	17.97	23.9	38.46	33.78	45.13	66.08		
35	PLACE1001551	2.55	6.26	6.15	4.72	6.59	6.71		
	PLACE1001564	1.37	4.87	2.88	4.01	3.57	3.7		
	PLACE1001570	2.62	5.95	4.18	2.19	3.82	4.32		
	PLACE1001571	2.04	4.51	6.07	5.69	6.27	5.81		
	PLACE1001595	4.73	4.64	10.04	11.6	8.27	5.28		
40	PLACE1001602	7.23	8.39	18.65	20.38	18.68	19.71		
	PLACE1001603	2.01	3.83	5.37	6.86	5.86	4.56		
	PLACE1001608	3.44	7.22	5.9	5.82	7.73	8.7		
	PLACE1001610	3.77	8.4	8.22	9.26	9.49	9.85		
	PLACE1001611	1.94	7.34	3.65	2.28	3.85	1.88		
45	PLACE1001629	0.78	6.77	2.24	3.62	3.36	3.52		
	PLACE1001632	1.66	8.26	4.04	4.3	4.14	4.37		
	PLACE1001634	7.4	9.92	39.12	23.85	32.41	18.38		
	PLACE1001637	0.84	2.16	1.25	1.41	2.4	1.1		
	PLACE1001640	1.33	3.27	4.66	2.68	4.85	4.49		
50	PLACE1001655	0.83	2.93	2.06	2.82	2.14	2.02		
	PLACE1001672	1.84	7.04	4.01	3.3	4.41	4.09		
	PLACE1001676	1.38	8.49	3.54	4.63	4.77	3.85		
	PLACE1001683	12.79	23.62	24.61	25.33	30.22	27.13		
55	PLACE1001691	3.41	12.29	6.72	9.03	8.96	9.83		
	PLACE1001692	1.47	2.96	5.25	5.87	5.6	5.13		
	PLACE1001705	3.02	3.75	9.88	10.06	9.21	8.32		

EP 1 130 094 A2

	PLACE1001716	1.68	3	2.61	2.24	3.79	3.58		
5	PLACE1001720	1.49	2.62	2.21	1.56	2.45	1.71		
	PLACE1001728	1.43	6.19	4.24	1.96	2.04	2.51		
	PLACE1001729	2.12	8.13	4.44	3.8	4.52	4.36		
	PLACE1001739	2.61	9.55	4.04	4.95	7.24	6.16		
10	PLACE1001740	0.92	5.36	2.09	1.92	2.1	1.69		
	PLACE1001745	1.15	0.98	3.22	1.87	2.48	2.31		
	PLACE1001746	1.04	2.25	2.55	4.64	3.4	2.82		
	PLACE1001748	4.74	7.01	8.18	8.19	6.58	5.96		
	PLACE1001753	2.06	3.54	3.29	7.44	5.57	5.82	*	+
15	PLACE1001756	5.6	11.31	38.07	31.78	44.99	35.99		
	PLACE1001760	6.54	12.23	12.85	16.36	16.96	16.66	*	+
	PLACE1001767	11.26	14.98	59.72	45.37	61.46	45.39		
	PLACE1001771	1.96	6.64	4.03	4.32	5.22	4.54		
	PLACE1001775	2.23	2.81	6.72	5.1	3.11	4.79		
	PLACE1001777	83.34	145.9	190.82	142.92	71.27	59.69		
20	PLACE1001781	1.9	3.86	4.91	8.72	3.39	2.3		
	PLACE1001783	0.76	3.21	2.06	4.84	2.09	1.54		
	PLACE1001786	1.77	6.61	2.72	3.7	3.32	2.6		
	PLACE1001788	5.16	9.07	7.14	10.52	8.74	9.32		
	PLACE1001795	1.92	4.4	4.82	5.42	4.61	5.42		
25	PLACE1001799	0.69	3.62	2.11	1.86	2.83	1.97		
	PLACE1001810	0.89	1.52	1.76	2.73	3.91	1.73		
	PLACE1001817	5.53	6.12	10.88	10.56	9.4	6.38		
	PLACE1001821	4.68	6.07	7.11	8.37	9.92	4.99		
	PLACE1001836	0.91	3.12	2.38	2.69	4.12	2.63		
30	PLACE1001844	1.55	5.1	3.48	4.42	4.36	4.09		
	PLACE1001845	3.62	8.38	7.39	7.88	7.55	9.93		
	PLACE1001858	2.56	6.58	3.52	5.26	7.48	6.05		
	PLACE1001869	3.13	7.15	4.85	6.09	6.46	5.66		
	PLACE1001890	11.74	11.92	21.45	173.44	255.31	125.13	*	+
35	PLACE1001897	9.19	13.85	16.44	22.22	23.13	12.95		
	PLACE1001902	10.13	12.6	21.53	22.74	27.67	12.77		
	PLACE1001904	1.38	3.72	1.51	2.45	2.53	2.35		
	PLACE1001907	3.36	6.76	5.71	7.67	5.67	5.59		
	PLACE1001910	83.6	82.16	135.34	301.29	325.42	244.59	**	+
40	PLACE1001912	1.53	6.6	3.36	5.54	5.48	4.85		
	PLACE1001918	17.31	22.95	30.16	31.14	40.44	40.02	*	+
	PLACE1001920	2.07	3.51	5.43	11.97	13.8	11.4	**	+
	PLACE1001928	3.06	2.96	4.67	5.29	9.7	5.31		
45	PLACE1001930	1.17	3.92	2.2	2.9	4.73	3.22		
	PLACE1001949	1.16	3.67	1.78	3.84	4.24	3.18		
	PLACE1001959	1.36	4.7	3.16	2.63	3.17	2.26		
	PLACE1001969	2.09	7.83	7.21	6.56	10.73	6.57		
	PLACE1001974	7.39	11.98	11.87	11.43	16.09	16.06		
50	PLACE1001981	0.77	4.38	3.22	1.77	3.88	2.36		
	PLACE1001983	3.81	4.12	5.32	5.92	6.16	5.72	*	+
	PLACE1001989	2.34	4.15	5.02	4.37	5.91	3.72		
	PLACE1002004	3.07	4.06	8.05	9.22	9.69	7.18		
	PLACE1002008	8.4	11.76	17	23.36	22.19	22.42	*	+
55	PLACE1002015	26.96	30.92	67.62	105.75	88.42	94.15	*	+
	PLACE1002044	3.79	8.07	5.86	4.64	6.39	6.4		

EP 1 130 094 A2

	PLACE1002046	1.78	5.68	1.9	4.3	5.79	4.97		
5	PLACE1002052	1.09	4.98	2.26	1.38	2.41	2.32		
	PLACE1002066	4.79	6.3	8.29	10.24	10.77	9.93	*	+
	PLACE1002072	2.55	3.91	4.86	6	5.48	6	*	+
	PLACE1002073	0.51	2.83	2.29	2.35	4.06	2.91		
10	PLACE1002080	1.81	6.49	6.13	4.76	6.82	5.72		
	PLACE1002081	1.66	6.13	4.06	3.74	4.86	4.3		
	PLACE1002090	7.74	16.55	13.87	12.53	14.4	19.41		
	PLACE1002095	2.97	6.22	8.45	10.01	10.18	11.32	*	+
	PLACE1002102	4.26	8.56	8.81	9.47	9.56	10.67		
	PLACE1002109	2.57	5.08	3.81	4.66	6.17	6.32		
15	PLACE1002115	1.75	3.57	2.48	2.78	4.26	2.59		
	PLACE1002119	15.65	15.3	35.78	37.28	32.59	38.23		
	PLACE1002140	5.25	8.45	14.05	19.93	17.14	17.19	*	+
	PLACE1002150	1.54	8.26	4.25	3.23	5.36	4.12		
	PLACE1002153	1.6	5.75	2.58	3.47	5.76	4.48		
20	PLACE1002157	0.87	2.96	1.72	1.76	3.28	3.73		
	PLACE1002163	2.13	4.67	4.55	6.21	8.81	6.03		
	PLACE1002168	2.39	4.04	4.42	4.68	6.28	3.22		
	PLACE1002170	2.73	3.53	7.35	4.89	5.33	3.74		
	PLACE1002171	3.09	6.11	10.02	18.44	14.63	13.93	*	+
	PLACE1002180	3.16	6.23	6.77	4.63	8.54	8.39		
25	PLACE1002184	9.2	15.58	18.42	124.63	250.27	333.14	*	+
	PLACE1002200	1.35	5.67	2.38	2.97	2.89	2.26		
	PLACE1002205	3.3	6.47	18.07	17.08	18.38	14.61		
	PLACE1002213	2.2	4.16	4.93	5.52	8.03	6.03		
30	PLACE1002219	1.05	1.91	2.23	3.33	3.53	1.96		
	PLACE1002227	0.68	2.65	1.7	1.5	3.03	1.67		
	PLACE1002253	0.32	2.67	1.28	1.47	0.76	0.43		
	PLACE1002256	1.16	4.78	3.31	3.54	3.01	4.79		
	PLACE1002259	1.46	5.69	4.48	3.22	2.98	2.31		
35	PLACE1002285	1.16	10.74	2.29	1.55	2.38	1.24		
	PLACE1002301	9.42	17.5	14.68	12.7	10.48	11.7		
	PLACE1002310	4.28	10.16	9.86	8.82	7.87	9.94		
	PLACE1002311	1.84	2.94	3.87	2.96	2.87	2.03		
	PLACE1002319	2.31	2.64	2.94	3.21	3.23	3.92	*	+
40	PLACE1002329	0.56	2.54	2.5	4.07	3.58	3.07		
	PLACE1002333	1.34	3.1	1.96	1.22	2.44	2		
	PLACE1002342	4.19	9.04	9.44	5.06	8.52	8.17		
	PLACE1002343	0.49	6.98	2.94	2.08	1.9	2.52		
	PLACE1002355	1.31	9.39	2.36	3.33	4.35	2.63		
45	PLACE1002358	1.15	7.94	3.3	2.6	2.65	2.13		
	PLACE1002359	1.91	2.17	3.47	4.7	3.91	3.42		
	PLACE1002374	29.69	28.18	54.19	53.9	34.73	36.14		
	PLACE1002376	3.58	5.91	7.86	6.23	6.82	6.56		
	PLACE1002379	6.24	7.66	6.63	10.13	9.68	10.9	**	+
50	PLACE1002386	0.86	5.32	1.35	1.87	2.05	1.51		
	PLACE1002395	3.69	9.97	17.13	16.43	20.62	16.16		
	PLACE1002399	2.38	11.09	3.42	5.31	10.38	7.39		
	PLACE1002407	1.09	5.22	2.31	2.3	4.01	3.66		
	PLACE1002433	1.63	2.17	2.97	2.96	4.35	3.66		
55	PLACE1002437	0.79	1.4	1.47	1.41	3.28	1.35		

EP 1 130 094 A2

	PLACE1002438	0.74	2.38	1.96	1.8	2.43	3.38		
5	PLACE1002446	4.64	8.42	5.95	10.27	8.88	11.99	*	+
	PLACE1002447	1.26	6.06	2.05	3.92	3.14	4.32		
	PLACE1002450	1.19	5.92	3.24	4.32	4.21	5.05		
10	PLACE1002462	0.81	4.02	2.94	3.51	2.99	3.13		
	PLACE1002465	0.96	4.69	2.2	2.69	4.31	2.24		
	PLACE1002474	1.61	2.26	3.23	3.85	4.41	3.6	*	+
15	PLACE1002477	11.11	14.51	32.39	44.06	41.42	26.68		
	PLACE1002493	3.39	4.1	10.1	14.39	16.66	9.49		
	PLACE1002497	0.68	2.81	0.67	1.45	0.93	0.99		
20	PLACE1002499	2.12	4.73	3	5.98	6.44	5.28	*	+
	PLACE1002500	2.61	6.52	7.36	7.58	10.45	7.25		
25	PLACE1002514	0.3	4.49	1.84	1.74	2.47	1.75		
	PLACE1002518	2.86	7.65	6.9	5.62	7.55	4.67		
	PLACE1002529	1.14	1.56	2.21	3.19	3.4	1.44		
30	PLACE1002532	1.31	1.82	3.18	5.75	4.94	5.59	**	+
	PLACE1002536	3.59	3.75	3.44	5.84	6.07	3.85		
	PLACE1002537	1.63	4.06	2.7	2.69	4.07	3.08		
35	PLACE1002539	1.86	5.68	2.75	4.53	5.29	4.78		
	PLACE1002547	6.09	8.06	7.3	12.32	11.02	11.26	**	+
	PLACE1002571	2.84	6.85	5.19	6.84	8.65	6.23		
	PLACE1002578	3.57	8.34	8.35	11.11	12.19	8.11		
40	PLACE1002583	1.33	1.61	2.32	3.18	4.02	2.46		
	PLACE1002591	0.82	1.62	2.34	3.25	4.43	1.92		
	PLACE1002598	6.56	10.95	12.39	11.93	9.04	7.74		
45	PLACE1002604	1.73	3.57	2.69	3.75	5.38	3.51		
	PLACE1002612	2.89	8.47	5.95	11.25	10.88	8.06		
	PLACE1002625	1.25	4.79	3.18	2.7	3.25	1.82		
50	PLACE1002638	2.94	8.01	6.66	7.78	6.81	7.29		
	PLACE1002655	1.39	6.51	5.57	7.19	7.62	6.46		
	PLACE1002665	4.57	3.88	5.4	7.47	12.16	10.75	*	+
55	PLACE1002685	0.58	1.12	1.3	0.67	2.43	0.98		
	PLACE1002692	7.42	8.56	16.7	19.27	22.67	16.29		
	PLACE1002714	1.8	3	2.11	2.43	3.14	2.24		
	PLACE1002721	2.94	4.37	3.88	5.88	7.1	4.28		
	PLACE1002722	0.92	5.42	1.97	1.37	3.28	1.85		
60	PLACE1002726	1.6	6.24	3.66	4.6	5.7	5.26		
	PLACE1002756	1.57	4.5	7.04	5.92	9.63	7.78		
	PLACE1002768	1.05	3.72	2.16	2.1	2.34	1.71		
	PLACE1002772	0.54	2.15	1.32	2.49	2.86	2.3		
	PLACE1002775	4.33	4.71	9.15	7.05	7.08	8.67		
65	PLACE1002780	185.63	218.72	325.36	272.21	244.38	305.38		
	PLACE1002782	0.4	3.76	1.1	1.62	1.69	1.14		
	PLACE1002794	1.5	6.71	3.27	2.26	4.59	4.36		
	PLACE1002795	1.92	6.45	0.81	2.37	3.63	2.77		
70	PLACE1002811	0.6	1.57	1.34	1.9	1.46	1.16		
	PLACE1002815	6.39	7	10.49	7.24	3.16	9.21		
	PLACE1002816	8.5	9.72	9.05	7.22	8.2	7.97	*	-
	PLACE1002822	0.58	2.51	2.06	2.2	2.87	1.94		
	PLACE1002833	9.98	15.11	16.78	15.42	15.99	16.56		
	PLACE1002834	3.2	8.08	6.57	6.23	6.79	8.41		
75	PLACE1002835	0.62	4.14	1.72	0.85	1.83	1.79		

EP 1 130 094 A2

	PLACE1002839	1.13	5.75	2.72	2.89	4.72	2.81		
5	PLACE1002851	1.52	1.87	1.41	1.98	2.15	2.7		
	PLACE1002853	4.18	6.23	9.15	6.26	5.6	7		
	PLACE1002881	3.42	5.2	11.04	8.35	11.57	10.26		
	PLACE1002901	9.66	12.66	20.09	24.14	25.51	30.67	*	+
10	PLACE1002904	0.89	7.35	1.41	1.98	1.95	3.09		
	PLACE1002905	1.36	5.46	3.26	4.04	4.46	3.4		
	PLACE1002908	1.6	5.19	3.18	3.84	5.27	3.81		
	PLACE1002911	3.91	6.96	6.9	4.66	7.89	6.75		
	PLACE1002941	1.57	2.2	2.48	3.94	2.02	2.31		
	PLACE1002950	9.59	9.15	14.74	5.31	8.02	14.51		
15	PLACE1002955	47.83	40.69	72.7	82.17	62.5	84.64		
	PLACE1002958	19.36	26.92	35.27	35.6	35.35	59.02		
	PLACE1002962	1.03	4.03	2.2	1.41	2.63	1.67		
	PLACE1002967	1.34	4.83	3.19	4.37	3.52	2.81		
	PLACE1002968	1.2	5.14	2.7	2.55	3.05	1.81		
20	PLACE1002976	8.94	12.08	24.23	24.5	36.89	30.05		
	PLACE1002991	2.68	3.05	6.66	3.49	4.56	3.6		
	PLACE1002993	2.72	3.86	5.52	8.21	6.92	5.56		
	PLACE1002996	2.02	3.03	3.43	5.54	3.52	3.01		
	PLACE1003010	1.91	3.69	4.27	4.31	3.86	3.32		
25	PLACE1003025	2.85	7.01	6.1	8.57	11.37	10.11	*	+
	PLACE1003027	5.02	13.08	9.31	8.55	12.45	12.76		
	PLACE1003044	1.95	8.24	2.61	3.64	4.16	2.74		
	PLACE1003045	1.41	7.75	1.77	1.88	2.64	1.01		
	PLACE1003052	2.19	3.16	5.74	4.44	3.6	1.99		
30	PLACE1003083	1.59	3.04	3.23	3.06	1.61	2.25		
	PLACE1003085	3.91	6.19	5.6	9.46	5.89	3.33		
	PLACE1003092	3.94	4.87	6.25	7	5.6	6.17		
	PLACE1003097	0.37	3.06	1.44	2.12	1.88	1.63		
	PLACE1003100	1.65	7.1	4.2	3.88	4.74	4.29		
35	PLACE1003108	1.26	10.37	2.91	3.32	4.44	2.39		
	PLACE1003115	11.39	18.3	58.59	73.64	99.24	69.1	*	+
	PLACE1003120	3.1	3.08	9.71	11.34	8.32	10.19		
	PLACE1003135	0.72	2.04	1.09	1.56	2.89	1.08		
	PLACE1003136	3.95	5.82	6.05	9.03	6.55	7.34		
40	PLACE1003141	2.04	2.97	2.1	1.97	2.49	1.8		
	PLACE1003145	1.21	4.17	2.52	6.24	6.88	7.67	*	+
	PLACE1003147	2.87	7.85	5.71	5.02	5.25	6.28		
	PLACE1003153	0.54	7.63	2.14	1.66	3.2	1.82		
	PLACE1003163	6.09	13.55	8.19	8.39	14.09	12.26		
45	PLACE1003172	23.21	21.74	44.19	47.78	43.17	39.52		
	PLACE1003174	2.31	2.49	3.75	4.3	3.55	1.68		
	PLACE1003176	0.47	2	1.89	2.88	1.27	1.46		
	PLACE1003181	1.72	4.19	2.72	2.5	2.76	2.36		
	PLACE1003184	0.76	3.92	1.53	1.91	1.49	2.06		
50	PLACE1003190	2.39	9.81	8.67	10.73	7.98	10.34		
	PLACE1003200	0.29	4.48	1.84	0.72	1.92	1.16		
	PLACE1003205	3.94	7.07	9.68	6.82	10.38	7.2		
	PLACE1003209	1.43	2.18	2.62	2.28	1.82	2.89		
55	PLACE1003214	0.83	1.3	2	2.15	2.44	1.81		
	PLACE1003229	2.08	2.78	2.9	2.78	3.35	3.48		

EP 1 130 094 A2

	PLACE1003238	0.46	2.34	1.24	1.35	2	0.75
5	PLACE1003249	1.87	5.04	4.7	7.33	7.56	5.89
	PLACE1003256	3.47	7.69	7.94	8.82	7.68	6.08
	PLACE1003258	1.03	3.81	3.48	2.42	2.19	0.87
	PLACE1003279	3.09	7.19	9.02	11.15	13.56	11.58 *
	PLACE1003294	0.95	1.54	1.59	1.57	1.25	2.64
10	PLACE1003296	1.49	2.6	2.45	2.59	3.11	2.4
	PLACE1003297	7.52	10.15	31.88	23.01	23.49	19.3
	PLACE1003302	3.92	5.16	6.99	5.8	4.72	5.47
	PLACE1003334	1.51	4.41	1.91	2.4	3.59	3.09
15	PLACE1003337	13.69	16.3	29.83	28.53	34.27	25.76
	PLACE1003342	1.05	4.07	1.89	2.15	2.35	1.97
	PLACE1003343	1.07	4.98	1.61	2.02	2.75	2.12
20	PLACE1003344	6.25	5.33	12.83	11.18	11.35	11.98
	PLACE1003353	19.67	16.04	40.09	37.78	42.55	40.26
	PLACE1003361	1.82	3.64	3.72	5.85	5.31	4.6 *
	PLACE1003366	1.45	4.35	3.63	3.22	3.33	2.97
25	PLACE1003369	2.75	4.51	3.49	3.29	3.25	4.62
	PLACE1003372	2.08	5.73	2.68	5.45	4.72	3.39
	PLACE1003373	2.85	7.37	6.62	8.8	11.81	9.89
	PLACE1003375	1.42	4.91	1.92	2.59	2.95	3.21
30	PLACE1003378	0.94	0.94	0.98	0.7	1.66	1.08
	PLACE1003383	0.87	1.55	2.33	1.59	3.15	1.57
	PLACE1003394	10.55	12.49	24.08	11.75	22.99	17.27
	PLACE1003401	0.79	3.91	1.34	1.03	2.13	1.04
35	PLACE1003405	1.5	3.97	2.22	2.54	2.46	2.04
	PLACE1003407	2.39	6.06	5.16	3.96	6.3	4.02
	PLACE1003420	3.26	7.69	6.19	6.8	10.92	8.7
	PLACE1003428	0.63	3.3	2.62	2.07	2.94	1.96
40	PLACE1003432	6.14	5.81	8.2	6.64	7.05	5.42
	PLACE1003438	0.45	2.66	0.93	2.41	2.34	1.99
	PLACE1003452	1.87	5.02	5.08	4.53	3.43	3.84
45	PLACE1003454	2.49	5.59	7.34	7.31	6.95	5.61
	PLACE1003455	2.58	4.26	2.35	2.97	3.01	3.17
	PLACE1003456	3.22	7.74	8.62	6.9	7.2	7.79
	PLACE1003460	6.39	13.35	14.87	13.02	16.76	12.86
50	PLACE1003478	1.15	1.71	0.86	2.33	2.07	1.24
	PLACE1003484	12.06	12.21	45.33	28.12	31.5	34.2
	PLACE1003493	1.61	4.72	4.9	3.84	5.96	5.08
	PLACE1003503	85.45	87.35	107.79	115.17	111.85	172.81
55	PLACE1003505	1.99	6.77	4.78	7.44	6.63	8.87
	PLACE1003516	0.86	6.78	2.7	2.8	3.95	2.39
	PLACE1003519	17.58	26.29	50.41	45.77	36.97	58.75
	PLACE1003520	14.18	25.48	35.96	25.73	31.4	32.19
	PLACE1003521	2.71	3.64	4.93	5.97	4.71	7.4
	PLACE1003525	8.45	11.81	45.05	33.94	43.71	36.88
	PLACE1003528	39.18	44.68	136.4	106.04	122.76	127.22
	PLACE1003529	1.46	4.26	3.29	2.4	3.94	3.83
	PLACE1003537	4.41	9.05	11.05	11.36	13.77	13.3
	PLACE1003549	1.1	5.02	4.59	5.61	6.01	5.93
	PLACE1003553	1.6	5.89	3.88	4.02	4.17	4.23
55	PLACE1003566	5.93	9.8	17.51	13.03	19.09	14.58

EP 1 130 094 A2

5	PLACE1003568	3.01	2.71	5.76	5.69	4.43	4.04
	PLACE1003573	0.98	2.43	1.19	2.16	1.87	1.48
	PLACE1003575	2.16	3.09	3.44	3.34	3.5	4.15
	PLACE1003583	0.97	3.45	3.34	2.29	4.16	2.23
	PLACE1003584	1.23	4.46	4.01	3.56	3.8	2.65
10	PLACE1003592	4.4	8.48	9.48	7.11	10.48	9.53
	PLACE1003593	0.84	5.55	2.4	2.23	3.02	1.55
	PLACE1003594	4.24	6.76	6.01	5.78	6.68	7.36
	PLACE1003596	13.77	11.31	22.53	15.68	17.69	8.25
	PLACE1003598	2.83	3.63	5.02	4.89	3.7	2.95
15	PLACE1003602	1.8	4.24	6.36	4.37	3.54	2.68
	PLACE1003605	17.43	21.72	45.86	94.65	95.6	91.55 ** +
	PLACE1003611	2.34	5.18	6.07	5.65	7.14	6
	PLACE1003618	0.67	7.39	2.09	1.58	2.4	1.32
	PLACE1003625	1.78	10.41	2.75	3.33	5.48	2.8
	PLACE1003626	8.77	15.99	17.14	10.87	14.46	13.19
20	PLACE1003630	1.8	2.57	5.8	7.05	4.67	5.86
	PLACE1003635	2.15	1.83	3.19	2.96	2.82	2.44
	PLACE1003638	1.3	2.58	3	5.21	4.19	3.13
	PLACE1003644	4.01	5.7	7.25	7.81	9.13	8.76 * +
	PLACE1003654	2.56	6.14	4.04	3.54	6.96	6.4
25	PLACE1003656	2.69	7.79	6.12	6.54	5.63	4.77
	PLACE1003660	0.26	9.54	3.5	3.08	4.92	4.11
	PLACE1003669	2.43	9.05	3.67	2.59	4.26	3.08
	PLACE1003670	5.37	5.7	9.44	11.01	8.26	8.76
	PLACE1003671	1.66	1.22	3.57	3.11	2.57	1.57
30	PLACE1003697	7.27	7.99	9.8	8.23	6.06	6.42
	PLACE1003704	3.12	3.97	5.17	5.96	7.25	5.97 * +
	PLACE1003709	0.89	2.63	0.8	1.19	1.24	2.44
	PLACE1003711	0.74	5.48	1.35	1.87	1.8	1.39
	PLACE1003723	1.07	6.99	4.7	4.2	5.31	4.16
35	PLACE1003724	3.31	10.74	9.1	9.11	11.79	10.49
	PLACE1003737	2.14	2.21	4.72	3.35	3.1	3.29
	PLACE1003738	1.06	1.94	3.13	3.96	3.92	3.41
	PLACE1003742	2.25	3.58	5.71	6.81	6.18	2.85
	PLACE1003744	6.13	8.86	14.6	16.21	17.96	19.13 * +
40	PLACE1003758	0.85	4.55	0.96	2	1.46	1.16
	PLACE1003760	13.44	18.68	27.23	31.82	20.52	22.79
	PLACE1003762	1.45	4.97	3.7	3.77	3.78	3.49
	PLACE1003765	1.18	5.23	3.45	2.01	3.1	2.11
45	PLACE1003768	0.36	1.14	1.36	1.45	2.75	1.07
	PLACE1003771	1.28	1.94	2.07	1.84	3.13	1.43
	PLACE1003772	34.15	38.19	97.86	62.42	64.06	52.43
	PLACE1003783	1.48	3.02	2.22	18.65	19.53	16.61 ** +
	PLACE1003784	0.69	3.92	0.87	2.09	2.19	2.68
50	PLACE1003788	0.4	4.92	1.06	1.85	1.71	0.32
	PLACE1003795	1.01	4.1	3.57	4.73	4.38	3.54
	PLACE1003827	13.83	20.46	20.72	22.48	30.84	25.92
	PLACE1003833	0.98	1.49	3.9	3.65	4.33	3.31
	PLACE1003839	22.55	19.18	52.95	50.39	56.11	43.86
55	PLACE1003845	6.09	6.88	11.72	24.98	19.99	10.6
	PLACE1003850	3.16	4.84	7.19	5.45	5.95	6.39

EP 1 130 094 A2

	PLACE1003852	0.25	3.36	1.09	0.99	1.58	1.05
5	PLACE1003858	1.34	4.42	1.99	2.04	1.85	2.92
	PLACE1003861	0.95	4.51	1.63	2.98	2.78	1.73
	PLACE1003864	0.94	5.5	2.74	2.88	3.86	2.69
	PLACE1003870	3.84	3.4	13.2	10.71	16.12	12.03
	PLACE1003885	1.33	1.42	1.59	3.07	3.76	2.38 *
10	PLACE1003886	4.56	6.01	5.75	9.27	6.87	4.3
	PLACE1003888	0.75	3.79	1.96	2.87	3.42	2.68
	PLACE1003892	4.93	6.91	20.79	17.21	22.33	14.87
	PLACE1003900	2.27	5.92	7.17	6.34	9.75	6.6
	PLACE1003902	1.91	7.39	5.25	5.43	8.07	6.29
15	PLACE1003903	0.42	5.07	2.94	2.55	3.5	2.59
	PLACE1003915	8.15	7.04	10.78	8.31	9.79	9.84
	PLACE1003918	1.88	2.45	4.75	3.47	6.26	3.75
	PLACE1003923	2.06	3.73	5.63	2.7	5.54	3.32
	PLACE1003932	3.99	5.16	5.47	4.06	7.58	5.09
20	PLACE1003936	1.02	3.82	2.81	3.63	2.42	2.78
	PLACE1003966	3.11	7.43	7.76	4.89	7.32	4.21
	PLACE1003968	1.68	5.68	5.94	3.33	4.26	4.57
	PLACE1004018	25.49	33.73	48.16	32.56	40.53	28.62
	PLACE1004020	8.91	10.18	13.26	11.42	18.03	24.15
25	PLACE1004028	0.41	2.55	1.3	1.38	1.23	1.91
	PLACE1004034	3.56	4.53	5.22	8.42	9.03	13.04 *
	PLACE1004042	17.25	20.19	68.35	79.51	93.32	79.44 *
	PLACE1004078	1.14	4.1	3.3	4.95	6.51	4.45
	PLACE1004103	5.54	10.93	13.98	13.77	15.09	14.14
30	PLACE1004104	5.94	12.29	27.78	24.18	34.98	29.71
	PLACE1004113	1.37	3.7	3.28	2.75	3.27	1.29
	PLACE1004114	1.12	2.55	2.23	2.84	2.49	2.93
	PLACE1004118	1.58	3.52	2.09	2.74	3.64	2.5
	PLACE1004128	4.4	6.84	5.66	6.61	8.13	9.01
35	PLACE1004130	2.25	4.83	8.35	6.86	9.26	6.73
	PLACE1004149	3.59	7.3	9.86	10.23	13.29	10.12
	PLACE1004156	3.61	7.91	10.12	11.66	17.62	13.31
	PLACE1004160	5.45	9.54	14.36	13.1	19.65	14.53
40	PLACE1004161	2.2	4.86	3.54	4.85	5.73	7.48
	PLACE1004166	5.61	5.81	9.91	8.3	8.66	11.2
	PLACE1004168	3.35	4.97	3.73	4.73	6.65	6.79
	PLACE1004170	0.78	3.28	1.93	2.98	3.42	2.76
	PLACE1004178	0.83	5.23	2.37	2.4	2.59	2.36
45	PLACE1004183	0.89	7.99	4.41	3.53	4.32	4.84
	PLACE1004197	0.64	5.14	1.55	1.73	3.54	1.65
	PLACE1004199	1.66	4.52	4.09	3.78	5.88	4.35
	PLACE1004203	1.8	3.57	4.17	2.43	3.62	2.83
	PLACE1004242	3.8	5.64	11.04	8.55	8.14	8.64
50	PLACE1004249	31.4	56.31	117.88	127.93	152.54	151.22 *
	PLACE1004255	0.79	2.65	1.26	2.59	2.15	1.93
	PLACE1004256	9.06	11.68	13.63	14.66	14.18	23.37
	PLACE1004257	2.63	7.95	6.48	7.89	8.8	8.64
	PLACE1004258	1.87	5.21	3.13	4.59	3.15	3.11
55	PLACE1004270	0.72	3.8	2.5	2.7	4.01	1.65
	PLACE1004272	1.34	3.68	3.73	3.86	5.38	6.15

EP 1 130 094 A2

	PLACE1004273	92.91	89.59	212.62	212.05	129.56	99.82
5	PLACE1004274	2.09	3.61	6.51	6.42	7.14	6.74
	PLACE1004277	2.3	4.4	5.76	6.45	7.7	6.04
	PLACE1004279	0.54	3.39	2.23	3.16	2.64	2.02
	PLACE1004282	2.43	8.25	6.62	4.22	5.56	4.49
	PLACE1004284	4.59	11.31	7.84	7.38	8.16	7.15
10	PLACE1004289	1.28	7.85	2.46	3.06	3.63	2.1
	PLACE1004299	0.33	6.41	1.38	1.54	2.67	1.83
	PLACE1004302	1.01	2.98	3.27	2.41	2.45	1.12
	PLACE1004305	1.11	2.09	1.9	1.9	1.82	1.78
15	PLACE1004316	2.3	4.48	5.4	6.06	3.85	4.52
	PLACE1004322	2.49	3.41	5.25	6.35	7.14	5.75 * +
	PLACE1004325	2.43	6.38	3.84	3.85	3.66	4
	PLACE1004332	1.21	7.18	2.8	3.72	3.46	3.01
	PLACE1004336	2.87	9.6	5.36	6.88	9.21	6.71
	PLACE1004346	0.47	7.22	2.58	1.87	2.54	1.69
20	PLACE1004358	1.3	2.41	2.41	2.46	2.09	2.03
	PLACE1004376	11.07	10.15	23.35	19.16	17.04	16.46
	PLACE1004384	0.65	3.46	1.46	1.92	2.48	2.1
	PLACE1004385	1.4	2.89	1.69	3.52	1.88	2.67
	PLACE1004388	1.79	5.73	4.27	3.44	4.87	3.04
25	PLACE1004405	2.16	8.39	4.42	13.36	14.48	16.74 ** +
	PLACE1004407	5.05	13.12	13.37	11.2	16.24	11.85
	PLACE1004424	0.37	5.78	0.85	1.7	1.81	1.58
	PLACE1004425	1.14	1.94	3.57	3.28	3.27	3.44
	PLACE1004427	1.96	3.31	4.56	4.67	4.22	3.24
30	PLACE1004428	0.88	2.05	2.17	2.66	2.08	2.62
	PLACE1004433	5.7	8.3	10.82	12.94	15.67	12.05 * +
	PLACE1004435	0.72	4.17	1.43	1.95	1.9	2.15
	PLACE1004437	4.05	7.68	14.2	11.07	13.01	12.37
	PLACE1004441	7.82	11.68	34.06	30.75	43.19	26.41
35	PLACE1004446	1.5	4.36	0.9	1.03	1.35	1.39
	PLACE1004450	0.33	1.46	1.34	2.57	1.71	0.7
	PLACE1004451	0.51	1.45	2.14	1.89	2.69	0.88
	PLACE1004456	8.22	9.7	10.97	16.68	10.4	4.18
40	PLACE1004458	3.39	4.81	3.66	7.77	7.05	8.24 ** +
	PLACE1004460	0.84	4.58	2.1	2.91	2.69	1.75
	PLACE1004467	5.31	6.81	10.65	7.67	10.14	10.48
	PLACE1004471	2.65	5.93	6.64	6.79	7.34	6.14
	PLACE1004473	1.16	4.66	3.5	3.18	3.23	3.21
45	PLACE1004475	14.03	16.41	32.49	31.09	32.51	18.17
	PLACE1004482	8.37	6.7	10.79	10.04	9.76	9.15
	PLACE1004491	0.39	2.51	1.49	1.19	2.68	1.3
	PLACE1004492	61.52	74.8	127.94	129.92	127.64	123.82
	PLACE1004506	10.71	14.35	14.4	8.45	11.13	10.03
50	PLACE1004507	2.9	7.37	5.09	7.15	6.87	6.18
	PLACE1004510	2.51	6.23	6.33	6.59	7.8	8.16
	PLACE1004516	0.98	7.36	2.12	2.79	3.78	2.22
	PLACE1004518	1.64	1.78	3.03	2.41	3.88	2.83
	PLACE1004519	0.17	0.82	0.62	1.43	2.79	1.51 * +
55	PLACE1004520	6.08	8.09	10.06	7.44	9.11	2.52
	PLACE1004530	33.19	43.86	68.13	41.86	27.72	38.09

EP 1 130 094 A2

	PLACE1004545	1.13	3.83	2.12	3.03	3.31	3.65		
5	PLACE1004547	5	7.61	7.82	8.66	11.2	10.28		
	PLACE1004548	1.69	6.73	4.43	6.93	8.48	6.5		
	PLACE1004550	2.27	6.24	6.67	5.92	6.78	6.15		
	PLACE1004551	0.8	2.16	1.62	2.14	2.21	1.95		
	PLACE1004559	2.9	2.89	5.11	4.45	6.75	4.82		
10	PLACE1004562	8.67	11.27	16.07	13.01	14.38	13.34		
	PLACE1004564	1.84	5.19	4.36	4.64	5.98	4.49		
	PLACE1004604	1.69	4.21	9.88	2.49	4.34	1.97		
	PLACE1004611	2.73	5.87	4.89	3.86	4.17	3.99		
	PLACE1004629	9.42	15.75	19.92	23.93	30.49	29.01	*	+
15	PLACE1004630	16.66	20.82	35.1	16.76	23.04	19.17		
	PLACE1004637	5.03	8.82	10.34	6.61	9.17	8.29		
	PLACE1004645	36.5	39.28	92.04	85.16	87.94	74.59		
	PLACE1004646	1.07	2.91	2.87	3.68	2.19	2.28		
	PLACE1004648	0.8	3.42	2.52	2.53	3.15	1.22		
20	PLACE1004655	45.95	58.09	130.94	112.14	126.25	99.01		
	PLACE1004658	2.4	7.34	6.31	6.64	8.37	6		
	PLACE1004664	1.26	4.83	1.3	3.02	2.65	1.89		
	PLACE1004672	2.32	6.79	8.02	6.3	7.51	7.14		
	PLACE1004674	9.4	11.97	14.7	8.3	9.75	15.25		
25	PLACE1004681	1.97	3.84	5.62	5.05	5.69	4.39		
	PLACE1004686	2.74	4.33	7.46	9.22	10.77	8.59	*	+
	PLACE1004690	10.64	13.43	19.62	21.75	19.21	31.72		
	PLACE1004691	1.14	6.71	3.71	2.92	4.13	2.75		
	PLACE1004693	1.34	7.54	4.89	3.91	4.59	5.97		
30	PLACE1004701	13.01	18.45	24.24	25.21	24.46	25.1		
	PLACE1004705	1.29	3.33	2.27	1.8	1.96	1.47		
	PLACE1004708	37.69	46.37	80.19	41.34	39.66	50.98		
	PLACE1004716	6.37	8.81	11.08	4.22	12.55	14.26		
	PLACE1004722	1.31	3.05	2.6	2.26	3.28	2.51		
35	PLACE1004736	5.25	7.71	7.6	9.16	8.89	11.63		
	PLACE1004737	5.42	12.71	16.14	8.15	11.23	13.78		
	PLACE1004740	4.88	9.06	8.22	7.37	7.93	8.2		
	PLACE1004743	1.31	4.04	3.1	1.97	4	3.55		
	PLACE1004751	0.98	2.89	2.88	2.75	3.74	3.06		
40	PLACE1004757	3.45	4.34	10.53	8.4	9.6	7.22		
	PLACE1004761	6.41	7.32	12.59	9.99	10.44	9.72		
	PLACE1004773	1.05	2.34	1.7	1.94	2.31	2.72		
	PLACE1004775	0.35	3.26	1.37	1.29	2.14	1.07		
	PLACE1004777	2.1	7.57	2.97	3.68	4.25	4.4		
45	PLACE1004793	0.83	4.58	1.37	1.9	2.06	1.25		
	PLACE1004796	6.65	8.7	13.08	7.79	8.57	7.88		
	PLACE1004804	0.99	4.46	3.25	2.44	2.38	3.22		
	PLACE1004813	4.55	7.11	9.84	6.45	5.19	5.45		
	PLACE1004814	7.16	11.76	17.62	15.83	11.39	10.1		
50	PLACE1004815	0.7	2.81	2.43	3.12	2.61	3.44		
	PLACE1004816	1.16	2.63	2.04	2.36	2.26	1.84		
	PLACE1004824	3.25	7.37	5.27	8.1	9.13	8.85		
	PLACE1004827	1.4	10.89	3.17	2.57	3.05	1.3		
	PLACE1004836	1.72	12.95	4.26	6.25	7.99	4.49		
55	PLACE1004838	1.35	8.81	2.2	2.49	2.34	1.68		

EP 1 130 094 A2

5	PLACE1004840	1.59	2.06	2.21	1.85	2.08	1.37
	PLACE1004842	0.86	1.98	1.89	1.98	1.78	2.33
	PLACE1004850	0.81	2.35	1.63	1.83	2.76	2.36
	PLACE1004868	0.81	2.97	2.04	1.62	2.23	2
	PLACE1004885	1.5	7.09	3.51	3.4	6.03	4.77
	PLACE1004886	1.87	8.53	2.76	3.33	5.12	4.93
10	PLACE1004887	18.14	34.01	58.51	36.9	38.66	30.33
	PLACE1004896	8.39	14.15	15.4	9.39	11.14	14.03
	PLACE1004900	1.75	2.7	6.69	5.66	5.74	4.44
	PLACE1004902	5.42	6.25	9.27	6.39	4.2	3.6
	PLACE1004904	1.7	4.66	2.52	6.49	4.78	3.03
15	PLACE1004911	0.69	2.5	1.12	5.95	4.82	6.09 ** +
	PLACE1004913	3.63	5.72	7.38	4.49	5.45	4.79
	PLACE1004918	1.3	6.69	2.05	2.39	3.24	2.64
	PLACE1004930	2.74	8.84	5.93	10.63	16.57	14.71 * +
	PLACE1004934	1.14	4.3	3.34	2.97	2.03	2.5
20	PLACE1004937	2.1	4.03	4.91	2.74	3.59	2.36
	PLACE1004949	4.32	4.98	7.67	8.53	8.48	6.04
	PLACE1004969	0.74	1.74	1.99	1.39	2.34	1.4
	PLACE1004970	0.45	2.18	1.2	1.43	1.31	1.01
	PLACE1004972	1.63	6.56	2.69	5.66	3.17	4.76
25	PLACE1004974	1.27	5.21	4.2	5.6	5.7	5.62
	PLACE1004975	0.59	2.84	1.11	1.94	1.98	1.24
	PLACE1004979	1.58	4.06	4.26	4.91	5.69	4.75
	PLACE1004982	5.66	6.45	9.74	10.03	10.67	5.65
	PLACE1004985	1.4	1.47	1.46	2.5	2.17	1.2
30	PLACE1005003	2.85	4.22	6	6.05	6.37	5.78
	PLACE1005004	0.47	3.36	0.92	1.5	0.73	0.85
	PLACE1005005	3.35	6.9	5.32	6.67	9.65	7.17
	PLACE1005011	6.03	11.12	35.8	37.66	56.97	36.62
	PLACE1005026	0.79	4.18	2.29	2.44	2.49	2.16
35	PLACE1005027	2.46	6.72	6.69	5.36	6.92	5.68
	PLACE1005031	1.21	1.47	3.69	5.72	7.1	4.6 * +
	PLACE1005036	2.27	3.6	6.83	9.08	8.91	7.53 * +
	PLACE1005041	2.5	2.84	2.84	5.05	4.41	3.25 * +
	PLACE1005046	2.23	4.11	4.56	6.04	3.92	4.33
40	PLACE1005047	0.23	3.19	2.6	1.43	1.23	2.1
	PLACE1005052	4.24	8.53	6.36	8.08	8.15	8.1
	PLACE1005055	2.54	7.45	4.66	7.2	6.45	5.62
	PLACE1005066	4.33	8.26	7.58	12.9	14.14	16.49 ** +
	PLACE1005077	1.17	0.68	1.2	2.1	2.43	1.54 * +
45	PLACE1005085	1.41	1.97	3.06	3.34	4.14	3.45
	PLACE1005086	1.93	3.77	5.17	5.62	7.78	4.79
	PLACE1005088	24.66	32.47	46.03	43.45	31.47	27.46
	PLACE1005089	1.57	4.78	3.15	2.52	3.67	3.14
	PLACE1005101	3.37	8.11	5.46	6.11	8.96	6.39
50	PLACE1005102	2.56	7.14	5.01	4.11	5.51	3.8
	PLACE1005108	2	6.08	5.87	6.58	6.19	5.09
	PLACE1005110	1.34	1.89	3.08	1.75	2.75	2.15
	PLACE1005111	1.31	1.34	1.23	1.45	2.17	1.54
	PLACE1005123	26.23	26.21	47.58	34.26	49.34	34.98
55	PLACE1005124	3.2	4.66	4.18	4.2	6.91	5.44

EP 1 130 094 A2

	PLACE1005128	9.54	8.89	18.22	16.37	16.36	16.13		
5	PLACE1005130	2.65	6.57	5.54	2.84	4.98	3.58		
	PLACE1005141	6.3	9.92	11.25	16.15	20.75	18.95	**	+
	PLACE1005146	1.3	2.71	3.03	2.17	2.53	2.29		
	PLACE1005152	1.85	3.9	4.56	4.13	4.23	4.79		
10	PLACE1005157	2.66	5.19	5.3	4.38	4.09	7.01		
	PLACE1005162	2.79	3.72	9.31	6.57	7.45	7.1		
	PLACE1005170	17.34	18.92	29.76	21.38	18.18	23.73		
	PLACE1005176	0.57	5.6	1.7	2.33	2.47	1.94		
	PLACE1005181	0.53	5.14	0.96	0.89	1.36	0.37		
15	PLACE1005184	4.06	9.09	10.4	8.97	12.82	11.26		
	PLACE1005186	3.5	3.41	8.56	8.05	5.79	5.73		
	PLACE1005187	2.85	4	4.13	6.1	4.99	4.25		
	PLACE1005189	6.12	7.71	5.34	10.84	10.65	12.22	**	+
	PLACE1005193	1.48	3.78	1.71	3.84	2.91	2.61		
20	PLACE1005200	1.35	4.68	2.61	2.47	3.75	3.1		
	PLACE1005206	2.43	6.48	4.26	3.35	3.95	2.95		
	PLACE1005216	1.53	5.46	4.44	5.6	6.51	4.12		
	PLACE1005223	1.43	6.21	5	4.38	5.66	3.27		
	PLACE1005225	1.36	3.01	3.49	3.33	3.32	4.65		
	PLACE1005232	1.86	3.31	4.87	5.63	6.19	3.88		
25	PLACE1005239	1.06	4.3	2.32	2.84	2.86	2.41		
	PLACE1005243	4.35	7.32	5.41	8.48	7.49	10.75		
	PLACE1005250	4.24	10.31	7.98	4.38	5.9	8.88		
	PLACE1005261	3.21	7.43	4.74	4.78	5.82	3.51		
	PLACE1005266	1.05	4.47	2.82	2.28	4.43	2.76		
30	PLACE1005271	4.66	5.31	8.79	5.87	11.16	7.95		
	PLACE1005277	2.06	3.48	2.35	2.62	1.98	2.64		
	PLACE1005287	3.63	4.31	5.87	2.98	5.06	6.91		
	PLACE1005299	24.16	22.75	48.29	35.17	24.24	41.06		
	PLACE1005305	6.81	8.46	11.13	10.67	11.85	16.25		
35	PLACE1005307	1.59	5.44	4.14	3.15	5.42	4.84		
	PLACE1005308	2.41	4.96	3.95	5.32	5.99	5.79		
	PLACE1005313	1.08	3.83	1.6	1.8	2.05	1.8		
	PLACE1005320	1.36	3.65	3.34	3.39	4.05	2.26		
	PLACE1005327	10.78	8.74	16.8	10.36	7.95	4.43		
40	PLACE1005331	2.28	4.92	5.28	4.66	4.97	3.33		
	PLACE1005335	1.53	3.8	2.24	2.03	3.22	2.42		
	PLACE1005336	9.12	12.58	16.58	16.39	16.99	20.15		
	PLACE1005351	2.62	8.18	10.17	9.28	8.66	9.52		
	PLACE1005366	2.04	6.93	3	2.99	3.71	4.23		
45	PLACE1005373	1.77	6.34	4.44	3.91	5.36	3.37		
	PLACE1005374	3.29	9.47	11.4	7.35	10.22	12.41		
	PLACE1005383	8.16	7.54	12.81	7.21	5.93	4.03		
	PLACE1005388	0.33	2.04	1.56	1.92	3.67	2.2		
	PLACE1005409	2.97	5.02	4.99	3.9	4.23	2.97		
50	PLACE1005410	12.41	16.44	18.89	24.38	20.98	27.1	*	+
	PLACE1005426	5.16	7.48	9.06	5.51	7.67	5.45		
	PLACE1005431	12.6	15.65	22.53	19.64	26.25	23.75		
	PLACE1005453	1.4	10.38	3.93	4.85	4.45	3.28		
55	PLACE1005467	3.09	11.87	7	5.57	11.63	7.28		
	PLACE1005471	1.6	1.94	1.66	2.29	1.52	1.28		

EP 1 130 094 A2

	PLACE1005476	0.42	1.73	1.24	1.6	1.57	1.46
5	PLACE1005477	1.58	2.26	2.51	3	2.93	2.74
	PLACE1005480	0.77	2.01	1.86	1.93	1.4	0.53
	PLACE1005481	0.44	4.81	2.3	2.77	3.62	2.44
	PLACE1005494	0.27	6.66	1.68	1.21	1.73	1.06
	PLACE1005495	3.86	12.83	8.31	6.85	9.25	7.62
10	PLACE1005497	2.27	7.72	3.95	4.24	5.68	5.91
	PLACE1005499	5.71	5.86	11.07	10.82	7.9	6.49
	PLACE1005502	1.59	2.87	3.43	4.07	3.45	1.49
	PLACE1005513	1.77	4.14	3.35	1.86	2.85	1.98
15	PLACE1005515	2.89	4.76	4.22	4.58	5.29	3.78
	PLACE1005519	1.04	4.53	3.29	2.85	2.85	2.83
	PLACE1005526	0.58	5.55	1.38	1.3	1.59	0.71
	PLACE1005528	2.08	7.71	5.57	5.94	7.12	5.33
	PLACE1005530	2.16	7.09	4.32	5.17	8.23	4.67
20	PLACE1005536	1.74	1	2.74	3.12	2.43	2.88
	PLACE1005539	10.1	11.64	23.77	8.65	8.66	5.22
	PLACE1005543	1.7	3.57	5.62	3.54	4.32	2.57
	PLACE1005544	0.86	3.26	3.15	2.49	2.68	2.27
	PLACE1005550	4.32	7.61	7.85	10.16	7.25	6.86
	PLACE1005554	1.15	5.47	2.67	2.17	2.17	1.17
25	PLACE1005557	1.76	7.21	4.95	8.22	7.64	7.7
	PLACE1005563	0.51	4	1.89	1.45	2.07	1.06
	PLACE1005569	0.6	0.5	1.56	1.59	1.81	1.09
	PLACE1005574	1.07	1.88	2.49	2.48	4.43	2.22
	PLACE1005584	1.3	2.68	3.91	3.91	5.58	3.03
30	PLACE1005590	4.28	5.14	8.4	9.87	10.73	8.02
	PLACE1005595	3.08	4.03	2.89	3.65	3.81	3.89
	PLACE1005601	2	5.66	4.22	3.77	4	4.02
	PLACE1005603	1.08	4.9	1.04	2.49	0.95	1.94
	PLACE1005604	1.2	6.71	2.42	3.6	4.2	3.46
35	PLACE1005611	2.22	2.3	3.98	5.15	5.65	2.89
	PLACE1005622	0.65	1.71	1.98	2.94	3.88	1.26
	PLACE1005623	1.42	3.08	3.27	3.71	3.65	1.61
	PLACE1005630	3.31	5.81	7.75	87.83	72.15	89.12 ** +
40	PLACE1005639	0.75	4.36	1.28	1.66	2.02	1.18
	PLACE1005646	2.13	5.41	4.31	5.4	5.08	2.55
	PLACE1005647	2.77	9.69	6.72	7.34	9.11	6.25
	PLACE1005648	3	8.11	9.21	8.34	10.59	8.22
	PLACE1005653	1.99	1.43	2.74	2.74	2.13	2.67
	PLACE1005656	0.92	2.48	2.24	1.68	2.78	1.58
45	PLACE1005659	0.87	2.64	1.01	1.62	1.84	1.32
	PLACE1005660	3.91	8.03	5.77	8.87	8.88	8.34
	PLACE1005664	2.69	6.57	6.14	3.39	4.27	3.19
	PLACE1005666	0.89	5.91	3.55	4.63	4.93	3.97
	PLACE1005669	4.46	10.41	11.39	11.64	13.9	14.6
50	PLACE1005682	1.94	5.27	4.49	6.2	5.2	5.47
	PLACE1005698	0.6	2.7	2.92	2.01	2.67	2.38
	PLACE1005708	25.32	34.08	53.46	53.89	59.98	53.76
	PLACE1005725	3.25	3.75	6.41	5.64	5.82	7.29
55	PLACE1005727	2.97	4.54	4.15	3.9	3.49	4
	PLACE1005730	0.77	4.29	3.26	1.1	1.54	1.28

EP 1 130 094 A2

5	PLACE1005736	5.37	7.55	5.73	9.25	12.55	10.19	*	+
	PLACE1005739	0.81	4.96	1.38	2.46	3.17	1.74		
	PLACE1005745	8.03	7.11	11.52	11.98	6.97	11.44		
10	PLACE1005752	1.31	3.15	2.96	2.55	2.24	1.25		
	PLACE1005755	0.8	2.79	3.02	1.72	3.28	2.27		
	PLACE1005756	10.79	12.06	17.2	18.22	19.3	21.47	*	+
	PLACE1005760	10.22	15.24	68.06	49.69	68.81	53.09		
15	PLACE1005763	1.47	7.04	3.58	3.79	4.63	3.02		
	PLACE1005768	1.25	5.63	3.69	4.58	5.13	4.19		
	PLACE1005771	5.71	13.63	13.7	11.28	17.49	17.27		
	PLACE1005783	1.82	2.44	3.64	3.05	3.71	3.47		
20	PLACE1005799	4.79	5.25	8.37	6.12	8.78	8.62		
	PLACE1005802	1.07	3.78	3.64	2.7	3.64	1.96		
	PLACE1005803	3.06	6.15	4.78	5.6	4.94	7.36		
	PLACE1005804	0.92	8.41	1.33	2	1.91	2.44		
	PLACE1005813	17.23	18.71	78.06	70.01	94.17	74.89		
	PLACE1005815	1.43	5.6	4.38	3.8	5.01	4.1		
25	PLACE1005828	2.11	3.62	4.42	5.34	6.24	3.56		
	PLACE1005833	119.17	92.82	182.22	122	114.37	107.96		
	PLACE1005834	2.04	4.33	3.95	3.55	3.56	2.56		
	PLACE1005835	22.7	19.1	51.52	72.32	60.34	68.56	*	+
30	PLACE1005836	2.39	4.21	4.97	2.61	3.83	2.55		
	PLACE1005845	0.97	5.42	2.66	2.67	3.05	3.65		
	PLACE1005850	1.82	3.91	3.04	2.84	2.85	2.15		
	PLACE1005851	1.03	3.44	1.46	1.2	2.01	1.11		
	PLACE1005856	0.92	4.01	2.42	2.24	3.37	3.37		
35	PLACE1005875	1.78	3.89	4.77	3.3	3.48	3.17		
	PLACE1005876	1.33	3.99	4.76	6.87	6.34	6.9	*	+
	PLACE1005878	1.3	2.67	2.08	3.54	4.46	2.79		
	PLACE1005880	2.36	4.09	4.31	4.16	3.07	3.45		
	PLACE1005884	1.6	4.87	1.89	2.48	2.21	2.73		
40	PLACE1005890	1.9	9.57	3.7	2.26	3.09	1.88		
	PLACE1005898	3.29	10.87	5.34	7.36	8.12	6.36		
	PLACE1005913	1.46	9.31	8.05	4.99	6.47	4.33		
	PLACE1005921	0.99	1.92	2.03	1.49	2.22	0.79		
45	PLACE1005923	0.74	1.61	1.17	1.47	2.42	1.43		
	PLACE1005925	0.83	2.67	3.18	2.19	2.14	1.68		
	PLACE1005927	1.26	2.49	1.93	1.95	2.56	2.3		
	PLACE1005932	2.04	5.66	2.44	2.53	2.32	2.52		
	PLACE1005934	0.88	7.91	3.16	3.9	5.61	4.19		
50	PLACE1005936	1.31	8.96	3.02	2.02	2.84	2.3		
	PLACE1005939	54.61	68.58	111.22	157.61	194.58	212.18	**	+
	PLACE1005951	2.36	3.39	4.98	5.56	4.48	2.35		
	PLACE1005953	1.5	1.64	2.64	2.59	2.43	3.03		
	PLACE1005955	1.64	2.01	3.8	4.07	3.43	2.55		
	PLACE1005966	0.76	3.42	1.69	1.75	2	2.19		
55	PLACE1005968	1.52	4.96	3.2	4.71	5.15	6.12		
	PLACE1005975	2.58	7.11	5.42	6.18	7.01	6.49		
	PLACE1005990	0.7	7.7	1.54	2.1	1.87	0.88		
	PLACE1005997	88.15	118.52	196.48	189.6	226.97	172.1		
	PLACE1006002	3.38	3.97	8.87	8.4	7.71	9.18		
	PLACE1006003	1.55	3.02	4.83	5.09	4.44	5.33		

EP 1 130 094 A2

	PLACE1006011	1.85	3.63	3.46	4.48	2.68	1.91
5	PLACE1006017	0.84	2.74	2.81	3.4	3.4	3.58
	PLACE1006037	2.99	7.05	2.48	6.14	3.64	4.29
	PLACE1006040	2.2	7.87	3.97	6.64	6.9	7.77
	PLACE1006063	0.94	4.64	2.59	2.11	3.15	2.25
10	PLACE1006071	3.06	6.52	4.97	5.36	4.03	4.47
	PLACE1006073	2.74	3.53	6.43	7.19	6.81	6.93
	PLACE1006074	1.4	2.22	3.34	2.62	3.23	1.69
	PLACE1006076	1.36	2.51	2.98	3.15	2.47	2.75
	PLACE1006079	1.38	4.32	1.78	2.1	1.1	1.11
15	PLACE1006093	0.49	3.76	1	3.56	3.85	1.83
	PLACE1006116	2.99	6.44	4.04	5.28	5.01	4.91
	PLACE1006119	3.15	6.81	7.07	9.22	10.4	8.03
	PLACE1006129	2.12	5.6	3.98	6.59	7.62	5.65
	PLACE1006139	3.44	2.98	6.03	7.77	8.85	5.58
20	PLACE1006143	0.5	1.48	1.87	3.18	4.13	3.17 * +
	PLACE1006157	1.55	2.54	4.82	2.96	3.9	2.44
	PLACE1006159	0.69	3.61	0.94	2.68	1.98	1.04
	PLACE1006164	0.35	3.18	1.37	1.73	1.85	1.21
	PLACE1006167	2.18	6.5	3.37	3.95	4.52	3.13
	PLACE1006170	2.79	6.09	6.09	4.34	5.31	3.68
25	PLACE1006181	2.75	7.34	2.84	5.8	5.51	5.22
	PLACE1006187	0.76	1.3	2.15	2.01	2.41	1.48
	PLACE1006195	0.11	1.24	1.73	1.93	1.93	0.87
	PLACE1006196	1.8	4.01	4.15	4.32	5.77	2.19
	PLACE1006197	2.12	5.6	5.24	4	3.47	3.39
30	PLACE1006198	0.27	3.68	1.21	0.84	1.63	0.5
	PLACE1006205	0.89	5.59	0.99	2.43	2.18	1.28
	PLACE1006208	7.28	13.32	13.46	14.09	14.99	12.5
	PLACE1006211	2.6	8.05	7.92	6.07	9.08	9.35
35	PLACE1006219	6.77	5.77	8.94	14.88	22.25	15.35 * +
	PLACE1006223	1.55	1.46	3.19	1.39	3	1.64
	PLACE1006225	0.56	2.27	1.3	1.04	2.3	0.99
	PLACE1006236	1.53	3.2	2.92	3.06	5.01	2.29
	PLACE1006239	0.67	3.62	1.97	2.61	3.66	3.41
40	PLACE1006245	3.86	7.13	5.45	4.43	7.44	3.28
	PLACE1006246	1.66	6.56	6.19	5.59	7.66	6.33
	PLACE1006248	1.58	4.47	5.6	2.77	3.1	2.82
	PLACE1006262	0.93	2.24	1.49	2.08	1.61	1.4
	PLACE1006269	2.28	4.71	3.42	2.06	2.47	2.33
45	PLACE1006275	1.6	3.57	3.37	4.12	3.68	3.53
	PLACE1006277	1.01	2.42	1.4	1.79	3.01	0.88
	PLACE1006288	9.32	13.59	22.49	26.85	18.4	25.21
	PLACE1006290	1.79	6.81	5.99	8.87	7.56	9.13
	PLACE1006298	1.93	5.52	2.47	3.87	5.08	4.55
50	PLACE1006311	0.65	3.38	1.75	225.97	161.43	251.12 ** +
	PLACE1006318	3.52	4.03	4.17	4.04	3.17	4.01
	PLACE1006325	5.43	6.73	6.31	8.09	8.38	8.08 ** +
	PLACE1006331	1.87	3.36	3.21	4.44	3.59	2.56
	PLACE1006335	1.76	3.64	2.55	4.45	2.98	2.92
55	PLACE1006357	0.27	4.51	1.59	1.7	1.49	1.2
	PLACE1006360	1.1	5.11	1.79	2.46	2.74	2.62

EP 1 130 094 A2

	PLACE1006364	4.51	8.06	7.29	7.37	9.19	5.75		
5	PLACE1006365	1.68	4.65	1.97	1.8	2.12	0.97		
	PLACE1006368	1.53	3.11	2.57	3.01	3.04	4.27		
	PLACE1006371	1.38	3.2	1.46	1.68	3.01	1.67		
	PLACE1006373	2.21	5.21	5.75	7.83	8.02	7.56	*	+
10	PLACE1006382	0.9	4.67	2.81	3.3	1.92	2.95		
	PLACE1006385	1.59	6.33	1.86	2.68	2.59	2.71		
	PLACE1006391	1.19	5	1.95	1.96	2.79	1.63		
	PLACE1006412	1.88	5.53	5.92	7.07	9.93	5.27		
15	PLACE1006414	0.63	3.42	0.95	1.22	1.87	1.6		
	PLACE1006419	7.79	9.8	11.93	5.19	7.29	5.32	*	-
	PLACE1006438	0.99	6.07	3.42	3.29	4.56	5.14		
	PLACE1006443	2.05	5.01	5.12	5.01	5.31	6.44		
20	PLACE1006445	0.84	5.76	3.65	3.53	3.27	3.55		
	PLACE1006447	1.34	5.81	3.28	2.95	3.26	3.96		
	PLACE1006466	0.75	4.38	1.35	1.49	1.66	1.08		
	PLACE1006469	0.67	4.66	2.31	1.65	2.26	1.67		
25	PLACE1006470	2.47	3.71	3.74	5.25	7.02	4.35		
	PLACE1006472	24.4	23.44	52.17	26.23	28.52	9.36		
	PLACE1006476	2.52	4.31	8.67	6.21	7.23	5.93		
	PLACE1006482	1.64	3.35	4.43	4.25	4.67	4.98		
	PLACE1006488	14.12	19.42	32.69	40.76	34.77	41.4	*	+
30	PLACE1006492	2.03	6.41	4.38	4.04	4.98	3.02		
	PLACE1006506	1.78	6.67	4.04	4.41	5.71	4.17		
	PLACE1006515	1.65	5.7	3.08	3.19	2.84	4.08		
	PLACE1006516	1.1	7.32	7.05	4.89	5.69	7.28		
35	PLACE1006520	1.02	2.74	2.12	1.19	3	1.54		
	PLACE1006521	2.4	3.54	6.38	6.49	6.86	5.08		
	PLACE1006529	5.96	7.35	6.96	10.56	8.2	7.93		
	PLACE1006531	1.01	4.31	3.33	1.84	2.05	2.43		
	PLACE1006534	1.68	6.04	2.59	3.01	3.86	3.19		
40	PLACE1006540	2.68	9.7	7.77	8.71	11.21	4.46		
	PLACE1006549	0.6	9.45	2.09	1.6	2.28	1.65		
	PLACE1006550	1.76	8.82	4.07	2.77	2.94	4.14		
	PLACE1006552	1.3	2.48	2.14	1.97	1.3	0.81		
	PLACE1006557	2.38	4.01	3.79	2.84	2.51	2.45		
45	PLACE1006563	2.49	3.44	5.7	4.23	4.15	4.3		
	PLACE1006579	1.53	7.5	4.82	4.88	5.38	5.78		
	PLACE1006594	236.53	241.11	397.64	122.37	278.58	324.29		
	PLACE1006598	0.72	8.53	2.4	1.53	1.58	2.07		
	PLACE1006607	1.47	7.69	4.18	3.45	5.86	4.29		
50	PLACE1006610	9.46	13.73	38.26	27.65	32.76	22.64		
	PLACE1006615	6.22	9.09	18.78	20.25	15.74	15.86		
	PLACE1006617	0.91	1.54	2.66	1.87	2.49	2.09		
	PLACE1006618	5.42	8.01	9.24	5.33	8.59	5.76		
	PLACE1006626	1.53	4.11	1.3	2.47	2.78	1.16		
55	PLACE1006629	0.99	5.05	1.36	2.22	2.56	1.76		
	PLACE1006637	1.29	6.54	3.97	3.77	4.23	4.87		
	PLACE1006640	0.59	5.14	1.17	0.85	2.54	0.94		
	PLACE1006644	1.66	4.46	2.12	2.79	2.49	2.39		
	PLACE1006657	1.28	2.09	2.31	4.55	3.09	2.19		
	PLACE1006673	2.29	4.73	10.34	11.06	10.89	6.45		

EP 1 130 094 A2

	PLACE1006678	2.54	2.98	1.44	1.37	1.96	1.39		
5	PLACE1006682	3.5	5.93	2.58	15.44	20.96	23.99	**	+
	PLACE1006684	1.12	4.8	1.81	1.64	2.54	1.65		
	PLACE1006698	1.54	5.86	4.52	2.15	3.57	1.9		
	PLACE1006704	1.81	5.41	2.71	2.93	2.92	2.97		
10	PLACE1006708	1.69	5.07	3.49	3.46	4.11	3.7		
	PLACE1006711	14.21	16.18	29.77	24.34	26.25	22.42		
	PLACE1006714	2.27	3.26	4.74	4.57	5.23	3.53		
	PLACE1006716	1.51	2.75	3.7	6	7.05	3.99		
	PLACE1006731	1.65	3.77	2.83	2.71	4	3.09		
15	PLACE1006754	0.43	3.94	1.73	1.8	1.81	0.99		
	PLACE1006760	7.56	10.98	10.08	8.58	8.89	11.31		
	PLACE1006779	1.44	4.12	2.88	3.19	3.79	2.97		
	PLACE1006782	0.44	5.17	2.42	2.95	1.57	1.15		
20	PLACE1006783	9.34	11.46	18.65	157.98	223.05	66.46	*	+
	PLACE1006786	3.31	4.08	6.07	5.9	6.24	3.34		
	PLACE1006792	1.61	3.31	5.38	5.66	3.33	4.18		
25	PLACE1006795	0.89	2.43	0.74	0.81	1.27	1.01		
	PLACE1006800	1.62	4.94	2.53	4.7	4.56	3.93		
	PLACE1006805	3.94	7.79	5.5	10.83	9.8	8.79	*	+
	PLACE1006809	3.55	5.7	5.94	9.58	10.61	8.97	**	+
30	PLACE1006815	1.7	7.57	4.1	5.12	5.23	5.8		
	PLACE1006819	0.33	0.88	0.95	0.89	1.76	0.63		
	PLACE1006820	2.35	2.01	4.91	4.84	6.72	4.18		
	PLACE1006826	2.28	6.22	4.84	7.68	7.62	5.58		
	PLACE1006829	3.76	5.51	6.54	9.49	8.66	8.69	*	+
35	PLACE1006853	1.2	4.21	1.97	2.25	2.93	2.88		
	PLACE1006860	1	4.29	1.62	1.61	2.1	1		
	PLACE1006867	5.65	9.36	11.34	7.04	8.33	7.63		
	PLACE1006875	1.15	6.19	5.66	4.84	4.53	4.63		
	PLACE1006878	1.59	2.84	3.09	2.99	3.22	2.39		
40	PLACE1006883	3.21	5.08	6.78	6.83	7.38	6.19		
	PLACE1006898	1.67	4.23	3.67	3.54	4.77	4.59		
	PLACE1006901	2.59	4.75	4.03	3.71	3.28	4.14		
	PLACE1006904	0.91	3.59	2.7	3.26	2.92	2.04		
	PLACE1006917	3.63	7.13	6.1	5.8	7.21	7.03		
45	PLACE1006932	0.54	5.85	1.29	0.92	1.34	1.19		
	PLACE1006935	1.3	5.46	2.54	1.59	4.03	1.6		
	PLACE1006956	0.92	2.55	3.4	2.55	2.41	2.09		
	PLACE1006958	0.78	2.41	1.35	1.76	4.2	3.39		
50	PLACE1006959	4.97	8.48	9.98	11.46	9.58	13.62		
	PLACE1006961	8.03	9.85	14.42	13.73	11.57	14.2		
	PLACE1006962	2.97	7.44	6.56	5.04	7.26	6.22		
	PLACE1006966	2.02	6.94	3.46	3.15	3.89	2.89		
	PLACE1006979	0.95	4.44	2.03	1.46	2.64	1.77		
55	PLACE1006989	2.19	5.05	3.02	3.27	3.9	5.06		
	PLACE1007001	4.98	6.79	10.71	4.03	7.43	7.38		
	PLACE1007014	1.37	3.03	3.45	1.79	2.18	2.2		
	PLACE1007021	0.74	3.03	2.11	0.75	2.2	1.73		
	PLACE1007026	2.1	9.23	3.93	4.15	4.27	5.42		
	PLACE1007028	4.12	8.5	10.56	7.89	8.34	9.35		
	PLACE1007038	237.33	267.91	446.14	406.27	622.67	671.17		

EP 1 130 094 A2

	PLACE1007040	1.55	3.14	2.85	1.57	3.31	2.45		
5	PLACE1007045	1.08	3.74	2.85	2.9	5.03	2.74		
	PLACE1007048	147.06	149.67	259.53	121.61	211.26	109.43		
	PLACE1007053	4.9	6.69	10	3.59	4.91	4.71		
10	PLACE1007068	7.56	10.33	62.76	39.52	45.9	36.69		
	PLACE1007070	5.97	10.85	10.28	8.65	9.6	14.3		
	PLACE1007076	8.22	14.4	14.19	16.53	23.62	24.67	*	+
15	PLACE1007077	2.65	6.45	4.01	5.2	5.28	5.43		
	PLACE1007081	0.36	4.47	1.94	1.92	1.92	1.37		
	PLACE1007082	1.23	4.66	4.95	4.32	4.5	3.99		
	PLACE1007092	2.49	4.12	7.26	4.77	5.22	4.34		
20	PLACE1007096	0.72	2.19	0.74	1.35	1.63	0.97		
	PLACE1007097	0.54	2.49	1.35	1.61	1.28	1.04		
	PLACE1007099	1.58	4.66	2.56	2.77	3.64	3.72		
	PLACE1007105	1.18	6.51	3.44	2.65	4.13	2.21		
25	PLACE1007108	3.55	13.02	7.41	5.03	6.87	5.75		
	PLACE1007111	1.33	9.51	1.52	1.74	2.37	1.52		
	PLACE1007112	1.23	7.26	1.79	2.09	3.12	2.36		
	PLACE1007130	0.54	2.02	1.92	0.87	1.47	0.33		
	PLACE1007132	1.46	3.32	4.63	3.58	3.38	2.88		
	PLACE1007140	0.61	2.58	2.41	1.98	1.98	1.32		
30	PLACE1007143	2.79	6.32	4.62	4.9	5.34	5.33		
	PLACE1007169	2.21	8.59	3.46	5.44	8.46	7.99		
	PLACE1007178	0.82	8.66	2.48	3.28	6.28	4.1		
	PLACE1007190	3.31	10.9	6.7	10.51	13.57	11.14		
	PLACE1007201	0.81	5.82	1.41	1.72	3.04	2.51		
35	PLACE1007202	37.76	34.95	76.28	58.23	34.42	37.86		
	PLACE1007226	2.01	2.39	2.73	1.89	3.14	2.29		
	PLACE1007238	1.64	3.07	1.83	2.39	2.73	2.2		
	PLACE1007239	1.81	3.68	2.99	1.76	2.72	2.44		
40	PLACE1007242	0.61	5.18	1.87	1.54	1.14	1.67		
	PLACE1007243	2.21	7.36	2.29	2.24	3.27	3.31		
	PLACE1007247	0.36	6.17	1.71	1.11	1.36	1.34		
	PLACE1007257	1.67	5.33	3.34	3.3	5.27	4.25		
	PLACE1007274	1.46	2.18	4.43	4.38	4.03	4.06		
	PLACE1007276	0.93	2.02	1.1	2.13	2.1	1.74		
45	PLACE1007282	2.51	4.2	5.72	4.28	3.62	4.66		
	PLACE1007286	2.97	4.8	7.85	10.14	12.47	8.79	*	+
	PLACE1007296	10.55	19.45	24.46	31.43	17.57	27.05		
	PLACE1007301	0.65	5.17	1.55	1.19	1.54	1.11		
50	PLACE1007314	3.11	6.61	8.64	7.98	8.96	10.24		
	PLACE1007317	1.19	3.34	1.27	1.88	1.62	1.79		
	PLACE1007329	0.89	0.73	1.78	2.38	2.35	2.09	*	+
	PLACE1007338	3.96	6.47	9.58	11.59	8.93	2.32		
55	PLACE1007342	0.71	1.8	1.3	1.1	1.1	0.7		
	PLACE1007345	1.72	4.57	2.54	2.72	3.6	3.29		
	PLACE1007346	1.43	4.61	3.89	5.77	4.53	4.1		
	PLACE1007359	0.74	4.55	2.16	2.59	2.44	3.53		
	PLACE1007367	4.53	8.63	15.16	12.49	13.49	11.75		
	PLACE1007375	0.36	3.24	2.02	1.75	2.56	1.59		
	PLACE1007377	1.49	2.01	3.18	3.29	3.96	2.36		
	PLACE1007386	1.55	1.75	1.47	2.37	1.68	1.36		

EP 1 130 094 A2

	PLACE1007392	1.57	2.99	2.49	2.79	4.48	3.51	
5	PLACE1007402	2.41	5.66	3.08	1.52	2.91	1.8	
	PLACE1007409	1.05	4.57	1.04	2.51	2.68	2.02	
	PLACE1007416	3.45	6.97	6.5	7.05	9.14	6.52	
	PLACE1007420	12.12	12.66	20.8	25.26	23.9	22.88	* +
	PLACE1007431	1.87	7.4	5.51	7.17	5.28	5.91	
10	PLACE1007450	0.79	1.22	2.65	3	2.99	2.39	
	PLACE1007452	0.42	2.36	1.76	2.09	2.98	1.45	
	PLACE1007454	23.74	28.02	76.56	59.97	75.95	46.61	
	PLACE1007460	0.75	3.52	2.35	2.34	1.93	2.58	
	PLACE1007478	0.41	3.07	1.33	1.35	2.18	1.92	
15	PLACE1007484	0.6	4.8	2.57	2.56	1.45	1.69	
	PLACE1007488	0.4	6.24	1.64	1.74	2.61	1.46	
	PLACE1007507	2.91	6.36	4.49	5.31	8.29	8.11	
	PLACE1007511	0.53	1.29	1.06	1.06	1.29	0.42	
	PLACE1007513	10.57	10.43	24.05	12.24	16.88	16.9	
20	PLACE1007524	1.55	3.33	3.53	3.96	4.72	2.96	
	PLACE1007525	1.24	2.95	3.14	2.38	2.85	2.24	
	PLACE1007537	8.6	9.68	49.88	43.78	63.66	40.1	
	PLACE1007544	1.55	6.45	4.97	3.2	3.92	4.61	
	PLACE1007547	1.36	5.03	4.15	2.37	2.84	2.4	
25	PLACE1007557	1.12	3.16	3.14	3.07	3.9	3.41	
	PLACE1007560	9.38	8.86	12.57	11.03	9.62	17.59	
	PLACE1007565	0.37	2.27	1	1	1.16	0.91	
	PLACE1007580	1.06	3.71	3.06	10.8	11.15	13.74	** +
	PLACE1007583	0.76	3.88	1.78	2.51	2.37	1.09	
30	PLACE1007591	0.79	4.62	1.7	2.2	2.53	2.07	
	PLACE1007598	1.13	6.98	3.86	2.71	3.46	4.71	
	PLACE1007610	0.41	5.63	1.28	1.33	3.18	1.5	
	PLACE1007618	1.57	1.91	2.01	1.75	2.2	2.41	
	PLACE1007621	1.78	2.83	3.64	3.33	3.57	4.38	
35	PLACE1007626	23.99	25.61	32.78	30.53	30.94	13.53	
	PLACE1007632	2.03	3.26	2.52	2.65	3.81	4.63	
	PLACE1007635	1.61	4.62	6.42	2.8	4.19	3.37	
	PLACE1007645	10.59	11.55	15.06	9.99	11.58	11.95	
40	PLACE1007649	1.7	5.88	3.47	2.78	4.95	3.13	
	PLACE1007659	1.33	5.85	3.61	4.88	6.22	4.9	
	PLACE1007669	2.01	2.1	3.74	2.97	4.63	4.4	
	PLACE1007677	1.25	2.29	2.81	2.68	3.07	2.91	
	PLACE1007688	3.4	5.69	5.43	1.98	4.53	4.98	
45	PLACE1007690	1.4	4.03	2.12	3.74	3.37	4.61	
	PLACE1007697	0.69	7.13	1.37	1.84	2.56	1.8	
	PLACE1007702	2.03	7.08	5.7	4.03	3.91	4.08	
	PLACE1007705	1.38	3.93	1.59	1.74	4.45	2.75	
	PLACE1007706	3.11	6.08	4.69	5.25	8.84	7.49	
50	PLACE1007725	3.41	4.69	6.65	5.1	3.29	5.39	
	PLACE1007729	0.98	2.65	1.8	2.7	3.11	1.99	
	PLACE1007730	1.25	4.29	3.07	3.66	3.75	4.32	
	PLACE1007737	1.43	4.79	3.39	3.79	4.7	4.17	
	PLACE1007743	1.38	4.26	2.29	2.3	2.83	2.03	
55	PLACE1007746	6.56	9.02	10.42	9.65	13.29	12.97	
	PLACE1007753	0.53	4.48	1.71	1.35	2.86	1.94	

EP 1 130 094 A2

	PLACE1007769	1.31	4.31	3.5	3.27	4.51	4.58		
5	PLACE1007780	5.77	4.63	7.11	6.51	3.75	2.17		
	PLACE1007791	1.82	3.29	3.38	3.16	3.69	2.87		
	PLACE1007807	0.67	2.79	1.72	2.33	1.76	1.29		
	PLACE1007810	0.39	4.45	2.63	4.11	4.08	3.27		
	PLACE1007814	3.57	5.98	5.04	4.2	4.62	6.3		
10	PLACE1007828	2.01	7.64	3.34	2.69	4.64	3.44		
	PLACE1007829	1.32	6.9	2.88	2.87	4.87	3.06		
	PLACE1007841	1.64	7.26	1.87	2.25	3.14	3.39		
	PLACE1007842	1.1	3.32	2.44	2.09	3.96	1.39		
	PLACE1007843	1.2	1.92	1.43	2.13	1.48	1.86		
15	PLACE1007845	1.76	3	4.11	3.45	3.42	2.36		
	PLACE1007846	0.99	3.26	1.64	2.02	2.73	1.5		
	PLACE1007848	1.09	3.51	2.23	2.39	2.62	2.25		
	PLACE1007852	2.26	7.88	3.82	2.94	4.61	3.24		
	PLACE1007858	3.65	11.57	5.81	61.71	80.46	57.09	**	+
20	PLACE1007866	19.42	25.98	40.48	43	80.39	56.73		
	PLACE1007871	8.1	7.9	15.45	16.17	12.35	11.08		
	PLACE1007877	1.09	2.09	1.45	1.4	2.39	1.53		
	PLACE1007878	5.98	9.75	14.61	13.65	7.49	8.9		
	PLACE1007881	0.43	2.66	1.34	1.59	1.94	1.93		
25	PLACE1007885	4.35	7.85	6.76	5.57	6.53	7.01		
	PLACE1007897	0.27	6.51	1.85	1.72	1.53	1.41		
	PLACE1007908	3.14	12.29	5.73	5.96	7.9	8.24		
	PLACE1007922	6.08	11.75	8.75	5.24	7.15	4.54		
	PLACE1007946	1.07	2.03	1.86	2.71	2.28	1.94		
30	PLACE1007950	6.98	7.6	18.21	16.17	19.34	12.63		
	PLACE1007954	-0.03	2.45	1.15	2.46	1.57	1.51		
	PLACE1007955	0.92	4.01	2.17	2.05	2.52	3.05		
	PLACE1007956	0.6	3.61	2.91	2.35	2.1	2.22		
	PLACE1007958	0.75	6.31	1.34	0.79	1.21	0.8		
35	PLACE1007965	0.64	5.88	3.25	3.38	2.91	2.17		
	PLACE1007969	1.09	6.37	3.06	2.35	3.29	2.21		
	PLACE1007971	2.73	4.17	5.21	6.1	4.41	5.92		
	PLACE1007990	1.95	2.33	2.31	3.22	3.09	1.88		
	PLACE1008000	0.32	2.16	1.98	1.85	1.27	0.66		
40	PLACE1008002	0.99	3.38	1.7	1.81	2.04	0.51		
	PLACE1008037	0.57	4.19	1.7	4.59	2.86	2.02		
	PLACE1008044	1.42	5.81	2.46	4.18	4.93	4.16		
	PLACE1008045	0.4	4.07	1.54	1.75	2	1.65		
	PLACE1008080	2.05	6.08	3.22	4.23	4.03	4.78		
45	PLACE1008092	1.56	1.56	1.48	1.48	2.98	1.86		
	PLACE1008095	0.59	2.14	1.48	2.38	2.73	1.23		
	PLACE1008105	0.95	1.76	1.71	2.24	2.71	0.74		
	PLACE1008107	0.27	2.33	0.7	1.72	1.44	1.68		
	PLACE1008111	1.73	5.01	2.12	4.57	5.4	4.04		
50	PLACE1008113	5.88	9.24	12.48	16.57	20.29	19.24	*	+
	PLACE1008122	1.22	5.54	2.55	1.61	1.57	1.5		
	PLACE1008129	1.5	5.64	2.8	2.43	5.36	2.91		
	PLACE1008132	5.51	4.47	8.34	6.61	11.2	7.63		
55	PLACE1008137	0.96	1.82	1.02	2.12	3.88	0.8		
	PLACE1008174	0.77	3.16	2.43	5.12	4.39	2.46		

EP 1 130 094 A2

	PLACE1008177	1.62	4.87	3.09	3.79	3.26	3.77		
5	PLACE1008181	1.76	3.87	1.6	2.06	2.43	1.43		
	PLACE1008195	2.66	6.08	2.97	4.34	4.14	3.9		
	PLACE1008198	1.06	5.56	2.52	2.55	3.31	1.54		
	PLACE1008201	1.22	4.45	3.58	5.92	7.69	5.64	*	+
	PLACE1008209	2.35	2.29	4.46	2.51	5.31	4.44		
10	PLACE1008226	1.8	2.35	5.25	4.72	5.68	7.08		
	PLACE1008227	0.77	2.67	3.02	2.38	4.6	3.54		
	PLACE1008231	1.26	3.85	1.85	1.05	1.83	0.78		
	PLACE1008238	1.22	3.21	2.9	2.47	2	1.72		
	PLACE1008244	1.01	4.69	1.56	1.68	3.2	1.56		
15	PLACE1008249	0.8	4.94	2.55	1.22	2.17	2.01		
	PLACE1008266	11.31	18.61	43.04	60.04	82.48	59.04	*	+
	PLACE1008273	1.47	3.95	3.81	3.53	3.8	4.47		
	PLACE1008275	1.59	3.67	2.17	2.62	2.57	2.34		
	PLACE1008280	0.85	2.6	1.84	2.42	2.48	2.36		
20	PLACE1008282	4.71	8.19	6.89	7.27	9.02	6.38		
	PLACE1008297	2.32	4.7	3.36	2.89	3.42	3.21		
	PLACE1008303	1.65	6.68	1.24	4.12	3.83	2.65		
	PLACE1008309	0.43	6.52	0.82	1.77	1.5	1.29		
	PLACE1008315	5.3	5.93	8.61	4.92	4.79	9.83		
25	PLACE1008329	0.47	2.23	2.06	2.32	2.8	2.49		
	PLACE1008330	0.72	4.06	3.16	2.48	3.36	2.96		
	PLACE1008331	0.84	5.01	2.1	4.5	2.17	2.91		
	PLACE1008351	4.34	8.66	7.41	7.91	7.31	7.1		
	PLACE1008356	1.56	8.23	1.93	2.86	4.16	3.35		
30	PLACE1008359	1.57	4.11	2.89	2	2.97	2.94		
	PLACE1008368	2.27	6.38	7.43	5.72	7.33	6.95		
	PLACE1008369	0.57	2.46	1.45	1.12	1.59	1.68		
	PLACE1008392	0.8	3.09	2.54	2.44	3.22	3.24		
	PLACE1008394	2.08	4.84	3.75	3.98	5.03	4.76		
35	PLACE1008398	5.32	9.36	11.44	11.36	11.3	12.33		
	PLACE1008401	1.19	7.06	3.21	2.82	3.43	3.33		
	PLACE1008402	3.21	6.45	7.2	7.23	10.15	9.26		
	PLACE1008405	10.3	10.95	18.42	17.17	18.82	20.4		
	PLACE1008409	1.88	5.19	5.69	4.97	5.41	5.65		
40	PLACE1008420	1.4	1.87	1.96	2.67	2.69	2.27	*	+
	PLACE1008424	0.88	2.69	2.54	1.69	2.34	1.71		
	PLACE1008426	0.98	2.58	1.58	1.7	2.66	2.32		
	PLACE1008429	0.92	3.17	2.14	1.91	3.4	1.84		
45	PLACE1008430	1.63	4.85	3.04	2.93	3.52	3		
	PLACE1008437	0.87	3.64	3.01	2.83	1.82	1.57		
	PLACE1008453	1.16	4.8	1.02	1.64	2.06	1.17		
	PLACE1008454	2.14	6.46	9.23	5.46	9.02	5.92		
	PLACE1008455	2.06	4.33	7.2	5.26	6.68	4.87		
50	PLACE1008457	0.51	2.6	2.01	2.28	2.43	2.47		
	PLACE1008465	0.49	2.41	1.72	1.56	2.13	0.48		
	PLACE1008469	2.42	4.36	5.32	5.16	4.75	7.1		
	PLACE1008488	0.81	5.48	1.97	2.44	2.03	1.8		
	PLACE1008519	1.48	10.85	6.17	4.41	4.99	4.51		
55	PLACE1008524	1.04	11.09	1.72	2	3.22	2.02		
	PLACE1008531	0.64	8.37	1.92	1.33	2.05	1.72		

EP 1 130 094 A2

	PLACE1008532	2.12	3	5.51	5.66	4.72	4.19
5	PLACE1008533	2.01	4	4.07	5.53	5.18	3.77
	PLACE1008542	1.61	2.36	0.96	2.05	2.1	1.72
	PLACE1008549	0.96	3.06	0.67	1.45	2.1	1.53
	PLACE1008560	1.18	4.23	2.28	2.29	3.93	3.47
10	PLACE1008567	0.87	7.26	1.85	2.33	3.67	2.38
	PLACE1008568	2.37	10.67	5.49	2.97	7.47	4.21
	PLACE1008569	3.94	10.32	6.74	6.1	8.6	7.6
15	PLACE1008584	0.88	1.4	1.58	2.86	3.38	1.31
	PLACE1008585	4.96	4.8	7.56	11.08	4.84	3.57
	PLACE1008603	5.9	7.25	31	30.55	43.67	29.76
	PLACE1008621	0.55	2.28	0.95	0.72	1.89	1.16
20	PLACE1008625	0.64	4.01	0.9	1.18	1.41	2.03
	PLACE1008626	0.55	6.06	0.9	1.03	0.83	0.95
	PLACE1008627	0.46	8.32	1.86	1.87	3.34	2.7
	PLACE1008629	3.22	9.18	5.84	5.44	6.75	4.41
25	PLACE1008630	1.68	3.39	4.23	4.21	3.01	3.51
	PLACE1008643	1.31	0.93	1.98	1.72	2.34	1.94
	PLACE1008650	0.25	3.05	1.62	2.23	1.63	1.24
	PLACE1008657	1.17	2.39	2.51	2.34	4.04	2.91
	PLACE1008664	0.91	5.93	2.37	2.91	2.51	1.13
30	PLACE1008693	0.97	4.93	3.09	2.53	3.81	2.2
	PLACE1008696	0.88	3.84	2.21	2.26	2.11	1.47
	PLACE1008715	1.05	4.71	2.11	1.34	2.65	2.65
	PLACE1008716	2.48	3.94	4.19	5.75	6.9	7.07 * +
	PLACE1008722	3.85	4.34	7.37	7.64	7.19	3.45
35	PLACE1008738	5.17	9.13	12.7	9.49	5.83	4.8
	PLACE1008742	6.57	6.87	14.66	14.94	15.06	12.41
	PLACE1008744	3.52	6.98	5.61	5.83	4.55	2.74
	PLACE1008748	0.63	4.39	2.75	2.44	1.67	1.61
	PLACE1008757	0.99	4.74	4.51	2.77	5.74	2.17
40	PLACE1008766	2.66	6.75	3.77	3.51	6.47	4.06
	PLACE1008785	1.39	1.68	2.6	3.26	3.8	3.89 * +
	PLACE1008790	1.57	1.8	2.29	3.5	5.39	2.96
	PLACE1008798	1.71	3.82	4.45	6	5.93	3.32
45	PLACE1008807	1.34	3.95	1.61	2.54	2.62	1.8
	PLACE1008808	1.6	4.53	3.01	4.24	3.69	5.04
	PLACE1008813	1.38	4.85	1.97	1.9	1.95	2.3
	PLACE1008836	1.34	5.81	3.68	3.89	6.17	4.1
	PLACE1008851	1.21	6.65	3.94	4.85	10.04	4.54
50	PLACE1008854	0.56	0.48	1.14	1.16	1.41	1.6
	PLACE1008864	1.98	1.92	2.96	2.73	2.65	2.49
	PLACE1008867	1.2	6.57	6.22	6.43	5.71	4.82
	PLACE1008876	11.7	16.5	27.29	26.74	20.94	23.24
	PLACE1008887	1.37	4.31	1.44	3.26	2.07	3.28
55	PLACE1008902	1.33	5.62	2.93	3.17	4.58	2.06
	PLACE1008911	4.04	8.56	10.48	11.31	13.99	15.66
	PLACE1008917	0.6	4.53	2.72	1.7	2.9	1.71
	PLACE1008920	0.75	0.77	0.87	0.61	1.58	1.44
	PLACE1008925	0.25	0.9	1.04	0.94	1.91	0.84
	PLACE1008930	4.12	7.32	9.83	5.11	10.36	7.17
	PLACE1008934	0.9	3.42	2.9	2.89	2.28	1.7

EP 1 130 094 A2

	PLACE1008941	1.57	4.14	2.8	2.06	2.59	4.05		
5	PLACE1008947	2.3	5.41	5.51	3.96	5.84	5.16		
	PLACE1008984	1.26	6.31	3.25	3.1	3.93	3.19		
	PLACE1008985	0.94	2.75	2.74	2.84	2.43	2.7		
	PLACE1008994	0.27	1.72	0.65	1.11	0.78	0.68		
10	PLACE1009020	0.46	3.49	2.42	2.49	3.1	2.16		
	PLACE1009027	0.89	2.7	1.59	2.24	1.75	2.09		
	PLACE1009039	-0.06	3.31	3.42	2.39	1.59	1.49		
	PLACE1009045	1.53	6.33	6.05	23.13	20.76	22.2	**	+
	PLACE1009048	0.41	5.97	2.3	0.61	1.04	0.54		
15	PLACE1009050	0.97	4.9	1.68	1.07	1.47	1.55		
	PLACE1009060	5.61	8.4	9.51	10.74	8.55	11.96		
	PLACE1009067	1.14	2.8	2.03	1.6	2.34	3.4		
	PLACE1009071	1.44	4.05	3.9	3.79	7.24	9.82		
	PLACE1009090	1.27	6.46	2.35	3.11	4.73	2.86		
20	PLACE1009091	5.58	10.22	38.11	38.77	49.35	36.29		
	PLACE1009094	0.26	5.68	1.88	1.67	5.04	1.71		
	PLACE1009099	1	5.52	3.47	3.49	3.36	3.84		
	PLACE1009110	1.59	5.82	1.16	1.68	4.3	4.39		
	PLACE1009111	1.88	5.24	2.65	3.95	3.77	2.88		
25	PLACE1009113	2.24	3.52	3.62	6.14	4.87	7.29	*	+
	PLACE1009130	4.46	6.8	7.84	6.68	9.36	10.47		
	PLACE1009150	0.88	3.54	1.95	3.23	3.3	3.01		
	PLACE1009155	1.11	5.06	2.98	4.46	4.43	3.87		
	PLACE1009158	1.06	5.77	1.95	1.77	2.35	2.88		
	PLACE1009166	0.76	4.8	1.53	1.59	2.16	1.3		
30	PLACE1009172	1.43	3.96	2.45	2.26	5.85	2.61		
	PLACE1009174	1.13	3.45	2.42	1.67	3.02	2.38		
	PLACE1009183	1.62	3.54	4.47	4.1	6.33	8.06		
	PLACE1009186	1.04	5.07	2.3	2.46	2.86	2.91		
	PLACE1009190	0.75	2.32	1.44	1.53	1.9	1.65		
35	PLACE1009196	0.81	4.01	2.73	2.24	2.38	1.99		
	PLACE1009200	1.01	4.44	2.94	2.84	4.39	2.91		
	PLACE1009217	2.55	4.91	3.43	4.46	7.29	7.23		
	PLACE1009230	1.9	5.55	6.63	5.63	9.16	9.46		
	PLACE1009236	4.97	7.07	12.6	8.21	10.79	7.13		
40	PLACE1009246	11.71	11.96	24.75	14.59	16.36	9.05		
	PLACE1009265	6.95	7.82	14.01	15.61	5.19	12.17		
	PLACE1009279	0.67	2.07	2.46	1.93	2.54	1.63		
	PLACE1009298	5.54	9.92	9.52	10.21	11.25	17.55		
45	PLACE1009308	1.13	6.82	2.04	2.48	2.48	2.34		
	PLACE1009319	2.04	9.25	3.15	2.92	3.54	2.5		
	PLACE1009328	1.04	5.78	1.81	2.98	3.39	2.17		
	PLACE1009335	1.38	6.55	4.72	2.24	3.21	3.01		
	PLACE1009338	2.56	4.14	5.1	3.24	4.3	1.57		
50	PLACE1009344	0.73	2.45	1.08	1.31	1.55	0.84		
	PLACE1009355	5.41	7.37	9.95	13.44	10.76	13.55	*	+
	PLACE1009368	1.3	2.56	2.41	2.43	2.32	2.19		
	PLACE1009375	1.21	6.41	3.05	3.04	4.46	2.53		
	PLACE1009388	1.18	8.68	3.01	3.46	4.53	2.72		
55	PLACE1009398	1.19	9.2	3.74	3.17	4.28	3.96		
	PLACE1009404	2.78	9.18	4.51	5.33	6.73	6.94		

EP 1 130 094 A2

	PLACE1009410	1.27	2.35	2.33	2.51	2.31	1.44		
5	PLACE1009417	0.95	2.25	4.34	2.55	3.08	1.71		
	PLACE1009424	1.88	3.61	3.18	2.85	3.24	3.93		
	PLACE1009434	0.84	3.94	2.91	1.29	1.82	2.19		
	PLACE1009443	1.21	7.2	2.55	2.42	3.43	3.17		
	PLACE1009444	1.33	7.71	4.05	2.51	3.17	3.79		
	PLACE1009459	0.23	7.99	1.55	1.71	1.83	0.86		
10	PLACE1009460	1.75	6.84	3.26	5.15	4.31	4.08		
	PLACE1009468	0.99	2.83	3.42	4.43	4.42	2.97		
	PLACE1009476	0.21	1.21	0.73	1.05	0.67	1.33		
	PLACE1009477	1.35	3.13	2.67	3.06	2.35	2.2		
	PLACE1009493	0.87	3.35	0.94	1	1.87	1.41		
15	PLACE1009502	0.76	4.64	2.13	1.19	1.89	1.66		
	PLACE1009524	1.32	4.22	1.63	0.94	2.14	1.6		
	PLACE1009527	0.95	4.51	2.11	1.64	2.55	1.28		
	PLACE1009531	20.82	28.24	41.52	46.25	43.25	49.96		
20	PLACE1009535	1.1	1.56	2.68	2.42	2.15	1.11		
	PLACE1009539	2.15	3.41	4.18	3.88	2.65	2.57		
	PLACE1009540	5.89	8	11.66	14.8	4.47	3.84		
	PLACE1009542	1.11	3.37	1.42	1.51	2.06	1.44		
	PLACE1009546	0.62	5.27	0.97	2.24	1.64	1.25		
25	PLACE1009556	0.35	4.46	3.46	3.36	2.86	3.16		
	PLACE1009569	0.05	3.93	2.46	3.34	2.7	3.11		
	PLACE1009571	1.67	4.27	2.52	3.04	2.85	2.67		
	PLACE1009573	3.81	2.97	6.73	6.92	8.12	6.49		
	PLACE1009576	1.92	2.51	4.3	2.73	3.66	2.08		
30	PLACE1009580	1.42	1.81	1.74	2.73	3.47	2.33	*	+
	PLACE1009581	0.89	4.25	2.03	2.91	4.38	2.74		
	PLACE1009587	0.96	4.91	2.29	2.43	3.2	1.99		
	PLACE1009593	2.71	6.73	4.37	4.94	6.85	5.03		
	PLACE1009595	1.81	5.44	2.66	2.67	5	2.79		
35	PLACE1009596	1.57	6.83	2.6	3.44	3.97	2.7		
	PLACE1009600	3.03	4.27	4.48	5.48	9.14	4.42		
	PLACE1009604	2.32	4.64	5.02	4.22	6.11	3.23		
	PLACE1009607	1.29	2.48	3.18	3.19	4.17	3.18		
	PLACE1009613	1.94	5.23	2.94	2.65	3.08	2.23		
40	PLACE1009621	1.66	6.72	3.32	8.21	8.67	8.06	*	+
	PLACE1009622	1.78	5.93	3.78	3.9	4.1	3.9		
	PLACE1009624	1.16	5.77	3.42	3.2	3.65	3.5		
	PLACE1009637	2	6.88	3.36	3.07	4.59	3.91		
	PLACE1009639	1.94	1.76	4.15	3.44	3.67	4.99		
45	PLACE1009654	20.88	17.13	34.95	14.94	24.53	20.64		
	PLACE1009659	2.77	6.78	7.45	6.38	8.38	6.55		
	PLACE1009665	1.04	4.21	1.93	1.19	2.72	1.93		
	PLACE1009669	7.73	9.64	14.54	9.85	16.89	8.82		
50	PLACE1009670	1.76	5.36	2.54	2.77	4.47	4.01		
	PLACE1009708	2.1	5.57	5.09	3.64	6.54	5.84		
	PLACE1009721	1.34	4.28	3.56	5.78	5.81	3.01		
	PLACE1009731	1.36	3.59	3	3.58	6.53	5		
	PLACE1009735	1.94	3.94	3.21	5.16	7.52	4.78		
55	PLACE1009737	1.89	4.29	2.95	4.83	5.61	5.47	*	+
	PLACE1009741	1.3	4.32	3.45	2.09	5.03	3.07		

EP 1 130 094 A2

	PLACE1009752	1.34	5.64	2.65	2.3	3.33	1.68
5	PLACE1009763	3.95	9.73	6.82	7.13	7.44	8.39
	PLACE1009766	1.46	6.98	3.32	3.07	5.19	3.75
	PLACE1009772	0.48	5.19	0.6	1.01	2.46	0.89
	PLACE1009782	0.91	2.39	2.03	2.88	2.91	3.74
10	PLACE1009794	2.58	4.45	5.11	3.54	3.66	5.03
	PLACE1009798	1.59	5.37	4	6.26	5.57	5.67
	PLACE1009845	1.05	6.02	2.92	2.79	3.39	3.92
	PLACE1009849	0.96	6.61	2.35	1.79	3.41	2.59
15	PLACE1009857	0.79	4.86	1.45	1.19	1.27	1.56
	PLACE1009861	1.43	4.67	3.87	4.1	3.47	3.11
	PLACE1009872	53.53	52.43	88.5	74.95	49.47	81.73
20	PLACE1009877	5.45	7.59	12.08	10.03	10.3	12.32
	PLACE1009879	0.82	3.28	1.59	1.55	2.99	1.34
	PLACE1009886	0.68	4.04	1.53	1.62	3.04	1.72
	PLACE1009888	1.03	7.4	3.23	5.34	5.84	7.94
25	PLACE1009908	1.56	7.63	8.64	3.37	6.71	5.9
	PLACE1009919	4.5	7.53	8.26	5.84	10.72	10.15
	PLACE1009921	0.96	3.94	3.32	1.63	4.28	2.47
	PLACE1009923	3.82	5.56	6.85	6.32	8.13	5.57
	PLACE1009924	3.01	2.49	4.53	4.43	4.31	1.04
30	PLACE1009925	0.61	2.77	1.84	2.51	2.2	2.5
	PLACE1009931	2.78	5.21	9	8.71	6.93	8.09
	PLACE1009935	0.74	3.71	2.1	1.19	1.08	1.5
	PLACE1009947	0.47	3.83	1.64	1.51	2.46	2.03
	PLACE1009961	0.43	4.08	1.39	1.69	2.18	1.9
35	PLACE1009971	0.92	4.9	1.98	1.35	1.74	1.45
	PLACE1009982	40.34	48.71	89.8	53.8	57.87	66.96
	PLACE1009992	0.94	1.9	2.59	1.47	2.52	0.68
	PLACE1009995	6.47	10.83	15.72	7.79	9.03	11.23
40	PLACE1009997	0.55	3.7	3.03	2.76	3.2	2.64
	PLACE1010002	1.4	4.14	2.82	2.89	3.04	3.46
	PLACE1010011	2.09	8.13	3.85	4.4	5.21	4.68
	PLACE1010013	0.18	12.85	1.74	0.92	1.81	0.68
	PLACE1010021	3.18	11.98	5.42	4.12	4.13	6.06
45	PLACE1010023	2.15	8.45	5.16	5.62	6.52	6.14
	PLACE1010031	4.6	4.35	7.23	6.79	4.91	1.82
	PLACE1010039	1.17	3.3	1.45	1.28	1.23	1.19
	PLACE1010045	1.1	2.83	3.66	2.52	3.55	2.64
	PLACE1010053	1.42	3.56	1.65	2.21	2.76	2.37
50	PLACE1010060	1.63	6.1	4.13	4.11	4.6	4.05
	PLACE1010069	0.41	7.96	2.32	1.48	2.91	1.3
	PLACE1010070	0.92	8.04	1.5	0.45	1.78	1.09
	PLACE1010074	5.25	11.67	11.8	12.32	9.51	11.22
	PLACE1010076	12.75	11.95	29.01	19.58	15.88	16.82
55	PLACE1010078	2.96	2.42	4.36	4.64	4.39	3.85
	PLACE1010081	2.74	4.1	3.7	6.85	7.81	4.59 *
	PLACE1010083	0.69	2.53	1.51	1.22	1.86	2.26
	PLACE1010089	1.86	4.89	3.35	3.45	3.47	3.48
	PLACE1010096	2.17	7.73	2.91	3.43	4.19	3.2
	PLACE1010102	3.89	10.9	5.33	7.1	9.64	7.57
	PLACE1010105	2.98	7.46	4.93	7.31	9.04	9.82

EP 1 130 094 A2

	PLACE1010106	2.46	2.95	4.48	5.47	4.88	5.8	*	+
5	PLACE1010130	0.53	1.79	1.17	2.27	2.55	1.23		
	PLACE1010132	2.49	4.65	5.3	5.07	4.39	4.19		
	PLACE1010134	0.8	3.32	1.15	1.97	2.31	1.67		
	PLACE1010139	6.67	10.51	12.98	14.99	16.1	14.58		
10	PLACE1010148	0.96	5.07	1.62	1.48	1.9	1.97		
	PLACE1010152	3.11	5.68	5.16	6.33	6.64	5.76		
	PLACE1010155	3.8	6.17	6.52	16.85	20.56	20.32	**	+
	PLACE1010156	13.71	15.43	32.21	132.45	85.59	134.99	**	+
	PLACE1010161	1.9	2.81	5.05	3.29	2.92	1.97		
15	PLACE1010181	0.73	2.22	1.51	2.58	1.99	2.53		
	PLACE1010194	0.64	3.35	1.03	2.26	2.14	1.64		
	PLACE1010202	0.4	4.14	1.2	2.91	1.65	2.16		
	PLACE1010231	1.1	3.78	2.39	1.31	2.99	2.73		
	PLACE1010235	1.26	4.24	1.94	2.68	2.42	3.16		
	PLACE1010237	1.01	3.4	2.1	1.14	1.97	0.87		
20	PLACE1010251	0.59	0.98	1.95	2.57	3.18	1.62		
	PLACE1010261	0.97	2.63	2.07	2.69	1.69	1.55		
	PLACE1010270	0.76	2.7	1.3	1.39	2.33	1.42		
	PLACE1010273	0.97	3.27	0.46	1.48	2.25	1.5		
	PLACE1010274	6.28	9.23	9.66	10.49	12.18	14.28		
25	PLACE1010277	6.03	10.14	12.68	14.6	16.06	15.84	*	+
	PLACE1010293	1.8	5.68	3.55	3.65	3.37	3.96		
	PLACE1010297	5.17	11.37	21	24.84	32.59	22.06		
	PLACE1010300	4.18	4.78	8.22	8	9.95	6.87		
	PLACE1010310	16.52	14.75	49.45	70.74	71	77.01	*	+
30	PLACE1010321	2.03	4.92	2.46	3.37	4.99	2.73		
	PLACE1010324	0.88	3.49	1.56	1.12	1.54	1.2		
	PLACE1010329	0.73	4.64	1.95	2.56	3.37	1.96		
	PLACE1010330	3.78	9.09	7.29	2.42	10.45	7.67		
	PLACE1010335	6.43	11.15	7.43	13.15	17.89	19.1	*	+
35	PLACE1010341	0.19	4.81	1.24	1.07	3.13	1.54		
	PLACE1010342	0.77	0.9	0.75	0.48	2.12	0.8		
	PLACE1010346	1.47	1.73	3.61	2.96	4.47	1.71		
	PLACE1010362	1.31	2.69	2.22	2.18	3.49	3.31		
	PLACE1010364	0.78	2.56	1.65	1.19	2.32	1.49		
40	PLACE1010368	1.66	5.44	3.51	3.41	3.87	4.48		
	PLACE1010373	9.05	10.48	16.82	12.13	15.45	12.28		
	PLACE1010383	1.91	5.52	5.13	5.58	6.39	4.9		
	PLACE1010385	0.3	3.01	1.07	0.04	0.6	0.9		
	PLACE1010389	6.28	7.98	13.24	22.3	13.64	22.94	*	+
45	PLACE1010401	0.73	2.72	1.32	1.99	2.87	2.21		
	PLACE1010410	3.15	4.83	6.71	4.78	7.55	7.32		
	PLACE1010418	1.88	4.73	4.2	4.71	5.14	4.66		
	PLACE1010425	0.93	4.78	1.43	1.78	1.96	2.15		
50	PLACE1010443	6.98	13.83	51.39	36.22	63.67	48.93		
	PLACE1010445	0.95	5.02	0.68	2.69	3.81	2.44		
	PLACE1010481	1.19	2.06	2.46	1.75	2	1.85		
	PLACE1010482	28.99	29.39	53.06	31.75	19.63	40.44		
	PLACE1010491	3.36	6.4	5.38	4.96	5.98	3.26		
	PLACE1010492	4	4.75	5.95	5.57	8.15	7.77		
55	PLACE1010509	0.8	4.32	3.15	3.09	3.01	2.99		

EP 1 130 094 A2

	PLACE1010518	3.33	6.72	6.58	7.3	8.25	8.24
5	PLACE1010522	2.3	5.96	4.35	1.87	3.52	2.64
	PLACE1010529	1.8	6.5	3.84	5.43	8.44	7.2
	PLACE1010547	0.79	1.57	1.76	1.51	1.93	2.45
	PLACE1010560	0.63	2.51	2.06	3.31	2.2	2.51
10	PLACE1010562	0.74	2.68	1.65	1.64	2.1	1.63
	PLACE1010579	1.11	7.13	2.63	3.45	4.67	3.26
	PLACE1010580	1.35	9.12	3.79	3.27	2.49	4.52
	PLACE1010599	3.56	6.07	7.94	8.32	9.26	8.13
15	PLACE1010606	1.17	4.42	1.64	3.39	4.17	3.51
	PLACE1010616	1.84	3.72	5.49	4.09	8.09	6.81
	PLACE1010622	2.1	3.43	3.91	5.07	4.74	4.69 * +
	PLACE1010624	1.43	3.35	3.98	4.21	6.17	5.22
	PLACE1010628	1.37	3.97	2.83	2.14	3.63	4.22
	PLACE1010629	1.08	4.64	2.24	3.01	3.3	3.5
	PLACE1010630	1.64	4.77	3.69	4.22	4.78	5.29
20	PLACE1010631	0.5	5.35	2.64	1.55	1.66	2.67
	PLACE1010651	14.24	15.75	24.44	37.62	40.09	52.12 * +
	PLACE1010661	1.62	4.09	2.28	3.56	6.43	3.22
	PLACE1010662	1.32	2.48	1.6	2.98	2.3	1.61
	PLACE1010668	12.87	15.91	27.82	37.63	30.53	28.75
25	PLACE1010702	1.46	2.34	4.24	3.59	3.6	3.2
	PLACE1010709	79.16	78.33	115.91	107.07	96.3	133.25
	PLACE1010713	7	10.81	14.7	9.14	8.16	15.14
	PLACE1010714	0.82	7.41	1.58	1.75	2.04	1.47
	PLACE1010716	0.71	6.19	4.31	2.08	2.3	1.93
30	PLACE1010717	0.9	6.49	2.13	2.17	3.9	2.61
	PLACE1010720	14.03	17.05	53.79	46.72	50.7	41.49
	PLACE1010739	0.9	1.2	1.11	1.73	1.21	1.93
	PLACE1010743	1.09	2.3	1.99	2.63	2.05	2.21
	PLACE1010752	0.87	2.92	1.85	1.76	2.05	1.53
35	PLACE1010761	3.6	8.83	13.51	12.07	16.4	17.08
	PLACE1010771	1.41	6.89	5.03	6.13	10.3	5.42
	PLACE1010784	0.9	9.66	1.97	2.07	1.72	1.34
	PLACE1010786	1.21	8.77	2.83	2.91	3.68	2.21
	PLACE1010789	0.6	1.16	1.52	1.8	1.89	1.17
40	PLACE1010800	2.18	2.86	3.25	3.95	3.24	2.93
	PLACE1010802	2.97	4.63	5.31	5.72	4.27	3.3
	PLACE1010811	0.89	2.19	1.96	1.83	1.75	2.18
	PLACE1010813	8.89	13.3	55.85	48.82	72.26	46.7
	PLACE1010827	1.54	6.43	3.94	4.3	5.52	4.81
45	PLACE1010833	0.93	8.13	2.63	2.68	3.64	2.09
	PLACE1010839	1.57	6.22	3.21	4.22	6.72	4.13
	PLACE1010856	7.58	8.94	12.34	8.02	6.53	8.59
	PLACE1010857	3.41	3.81	7.63	8.24	5.98	4.56
50	PLACE1010870	1.3	2.24	2.05	1.62	2.38	1.94
	PLACE1010877	1.67	4.66	2.69	2.77	3.92	2.62
	PLACE1010882	0.49	4.8	0.99	1.74	1.27	0.51
	PLACE1010891	1.1	7.73	1.12	1.85	1.73	0.95
	PLACE1010896	1.19	5.29	3.18	3.98	3.05	3.47
55	PLACE1010900	7.41	13.29	27.9	23.88	20.99	18.85
	PLACE1010916	1.55	1.18	2.06	1.89	1.9	2.2

EP 1 130 094 A2

	PLACE1010917	-0.04	0.82	0.36	1.05	2.25	0.56		
5	PLACE1010924	1.15	2.31	1.55	1.11	1.88	0.92		
	PLACE1010925	2.76	5.36	2.17	4.92	6.32	4.16		
	PLACE1010926	1.8	5.73	4.31	5.37	4.35	4.45		
	PLACE1010942	1.7	6.25	5.63	5.53	7.88	7.69		
	PLACE1010943	7.38	10.43	17.12	24.62	29.5	31.96	**	+
10	PLACE1010944	4.33	7.39	9.3	13.11	11.44	15.58	*	+
	PLACE1010947	1.43	0.9	2.41	2.57	2.8	2.25		
	PLACE1010954	3.56	2.92	7.4	7.92	8.55	7.64		
	PLACE1010960	2.06	3.44	6.07	4.23	7.89	2.6		
	PLACE1010965	2.33	3.81	3.54	6.09	4.92	5.03	*	+
15	PLACE1010968	1.55	4.69	1.38	4.95	6.51	3.68		
	PLACE1010978	3.63	6.12	7.05	9	8.94	6.45		
	PLACE1010982	2.23	5.77	5.6	4.74	5.66	4.88		
	PLACE1010990	0.88	5.4	2.04	3.11	3.03	2.19		
	PLACE1011017	5.6	3.78	22.57	25.64	35.47	20.97		
20	PLACE1011019	1.1	1.5	2.48	3.78	4.42	0.88		
	PLACE1011026	4.17	4.93	6.23	6	5.19	2.74		
	PLACE1011032	0.89	3.95	2.03	1.44	1.58	0.56		
	PLACE1011041	1.07	4.13	1.03	1.69	1.22	1.43		
	PLACE1011045	1.49	5.62	2.36	3.26	3.67	4.45		
25	PLACE1011046	0.83	5.25	1.79	2.57	3.17	1.87		
	PLACE1011054	2.33	5.33	6.64	5.26	7.29	5.05		
	PLACE1011056	5.78	5.43	16.22	14.56	19.78	15.67		
	PLACE1011057	2	2.18	3.5	3.29	5.68	3.9		
30	PLACE1011059	0.93	1.37	1.56	1.74	2.96	1.79		
	PLACE1011066	4.49	5.74	6.76	5.38	7.72	5.49		
	PLACE1011087	7.6	7.04	16.48	12.43	17.42	9.79		
	PLACE1011090	2.98	6.14	6.74	3.36	4.13	3.26		
	PLACE1011109	1.99	7.29	4.29	4.08	7.96	3.83		
35	PLACE1011114	1.62	4.4	3.13	3.33	4.68	3.29		
	PLACE1011116	4.89	5.94	6.66	7.43	6.81	8.98		
	PLACE1011122	0.93	2.52	1.84	2.1	1.61	1.64		
	PLACE1011133	0.83	2.22	3.03	3.48	3.52	2.77		
	PLACE1011134	12.47	15.29	66.86	44.95	68.68	51.65		
40	PLACE1011143	0.68	4.53	1.48	1.84	2.62	1.41		
	PLACE1011146	0.91	5.93	1.74	1.97	3.23	2.36		
	PLACE1011160	1.67	7.36	3.81	3.42	4.53	4.24		
	PLACE1011165	1.77	2.34	3.39	2.15	3.39	3.8		
	PLACE1011181	5.25	8.31	37.21	29.38	38.44	30.55		
45	PLACE1011185	2.47	4	3.57	4.66	5.15	4.8	*	+
	PLACE1011186	13.16	12.8	16.45	21.18	25.69	28.83	*	+
	PLACE1011203	1.08	4.64	2.19	1.75	2.94	1.96		
	PLACE1011214	9.02	16.55	59.24	46.39	62.58	47.89		
50	PLACE1011219	1.41	4.91	3.6	3.26	4.96	2.9		
	PLACE1011221	2.68	5.47	6.15	6.23	8.57	7.51		
	PLACE1011229	1.38	4.2	2.69	2.43	2.43	3.09		
	PLACE1011231	0.53	1.5	1.62	1.84	2.59	2.4		
	PLACE1011236	5.69	7.9	43.53	33.48	56.77	44.25		
55	PLACE1011247	8.36	10.08	19.16	24.17	26.33	29.74	*	+
	PLACE1011263	0.57	6.43	4.23	2.62	4.11	5.09		
	PLACE1011273	0.72	3.62	1.17	2.01	1.64	1.72		

EP 1 130 094 A2

5	PLACE1011278	2.42	5	6.12	3.98	4.84	4.31
	PLACE1011289	2.73	5.84	7.57	6.34	6.13	6.08
	PLACE1011291	3.2	5.19	8.31	7.32	8.04	7.95
	PLACE1011296	0.93	2.45	1.94	1.76	2.63	2.05
	PLACE1011310	1.72	2.64	3.36	4.51	2.77	4.48
	PLACE1011311	1.8	3.97	6.33	7.8	9.34	6.73
10	PLACE1011321	1.29	4.77	3.5	3.3	2.63	3.33
	PLACE1011325	0.63	4.2	1.84	2	2.74	1.59
	PLACE1011332	5.65	10.55	9.4	14.8	14.57	15.04 * +
	PLACE1011340	0.86	4.88	3.38	3.81	4.71	3.47
	PLACE1011353	5.39	5.53	8.39	10.06	8.58	4.43
15	PLACE1011360	1.09	3.29	2.18	2.11	3.06	2.41
	PLACE1011364	4.88	5.69	7.92	6.34	4.57	4.57
	PLACE1011365	0.92	3.36	2.95	3.01	3.6	2.06
	PLACE1011371	9.37	10.69	63.06	56.51	87.51	64.33
	PLACE1011375	1.62	9.37	3.35	2.61	2.74	1.62
20	PLACE1011386	3.91	12.96	4.18	6.88	5.51	5.93
	PLACE1011399	1.52	10.14	4.27	2.12	4.22	3.77
	PLACE1011406	1.25	2.05	1.81	5.03	3.26	2.38
	PLACE1011407	0.64	2.05	2.58	2.08	2.19	2.02
	PLACE1011419	2.83	3.2	6.02	6.23	4.18	3.72
25	PLACE1011433	3.09	4.43	6.13	3.41	4.74	4.99
	PLACE1011440	0.77	5.81	2.48	2.1	2.24	2.27
	PLACE1011452	1.06	8.86	2.43	2.87	2.71	2.68
	PLACE1011465	0.09	8.53	1.96	1.04	1.68	0.85
	PLACE1011472	1.52	7.67	3.98	0.97	2.87	1.59
30	PLACE1011477	11.18	12.29	54.35	31.86	55.86	45.67
	PLACE1011478	1.24	1.64	3.11	5.03	3.02	3.01
	PLACE1011492	2.24	3.54	5.01	5.45	6.74	5.27
	PLACE1011498	0.57	2.77	0.98	1.18	1.69	1.15
	PLACE1011501	0.49	4.67	1.8	4.87	5.63	7.5
35	PLACE1011503	0.44	5.37	0.79	0.5	0.82	0.35
	PLACE1011509	1.1	7.8	3.38	4.62	5.08	5.74
	PLACE1011514	5.86	11.61	11.98	13	17.7	13.17
	PLACE1011516	10.37	13.29	18.32	18.32	8.08	3.63
40	PLACE1011520	0.34	0.95	1.34	1.3	1.73	1.01
	PLACE1011538	52.87	99.27	185.04	129.45	86.87	63.9
	PLACE1011555	0.87	2.88	2.83	1.55	2.03	1.48
	PLACE1011561	3.2	4.53	1.98	6.81	5.31	3.08
	PLACE1011563	1.35	4.74	3.49	2.52	2.64	2.87
45	PLACE1011567	1.04	4.94	3.36	2.75	4.19	2.77
	PLACE1011569	0.32	4.35	2.77	2.38	2.46	2.28
	PLACE1011576	3.25	1.88	7.94	7.85	9.1	8.03
	PLACE1011586	3.24	2.5	6.22	4.43	4.35	2.94
	PLACE1011635	1.85	2.56	4.53	9.96	12.43	8.71 ** +
50	PLACE1011641	0.43	2.9	0.9	1.71	1.18	1.19
	PLACE1011642	5.05	6.96	10.37	12.13	10.86	10.09
	PLACE1011643	1.29	3.69	1.14	2.38	2.28	2.14
	PLACE1011646	8.68	12.8	30.53	39.05	54.16	37.76 * +
	PLACE1011649	1.35	5.7	3.88	4.5	4.61	5.46
55	PLACE1011650	1.15	1.45	2.54	2.47	3.24	3.75
	PLACE1011661	1.02	2.26	2.8	3.95	5.92	3.46

EP 1 130 094 A2

5	PLACE1011664	2.21	3.18	3.99	5.31	3.93	1.73
	PLACE1011672	0.88	4.14	0.72	2.69	3.57	2.04
	PLACE1011675	0.51	2.31	1.32	1.66	0.99	0.83
	PLACE1011682	2.04	4.56	2.23	2.22	4.03	2.12
	PLACE1011708	1.1	5.89	3.8	5.5	8.12	4.66
	PLACE1011719	1.07	4.58	1.66	3.55	3.88	3.03
10	PLACE1011725	1.23	1.19	2.72	3.73	5.19	4.3 * +
	PLACE1011729	0.86	1.03	1.8	2.38	3.26	1.22
	PLACE1011741	2.36	3.67	3.64	4.16	2.52	4.23
	PLACE1011749	1.58	3.89	4.09	3.49	4.85	3.27
	PLACE1011757	20.92	30.53	55.88	56.6	55.88	49.59
	PLACE1011762	0.4	4.34	2.69	3.91	2.14	2.3
15	PLACE1011778	0.51	4.39	1.99	1.34	2.02	1.34
	PLACE1011783	2.59	4.63	5.46	4.8	8.41	5.55
	PLACE1011795	0.74	1.28	2.24	1.47	1.8	1.22
	PLACE1011810	9.28	10.82	19.51	13.32	17.73	15.47
	PLACE1011824	5.38	8.17	38.05	25.52	42.89	16.75
20	PLACE1011825	10.61	16.39	22.6	17.63	18.92	16.07
	PLACE1011835	24.64	32.67	47.67	32.09	26.75	37.23
	PLACE1011836	18.11	18.97	31.43	33.14	47.23	13.95
	PLACE1011847	2.67	6.74	6.42	5.34	7.18	5.84
	PLACE1011855	0.9	6.06	3.53	3.23	4.47	3.49
25	PLACE1011858	5.83	7.44	9.37	6.88	6.25	8.35
	PLACE1011874	1.35	3.14	3.55	4.18	5.28	4.65
	PLACE1011875	0.57	2.29	1.11	2.66	2.48	2.64
	PLACE1011877	3.8	5.03	4.4	7.67	6.8	9.97 * +
30	PLACE1011891	0.17	3.81	1.31	1.13	1.34	1.26
	PLACE1011896	-0.1	5.22	1.45	-0.19	1.07	0.32
	PLACE1011920	0.21	5.87	1.04	1.1	1.92	1.76
	PLACE1011922	2.4	4.18	4.72	3.72	2.88	3.98
	PLACE1011923	3.42	4.82	7.51	8.09	5.38	12.28
35	PLACE1011937	3.16	2.24	3.76	3.81	5.58	4.64
	PLACE1011939	14.93	17.81	26.01	41.75	45.05	47.88 ** +
	PLACE1011940	6.13	7.58	12.68	5.73	7	7.23
	PLACE1011962	3.28	7.83	7.35	6.39	8.38	8.01
	PLACE1011964	0.39	5.05	1.66	1.04	1.95	1.46
40	PLACE1011978	1.55	4.65	3.35	4.48	5.91	5.14
	PLACE1011980	2.1	4.62	6.07	3.95	4.91	5.35
	PLACE1011981	5.77	7.28	38.2	27.22	35.24	34.99
	PLACE1011982	0.83	3.1	2.23	1.82	2.59	1.57
	PLACE1011995	0.81	3.4	3.73	2.51	3.59	2.86
45	PLACE1012023	1.38	5.37	1.87	2.09	2.46	1.91
	PLACE1012026	1.95	5.72	4.23	6.08	9.51	9.8
	PLACE1012031	2.49	5.81	4.54	4.34	6.35	4.03
	PLACE2000003	1.18	3.64	6.86	7.38	8.12	8.92
	PLACE2000005	1.16	2.41	2.16	2.76	2.03	1.89
50	PLACE2000006	2.52	4.13	15.6	11.34	16.58	13.4
	PLACE2000007	0.96	4.85	4.24	3.94	5.13	3.33
	PLACE2000011	1.72	3.27	3.34	4.3	5.06	3.62
	PLACE2000014	4.04	5.93	23.94	27.19	30.87	30.97 * +
	PLACE2000015	1.27	4.79	3.52	2.77	3.31	2.69
55	PLACE2000017	0.48	4.78	2.15	2.65	2.56	2.45

EP 1 130 094 A2

	PLACE2000021	1.99	5.06	4.09	3.72	6.24	5.61
5	PLACE2000022	1.8	2.8	4.31	3.35	4.64	2.71
	PLACE2000030	9.37	11.08	71.38	55.43	60.32	35.97
	PLACE2000032	1.23	2.89	3.51	3.53	3.24	2.32
	PLACE2000033	3.29	6.3	12.11	12.49	14.25	9.37
	PLACE2000034	0.6	4.3	1.92	1.79	2.19	2.44
10	PLACE2000039	2.75	8.06	3.92	6.27	8.01	4.81
	PLACE2000043	7	11.08	22.94	19.27	26.58	17.38
	PLACE2000044	0.63	6.92	1.12	1.8	1.71	1.29
	PLACE2000047	0.84	5.25	5.15	5.4	6.46	7.32
	PLACE2000050	1.48	2.68	4.78	2.92	2.98	1.2
15	PLACE2000061	0.47	2.07	1.17	0.95	1.34	0.25
	PLACE2000062	1.99	2.83	4.12	4.89	4.4	3.09
	PLACE2000072	0.78	2.45	1.57	1.85	1.62	1.69
	PLACE2000073	0.89	5.86	2.86	2.8	2.61	3.07
	PLACE2000097	8.54	19.93	23.93	27.69	35.36	26.36
20	PLACE2000100	1.87	7.79	3.53	4.23	6.29	4.22
	PLACE2000103	1.03	7.44	2.25	3.51	5.17	4.38
	PLACE2000106	1.53	2.42	4.19	5.71	3.29	4.01
	PLACE2000111	2.05	3.17	4.37	4.07	6.6	4.75
	PLACE2000115	0.3	2.06	0.75	0.31	1.29	0.97
25	PLACE2000118	10.15	17.04	21.09	13.73	15.21	22.01
	PLACE2000124	10.14	17.83	62.13	53.2	98.37	62.96
	PLACE2000132	0.06	6.26	1.48	0.99	1.5	1.56
	PLACE2000136	0.55	7.94	0.91	1.47	1.37	1.02
	PLACE2000137	0.96	4.46	2.4	2.65	4.12	3.14
30	PLACE2000140	2.91	5.24	14.34	13.2	12.08	9.43
	PLACE2000147	1.49	1.52	2.83	1.06	0.97	1.12
	PLACE2000153	0.3	3.44	2.15	1.69	2.45	1.95
	PLACE2000164	0.66	2.78	1.13	2.66	1.62	1.62
	PLACE2000170	1.54	6.18	4.69	5.26	9.09	6.24
35	PLACE2000172	0.33	4.34	2.15	1.25	1.93	2.43
	PLACE2000173	0.92	4.97	3.37	3.33	3.71	2.74
	PLACE2000174	1.17	4.68	2.43	1.85	2.89	2.05
	PLACE2000176	1.22	1.57	2.58	3.28	2.27	1.42
	PLACE2000187	1.01	2.08	2.55	3.45	3.66	2.19
40	PLACE2000216	7.03	9.28	11.47	14.09	9.13	3.68
	PLACE2000219	0.69	4.02	2.72	3.55	3.58	2.3
	PLACE2000221	2.49	6.81	6.53	7.22	9.33	8.56
	PLACE2000223	0.72	3.2	1.71	1.16	1.05	0.48
	PLACE2000231	1.02	3.97	3.11	3.43	2.61	2.47
45	PLACE2000235	1.82	5.27	6.17	6.02	7.45	6.97
	PLACE2000246	1.93	2	6.06	4.58	5.09	3.93
	PLACE2000264	0.67	1.39	1.85	2.45	3.74	3 * +
	PLACE2000274	0.65	2.4	2.12	3.09	4.11	2.1
	PLACE2000287	0.81	4.44	1.49	2	2.59	1.34
50	PLACE2000296	1.01	4.56	1.55	2.5	3.16	1.69
	PLACE2000302	1.34	4.67	2.86	3.52	3.35	3.45
	PLACE2000305	3.09	6.65	5.42	6.3	7.15	5.02
	PLACE2000317	0.92	6.34	2.26	3.15	2.95	2.4
55	PLACE2000324	1.19	1.25	3.09	4.2	5.84	3.3
	PLACE2000334	3.52	5	6.6	7.33	8.12	5.88

EP 1 130 094 A2

	PLACE2000335	1.47	4.35	4.24	5.68	6.25	4.76
5	PLACE2000340	0.64	3.47	1.63	1.58	1.52	1.65
	PLACE2000341	4.21	7.87	28.81	18.94	32.45	19.16
	PLACE2000342	2.07	5.11	4.32	4.84	5.82	4.49
	PLACE2000347	1.24	5.26	5.58	7.83	6.22	7.55
	PLACE2000357	8.49	13.56	15.35	17.83	18.98	21.24 * +
10	PLACE2000358	2.87	3.65	8.67	4.88	7.63	4.37
	PLACE2000359	1.27	1.79	4.45	3.28	6.65	3.61
	PLACE2000366	1.93	3.14	3.22	3.99	5.6	4.17
	PLACE2000371	4.29	5.2	6.08	5.95	9.06	7.32
	PLACE2000373	1.91	4.8	5.98	5.69	6.29	4.19
15	PLACE2000374	1.86	5.17	2.78	1.62	2.79	1.49
	PLACE2000379	0.34	4.85	1.32	1.28	0.92	0.04
	PLACE2000386	39.29	43.92	84.66	87.53	104.55	76.56
	PLACE2000388	1.96	3.35	3.89	2.78	3.48	3.49
	PLACE2000392	33.29	39.2	59.56	42.5	52.12	58.24
20	PLACE2000394	1.26	3.27	3.01	5.69	4.35	4.34 * +
	PLACE2000398	0.73	3.88	2.36	2.03	3.59	1.35
	PLACE2000399	3.7	6.82	7.01	7.15	7	6.79
	PLACE2000402	2.15	6.88	3.84	2.86	3.68	3.9
	PLACE2000404	5.2	9.96	10.67	10.03	11.04	6.47
25	PLACE2000411	3.21	7.2	5.21	5.27	5.73	6.68
	PLACE2000418	0.73	2.28	2.41	2.22	3.07	2.37
	PLACE2000419	0.99	2.32	2.54	4.95	4.55	3.29 * +
	PLACE2000425	1.26	3.98	3.11	4.28	4.81	5.2
	PLACE2000427	0.7	5.13	3.27	2.54	3.04	2.47
30	PLACE2000433	0.77	7.05	2.6	2.33	3.09	2.46
	PLACE2000435	0.48	5.19	1.49	1.69	1.63	1.5
	PLACE2000438	1.61	4.74	3.66	2.33	2.81	3.15
	PLACE2000450	3.01	4.38	5.67	6.51	7.39	5.63
	PLACE2000455	0.24	2.62	1.24	1.65	2	1.82
35	PLACE2000458	0.38	3.3	1.81	1.06	2.7	1.24
	PLACE2000464	2.15	4.91	5.3	7.43	9.68	8.83 * +
	PLACE2000465	1.43	6.72	6	6.51	8.27	6.31
	PLACE2000473	120.94	179.35	328.3	214.7	297.75	279.74
	PLACE2000477	0.43	3.87	1.34	1.13	2.22	0.97
40	PLACE3000004	2.22	4.63	6.39	5.27	7.51	5.2
	PLACE3000009	19.91	19.71	105.63	77.3	140.99	92.95
	PLACE3000020	10.03	9.03	49.6	36.74	46.52	23.82
	PLACE3000029	6.59	9.63	24.88	14.88	18.47	20.04
	PLACE3000038	0.52	2.37	2.47	1.44	2.4	2.05
45	PLACE3000052	5.13	7.95	23.92	25.01	29.61	24.94
	PLACE3000059	0.57	5	2.42	0.75	2.8	1.27
	PLACE3000067	2.51	5.79	7.44	5.66	8.53	7.75
	PLACE3000069	1.95	5.61	3.58	5.24	3.79	4.55
	PLACE3000070	2.57	5.57	9.04	9.5	10.42	10.57
50	PLACE3000103	3.85	7.84	11.87	6.6	8.32	4.37
	PLACE3000119	1.59	2.74	3.15	3.24	3.67	2.95
	PLACE3000121	7.58	8.44	38.1	30.63	42.28	32.64
	PLACE3000124	1.53	4.54	5.95	6.35	7.75	7.18
55	PLACE3000135	0.69	5.46	1.1	0.76	0.9	0.59
	PLACE3000136	0.77	10.46	4.46	2.12	2.77	2.01

EP 1 130 094 A2

	PLACE3000142	0.7	9.94	1.75	1.53	2.76	1.13			
5	PLACE3000145	8.69	17.55	55.33	42.85	49.12	39.96			
	PLACE3000147	15.7	12.92	39.97	64.96	54.76	30.34			
	PLACE3000148	0.7	2.08	1.48	0.82	1.4	1.38			
	PLACE3000154	0.48	1.86	0.67	1.5	0.87	0.44			
	PLACE3000155	1.28	4.26	2.53	3.97	4.76	3.04			
10	PLACE3000156	1.11	7.96	2.07	1.96	3.4	2.81			
	PLACE3000157	0.92	8.37	1.75	2.06	3.02	2.72			
	PLACE3000158	1.73	8.82	5.05	3.81	5.63	4.77			
	PLACE3000160	8.11	15.22	19.5	33.66	34.71	33.78	**	+	
	PLACE3000169	2.15	2.65	6.87	4.3	5.11	5.12			
15	PLACE3000181	1.06	2.14	3.94	3.22	2.62	3			
	PLACE3000194	0.31	2.83	1.77	1.89	2.58	2.42			
	PLACE3000197	1.18	2.66	2.09	2.42	2.46	2.21			
	PLACE3000199	0.22	4.8	1.63	0.55	0.86	0.43			
	PLACE3000205	11.79	17.95	57.49	51.4	63.83	42.63			
20	PLACE3000207	3.37	6.91	7.13	6.7	8.92	6.23			
	PLACE3000208	2.26	4.96	2.66	5.28	5.97	5.84			
	PLACE3000213	4.79	5.55	10.8	5.12	5.16	5.05			
	PLACE3000215	1.88	5.02	5.71	4.74	5	3.03			
	PLACE3000218	0	1.63	1.18	0.97	0.62	0.31			
25	PLACE3000220	1.96	3.55	4.58	6.74	7.52	6.69	*	+	
	PLACE3000221	14.42	25.34	40.15	43.8	51.16	36.99			
	PLACE3000225	1.15	4.68	3.11	2.11	2.67	1.28			
	PLACE3000226	1.37	5.65	5.16	3.78	7.42	3.68			
	PLACE3000230	0.83	3.46	1.36	2	2.8	1.73			
30	PLACE3000231	1.31	1.97	2.37	4.86	3.95	4.12	**	+	
	PLACE3000235	1.12	1.75	3.89	3.95	4.21	3.39			
	PLACE3000242	2.6	5.11	9.24	9.46	10.97	8.29			
	PLACE3000244	1.05	3.2	1.81	1.85	1.81	0.64			
35	PLACE3000253	0.7	3.75	1.64	2.67	2.11	1.27			
	PLACE3000254	2.5	4.75	4.04	6.19	6.09	5.75	*	+	
	PLACE3000271	2.67	6.06	6.81	10.96	10.99	9.5	*	+	
	PLACE3000276	1.1	5.78	2.27	1.48	1.9	1.78			
	PLACE3000304	5.55	4.69	10.81	11.19	11.49	10.5			
40	PLACE3000309	0.43	1.67	1.87	2.43	2.94	2.78	*	+	
	PLACE3000310	2.19	2.19	3.73	4.84	4.81	3.4			
	PLACE3000320	1.02	3.65	1.8	2.54	2.37	2.32			
	PLACE3000322	1.31	4.23	6.63	7.5	7.8	6.09			
	PLACE3000330	24.05	24.44	41.08	31.87	35.83	29.17			
45	PLACE3000331	1.21	5.86	4.14	4.34	5.7	4.31			
	PLACE3000336	2.61	6.99	4.42	4.24	5.72	5.11			
	PLACE3000339	7.36	5.1	11.41	16.25	18.28	17.37	**	+	
	PLACE3000341	1.65	1.32	2.41	4.08	4.35	3.65	**	+	
	PLACE3000350	5.88	6.4	12.86	15.45	18.5	15.41	*	+	
50	PLACE3000352	1.54	3.88	2.13	2.37	2.25	1.71			
	PLACE3000353	5.38	9.72	11.8	19.12	22.98	15.5	*	+	
	PLACE3000362	0.62	4.92	4.72	3.61	5.33	3.39			
	PLACE3000363	2.19	5.13	2.32	1.89	3.28	2.07			
	PLACE3000365	1.34	6.11	3.37	3.34	4.05	2.12			
55	PLACE3000373	0.89	1.52	3.66	2.93	6.08	2.3			
	PLACE3000374	1.07	1.85	2.91	2.72	2.99	2.15			

EP 1 130 094 A2

5	PLACE3000387	0.31	3.32	1.04	1.24	1.65	1.29
	PLACE3000388	1.18	3.22	1.94	2.76	3.49	2.22
	PLACE3000399	2.12	4.66	6.28	7.42	9.84	6.05
10	PLACE3000400	3.08	5.44	11.87	7.97	10.77	7.82
	PLACE3000401	7.52	11.42	18.59	22.61	29.55	23.4 *
	PLACE3000402	1.79	3.21	3.4	2.19	1.74	1.79
	PLACE3000405	3.37	3.74	5.82	5.54	7.22	6.01
15	PLACE3000406	2.1	2.91	3.11	3.48	3.68	2.42
	PLACE3000413	1.18	2.72	2.69	1.71	2.06	1.52
	PLACE3000416	1.05	4.03	4.04	3.43	2.67	2.72
	PLACE3000425	1.21	6.27	4.33	3.98	6.36	3.92
20	PLACE3000437	4.79	10.85	29.89	16.69	25.26	19.14
	PLACE3000455	2.97	8.07	10.62	8.97	10.39	7.91
	PLACE3000475	16.52	19.2	47.35	40.22	39.77	34.21
	PLACE3000477	5.44	4.79	5.56	8.05	5.52	8.42
25	PLACE4000003	0.38	2.97	1.61	3.14	2.33	2.31
	PLACE4000008	15.19	11.38	16.76	13.05	14.26	8.84
	PLACE4000009	1.17	6.19	3.39	3.93	3.37	1.82
	PLACE4000014	1.31	5.12	1.77	2.16	3.03	2.19
30	PLACE4000029	6.33	8.48	35.37	23.93	32.21	24.25
	PLACE4000034	2.27	6.24	5.22	6.46	6.52	4.91
	PLACE4000049	3.39	3.35	5.21	3.85	5.82	4.86
35	PLACE4000052	1.41	3.36	2.2	2.62	2.64	2.02
	PLACE4000062	1.6	4.94	5.06	4.25	5.06	3.71
	PLACE4000063	2.59	6.87	5.19	4.86	4.81	3.73
	PLACE4000089	1.52	6.31	3.35	2.81	3.91	2.84
40	PLACE4000093	0.44	5.6	1.61	1.28	1.65	1.98
	PLACE4000100	2.72	6.13	4.75	4.33	3.62	3.94
	PLACE4000103	0.63	4.48	5.64	4.4	5.67	2.9
	PLACE4000106	3.2	5.33	6.63	7.1	5.13	7.21
	PLACE4000128	1.93	3.97	4.88	4.15	4.96	4.4
45	PLACE4000129	0.74	3.26	1.64	1.57	2.11	1.78
	PLACE4000131	7.14	10.85	41.43	32.45	41.08	31.22
	PLACE4000147	0.34	3.65	0.54	0.45	0.93	0.61
	PLACE4000156	2.47	6.08	8.06	7.83	13.47	9.07
	PLACE4000175	0.72	4.08	1.48	0.98	0.91	0.84
50	PLACE4000190	14.55	18.47	70.34	49.15	74.82	60.76
	PLACE4000192	1.3	2.27	3.6	2.36	2	1.25
	PLACE4000206	5.35	6.65	12.44	7.13	7.1	6.02
	PLACE4000211	3.34	4.64	22.23	11.68	12.35	13.44
	PLACE4000214	0.86	3.61	2.68	2.08	2.53	1.69
55	PLACE4000222	0.93	5.28	4.36	4.13	4.75	3.5
	PLACE4000223	0.46	4.51	1.79	1.37	1.22	0.38
	PLACE4000229	1.9	5.79	2.11	2.81	3.36	3.48
	PLACE4000230	1.11	5.89	6.51	3.61	6.81	5.15
	PLACE4000233	1.26	3.02	5.66	2.92	2.98	3.51
	PLACE4000239	2.35	3.68	4.17	4.19	3.97	3.35
	PLACE4000247	0.52	2.37	3.38	2.64	3.1	2.35
	PLACE4000250	1.18	3.24	2.35	3.33	3.68	2.8
	PLACE4000252	1.06	4.99	2.25	1.92	1.75	1.64
	PLACE4000259	4.42	11.95	18.1	14.47	22.09	14.02
	PLACE4000261	0.87	10.29	1.07	2.03	1.9	1.12

EP 1 130 094 A2

5	PLACE4000264	15.86	24.96	36.9	11.96	21.82	22.51
	PLACE4000269	3.48	3.71	7.95	4.62	4.55	2.85
	PLACE4000270	0.43	1.42	1.87	1.75	1.83	0.59
	PLACE4000281	17.84	20.97	44.05	32.93	28.37	28.87
	PLACE4000300	0.67	2.06	2.04	3.21	2.88	3.58 * +
	PLACE4000320	1.33	5.86	3.1	2.84	5.32	3.21
10	PLACE4000323	1.63	7.43	5.13	4.03	4.65	4.82
	PLACE4000326	1.8	10.98	5.67	5.72	8.73	5.59
	PLACE4000344	0.22	5.75	2.62	1.66	1.6	1.18
	PLACE4000347	4.7	3.82	13.93	16.83	16.75	17.36 * +
	PLACE4000354	3.18	6.29	10.68	5.17	2.81	2.79
15	PLACE4000367	0.79	2.97	1.71	0.87	1.3	1.38
	PLACE4000369	1.35	3.97	2.36	1.99	1.96	0.82
	PLACE4000379	2.44	6.66	5.44	5.94	7.55	5.07
	PLACE4000387	0.88	5.86	2.11	1.28	0.84	1.12
	PLACE4000392	0.42	5.58	1.32	1.81	1.02	1.63
20	PLACE4000399	10.99	17.08	75.17	59.11	80.22	58
	PLACE4000401	0.72	0.7	1.53	1.17	0.83	1.4
	PLACE4000403	3.15	4.13	8.51	5.29	6.38	5.87
	PLACE4000411	2.22	2.28	4	2.27	2.6	1.82
	PLACE4000415	0.7	3.55	2.8	1.16	1.86	0.78
25	PLACE4000416	25.49	29.13	33.54	23.65	21.92	24.83
	PLACE4000424	1.61	5.59	3.33	3.27	3.92	2.51
	PLACE4000431	3.89	7.39	21.01	17.68	28.21	16.79
	PLACE4000443	0.07	4.33	2.15	1.52	2.83	1.14
	PLACE4000445	3.94	5.43	9.98	7.62	6.99	6.27
30	PLACE4000450	2.99	3.65	23.28	15.51	24.53	16.04
	PLACE4000455	5.18	7.39	9.55	8	7.21	4.63
	PLACE4000465	1.39	4.34	3.26	4.15	6.07	4.34
	PLACE4000466	120.96	98.04	201.25	113.83	170.96	145.31
	PLACE4000472	3.12	9.6	10.17	10.92	13.21	9.22
35	PLACE4000487	3.18	7.83	16.5	14.66	16.62	15.05
	PLACE4000489	0.93	4.69	3.41	1.95	3.88	1.69
	PLACE4000494	1.15	1.6	4.07	2.74	3.1	2.08
	PLACE4000502	6.3	5.39	10.92	11.65	15.08	6.37
	PLACE4000521	2.5	3.44	16.06	12.78	20.63	11.2
40	PLACE4000522	5.07	6.17	9.07	12.43	8.68	14.11
	PLACE4000537	0.98	4.28	1.27	1.67	1.61	1.22
	PLACE4000548	1.99	5.69	2.46	3.04	3.68	2.32
	PLACE4000558	0.87	6.72	1.97	3.15	2.41	2.15
	PLACE4000581	2.1	7.22	7.04	3.9	5.96	5.44
45	PLACE4000590	0.4	0.61	0.15	0.4	0.81	-0.25
	PLACE4000593	2.94	2.98	5.22	4.44	5.82	3.83
	PLACE4000612	0.68	3.33	3.33	1.5	3.02	2.74
	PLACE4000638	1.25	4.24	0.84	1.2	1.44	1.58
50	PLACE4000650	0.82	4.67	1.02	1.43	1.11	1.16
	PLACE4000651	2.42	6.4	7.48	5	7.01	6.07
	PLACE4000654	0.98	5.7	2.47	1.35	2.48	1.47
	PLACE4000670	0.5	4.06	2.92	0.76	1.29	0.67
	PLACE4000685	6.35	8.68	13.83	13.46	14.26	13.77
55	PLACE4000687	0.37	3.02	1.11	2.2	1.4	1.12
	PLACE5000003	1.1	2.74	3.31	3.21	3.55	3.07

EP 1 130 094 A2

	PLACE5000005	12.43	16.53	27.36	24.54	24.57	24.76
5	PLACE5000019	0.4	4.15	1.13	0.59	1.89	0.79
	PLACE5000021	0.74	4.59	1.61	0.39	0.93	0.32
	PLACE5000022	1.2	6.11	2.25	3.17	2.76	2.09
	PLACE5000024	1.77	2.58	2.27	2.92	3.39	3.84 * +
10	PLACE5000036	1.81	3.24	3.11	2.41	3.19	2.84
	PLACE5000059	14.41	17.79	26.55	25.98	30.03	34.87
	PLACE5000076	1.41	3.61	2.22	4.04	3.96	2.54
	PLACE5000117	7.44	12.48	15.66	16.87	18.78	20.64
	PLACE5000143	0.85	6.45	2.11	1.67	2.85	2.73
15	PLACE5000152	0.42	4.49	1.23	1.61	1.95	1.57
	PLACE5000154	18.23	23.5	45.06	21.81	25.65	31.8
	PLACE5000155	3.35	2.81	5.51	3.94	2.78	4.87
	PLACE5000165	3.78	4.4	6.67	4.51	5.99	5.82
	SKNMC1000004	9.7	11.62	16.77	10.19	12.16	13.96
20	SKNMC1000011	1.82	8.58	4.12	5.89	3.95	6.77
	SKNMC1000013	0.51	6.69	1.13	1.21	2.14	1.44
	SKNMC1000014	1.28	4.18	3.22	3.77	6.37	3.96
	SKNMC1000018	3.42	5.19	5.25	5.51	5.68	3.44
	SKNMC1000020	0.95	4.03	3.46	3.6	4.68	4.56
	SKNMC1000046	2	3.17	3.48	3.95	3.26	2.55
25	SKNMC1000050	4.99	8.04	10.32	5.4	6.28	6.12
	SKNMC1000062	9.79	12.6	20.18	19.2	15.42	18.73
	SKNMC1000075	1.45	4.3	2.01	1.98	1.89	2.92
	SKNMC1000082	1.12	4.39	2.13	1.85	1.78	2.39
30	SKNMC1000091	4.54	7.52	7.95	11.74	12.86	12.77 ** +
	SKNMC1000099	0.33	4.29	1.98	1.32	0.65	1.18
	SKNMC1000104	1.13	4.24	3.45	1.47	3.14	2.43
	SKNMC1000113	0.97	1.83	1.2	1.74	2.63	0.89
35	SKNMC1000119	1.73	2.64	5.07	4.48	5.34	4.67
	SKNMC1000142	0.04	2.87	0.99	1.27	0.75	1
	SKNMC1000170	0.91	4.75	2.34	1.71	1.49	1.11
	SKNMC1000178	3.02	8.39	7.08	5.77	9.65	9.02
40	SKNMC1000194	0.63	9.82	1.51	0.61	1.73	1.3
	SKNMC1000198	1.35	11.01	3.33	2.65	2.1	2.88
	SKNMC1000225	1.35	6.44	2.97	2.39	3.4	3.26
45	SKNMC1000249	0.49	2.14	0.75	0.57	0.51	0.52
	SPLEN1000007	0.74	2.15	2.11	1.7	2.26	1.99
	SPLEN1000012	0.39	1.9	1.72	1.19	0.8	0.84
	SPLEN1000014	1.78	4.4	4.9	5.75	4.33	3.99
50	SPLEN1000036	4.95	11.64	24.32	20.56	27.73	21.68
	SPLEN1000059	0.04	6.69	1.06	0.91	1.79	1.47
	SPLEN1000068	1.68	10.81	5.71	5.79	5.17	5.64
	SPLEN1000072	1	8.5	4.7	2.82	3	2.21
55	SPLEN1000101	20.01	18.4	45.64	29.93	25.24	12.63
	SPLEN1000108	0.56	1.54	0.98	0.75	1.11	0.76
	SPLEN1000113	1.33	2.27	3.04	2.72	4.13	3.04
	SPLEN1000114	2.97	4.19	6.03	3.59	4.76	6.32
	SPLEN1000132	0.85	4	1.72	2.25	2.67	1.99
	SPLEN1000135	3.13	8.76	14.93	11.12	15.28	10.52
	SPLEN1000136	12.41	21.47	15.14	20.24	27.48	21.8
	SPLEN1000141	2.26	7.07	10.79	4.03	5.41	4.51

EP 1 130 094 A2

5	SPLEN1000164	2.49	3.79	8.58	3.98	5.88	7.61
	SPLEN1000166	0.4	2.9	2.96	1.67	1.19	1.68
	SPLEN1000175	2.16	4.48	6.1	5.65	4.12	4.15
	SPLEN1000182	0.98	2.66	0.23	0.83	0.6	0.67
	SPLEN1000185	3.41	8.49	8.54	11.38	10.43	11.95
10	THYMU1000004	10.22	14.07	20.43	22.34	22.76	23.6
	THYMU1000009	9.48	10.13	14.9	13.48	23.86	22.1
	THYMU1000015	8.87	10.42	16.18	19.25	22.21	20.8 *
	THYMU1000016	6.24	5.96	13.03	10.3	8.45	9.38
	THYMU1000023	0.77	1.86	3.6	5.22	3.68	3.6
15	THYMU1000034	0.16	1.77	1.8	0.79	0.88	0.14
	THYMU1000035	0.62	2.8	0.97	1.17	0.95	1.31
	THYMU1000037	1.53	4.15	2.11	2.06	2.81	1.45
	THYMU1000042	5.97	10.24	12.23	12.03	13.98	13.28
	THYMU1000047	2.72	6.03	6.72	6.04	7.77	7.23
	THYMU1000080	0.56	4.31	2.6	3.26	1.85	2.11
20	THYMU1000094	2.77	3.47	7.91	9.17	8.35	4.55
	THYMU1000109	17.28	14.34	111.37	98.05	142.29	93.04
	THYMU1000127	2.75	5.95	10.76	8.18	9.98	6.74
	THYMU1000130	2.5	4.4	4.55	6.69	6.07	4.94
	THYMU1000137	3.53	7.18	10.26	12.67	18.55	13.05 *
25	THYMU1000146	4.37	8.38	6.52	8.29	7.46	7.74
	THYMU1000159	5.43	9.51	16.37	12.4	15.15	13.27
	THYMU1000163	5.85	12.26	37.58	45.53	58.37	36.93
	THYMU1000167	2.39	3.02	4.73	4.89	6.79	3.97
	THYMU1000186	0.69	1.05	1.45	1.31	2.45	0.66
30	THYRO1000017	0.94	3.45	2.54	2.02	3.54	2.11
	THYRO1000026	1.56	5.63	4.02	3.96	4.82	3.36
	THYRO1000034	0.49	4.16	1.59	1.99	2	1.82
	THYRO1000035	0.86	4.84	1.34	2.29	2.48	2.11
	THYRO1000036	0.93	8.32	4	3.08	4.36	5.59
35	THYRO1000040	2.58	7.02	4.76	4.66	4.83	4.93
	THYRO1000061	2.01	1.91	3.07	3.53	3.8	2.61
	THYRO1000067	1.98	2.8	5.12	3.37	4.14	3.3
	THYRO1000070	1.26	2.09	3.59	2.65	3.85	3.45
	THYRO1000072	1.33	3.37	4.22	2.54	4.08	2.06
40	THYRO1000084	8.07	12.69	22.39	2.99	5.61	4.42
	THYRO1000085	1.44	5.66	3.99	2.42	3.86	2.85
	THYRO1000086	-0.05	5.46	1.74	0.89	1.18	1.15
	THYRO1000087	0.72	3.86	1.01	0	0.58	0.17
45	THYRO1000092	2.32	5.1	4.66	3.75	4.43	4.5
	THYRO1000093	0.35	3.24	0.83	1.54	1.27	0.95
	THYRO1000099	0.45	2.53	2.73	2.8	1.67	2.39
	THYRO1000107	0.5	2.95	2.7	2.86	3.22	2
	THYRO1000111	0.85	4.58	1.78	1.4	2.06	2.36
50	THYRO1000121	1.33	5.72	2.52	1.94	2.4	2.95
	THYRO1000124	0.27	5.55	0.64	0.86	0.89	0.64
	THYRO1000129	0.36	2.1	0.11	0.94	1.11	0.92
	THYRO1000130	1.82	3.11	3.13	3.85	3.01	2.39
	THYRO1000132	2.4	3.62	9.43	11.14	6.99	6.26
55	THYRO1000134	1.5	4.07	3.22	4.06	3.65	3.73
	THYRO1000144	1.72	4.78	3.15	7.87	7.09	2.33

EP 1 130 094 A2

	THYRO1000155	1.6	4.1	1.45	1.77	1.9	2.23		
5	THYRO1000156	1.13	6.53	3.62	2.45	4.29	2.58		
	THYRO1000163	3.62	8.42	5.28	4.76	6.63	2.24		
	THYRO1000173	1.19	4.45	2.26	3.33	1.36	2.75		
	THYRO1000186	1.98	3.24	7.86	6.91	6.84	6.35		
10	THYRO1000187	2.7	3.58	5.3	4.92	6.24	5.22		
	THYRO1000190	1.12	3.32	2.94	3.73	4.55	2.71		
	THYRO1000196	0.3	5.28	0.81	0.66	1.21	0.52		
	THYRO1000197	2.05	7.28	4.69	4.08	6.24	3.89		
	THYRO1000199	0.76	6.28	4.13	1.93	2.08	1.98		
15	THYRO1000206	8.47	6.92	9.25	8.44	11.6	7.5		
	THYRO1000221	1.9	3.17	4.42	4.02	5.87	4.54		
	THYRO1000222	3.65	4.26	4.23	4.68	4.96	4.93	*	+
	THYRO1000228	0.81	3.67	2.85	2.24	3.04	2.94		
	THYRO1000241	1.76	3.7	6.29	4.62	5.54	4.01		
	THYRO1000242	0.63	4.16	4.46	2.49	2.56	2.62		
20	THYRO1000246	1.61	5.5	3.9	3.43	4.7	3.91		
	THYRO1000253	1.07	4.05	1.73	1.99	3.35	2.31		
	THYRO1000270	1.15	5.12	1.39	1.22	2.5	1.26		
	THYRO1000279	0.42	2.84	0.25	0.65	1.01	0.58		
	THYRO1000285	2.75	4.65	7.31	7.03	7.75	4.88		
25	THYRO1000288	7.76	7.59	11.77	5.68	5.07	7.22		
	THYRO1000296	4.18	6.04	6.22	7.4	11.24	8.96	*	+
	THYRO1000320	1.54	5.83	4.97	3.65	4.45	3.34		
	THYRO1000322	1.1	5.48	2.48	1.76	3.93	1.76		
	THYRO1000327	1.75	7.69	4.77	6.21	5.23	4.41		
30	THYRO1000343	2.5	6.12	5.35	5.06	5.04	6.13		
	THYRO1000345	1.36	7.34	11.92	7.82	5.84	9.49		
	THYRO1000358	1.82	3.39	3.08	1.92	2.32	1.54		
	THYRO1000368	0.76	2.39	2.73	1.43	2.82	0.58		
	THYRO1000375	3.2	7.03	4.79	7.38	6.09	9.77		
35	THYRO1000381	0.92	2.88	2.19	3.87	3.11	2.74		
	THYRO1000387	0.98	6.66	3.22	2.53	3.56	2.51		
	THYRO1000394	1.31	9.88	4.59	4.29	5.19	2.61		
	THYRO1000395	0.8	10.44	2.26	1.97	2.07	2.02		
	THYRO1000400	0.57	8.1	2.82	2.35	2.96	2.52		
40	THYRO1000401	0.86	1.94	2.5	1.87	1.16	1.57		
	THYRO1000407	1.97	2.3	1.36	1.37	1.58	0.55		
	THYRO1000420	1.8	2.67	4.46	3.52	3.53	3.39		
	THYRO1000438	1.78	4.37	3.26	2.94	3.33	3.15		
	THYRO1000452	2.62	7.99	6.45	3.71	5.75	4.38		
45	THYRO1000455	0.32	6.67	2.31	0.25	0.97	0.87		
	THYRO1000471	0.99	8.03	2.05	1.11	2.08	1.02		
	THYRO1000481	1.33	6.23	4.68	3.79	3.45	4.55		
	THYRO1000484	1.2	1.42	2.41	2.35	3	2.21		
	THYRO1000488	1.18	2.64	2.44	1.49	2.02	1.7		
50	THYRO1000501	1.12	4.01	2.78	3	1.92	1.82		
	THYRO1000502	0.34	3.7	1.69	1.79	1.44	1.2		
	THYRO1000505	0.13	4.64	1.19	1.14	1.02	0.6		
	THYRO1000535	11.1	20.54	39.24	54.13	69.59	62.96	*	+
	THYRO1000556	1.89	6.36	4.13	3.77	5.17	3.69		
55	THYRO1000558	0.25	2.82	1.12	1.16	0.81	0.61		

EP 1 130 094 A2

	THYRO1000569	2.88	4.12	6.05	5.78	4.46	4.88
5	THYRO1000570	2.31	3.28	8.46	8.53	6.04	3.49
	THYRO1000572	0.43	2.04	1.11	0.17	0.97	-0.42
	THYRO1000573	0.69	4.02	1.73	2.02	2.2	1.78
	THYRO1000577	1.06	5	1.34	0.96	1.22	0.71
	THYRO1000580	0.79	3.72	3.01	2.82	2.2	1.79
10	THYRO1000584	2.18	6.88	8.8	7.57	6.61	7.58
	THYRO1000585	4.83	9.37	9.83	5.76	6.27	9.52
	THYRO1000596	0.22	0.93	1.19	0.44	1.36	0.21
	THYRO1000602	2.08	2.95	4.01	4.05	4.65	4.97
	THYRO1000605	0.37	3.01	0.98	2.13	2.14	1.56
15	THYRO1000615	1.02	3.62	1.24	1.55	1.36	1.29
	THYRO1000625	0.71	5.48	2.28	2.46	2.9	1.78
	THYRO1000636	3.67	5.65	6.9	6.53	7.84	6.67
	THYRO1000637	0.91	3.96	1.71	1.18	2.03	1.54
	THYRO1000641	0.38	4.19	2.49	1.36	1.67	1.64
20	THYRO1000657	2.99	3.69	5.42	7.67	12.28	3.86
	THYRO1000658	2.68	3.62	5.39	5.4	5.55	6.09
	THYRO1000662	1.1	3.19	2.09	2.42	2.69	1.66
	THYRO1000666	0.57	3.19	2.28	1.63	1.48	1.43
	THYRO1000676	1.37	4.53	2.01	1.75	1.83	1.56
25	THYRO1000678	0.52	5.86	0.99	1.29	1.4	0.53
	THYRO1000684	0.95	4.98	2.94	1.92	2.65	1.47
	THYRO1000694	2.08	6.64	4.65	2.8	2.48	3.59
	THYRO1000699	2.98	2.14	5.55	4.86	7.08	7.12
	THYRO1000712	1.88	4.25	5.9	6.25	6.75	7.78
30	THYRO1000715	5.74	5.67	27.37	21.74	28.63	16.99
	THYRO1000716	0.92	3.26	3.2	1.88	1.78	1.35
	THYRO1000717	1.58	5	4.36	2.98	4.63	1.91
	THYRO1000723	0.6	4.54	1.6	0.55	1.06	0.85
	THYRO1000734	-0.01	4.81	1.89	1.49	1.73	1.07
35	THYRO1000748	0.98	5.51	5.23	2.35	3.85	3.18
	THYRO1000755	1.74	3.26	4.32	4.33	3.47	4.38
	THYRO1000756	2.79	4.24	3.24	3.46	4.2	3.41
	THYRO1000776	0.48	2.17	3.02	3.36	3.99	3.34
	THYRO1000777	1.81	3.39	4.54	4.99	2.05	2.37
40	THYRO1000779	1.45	3.55	0.88	0.18	1.01	-0.26
	THYRO1000782	3.92	10.13	12.52	10.76	15.05	14.05
	THYRO1000783	0.12	5.51	1.2	1.11	1.41	0.92
	THYRO1000786	6.65	9.54	19.71	15.74	7.92	13.7
	THYRO1000787	0.23	1.88	1.67	1.31	1.54	0.78
45	THYRO1000792	1.51	3.13	2.29	3.09	3.13	2.11
	THYRO1000793	0.11	3.13	0.84	1.51	1.86	1.16
	THYRO1000795	1.23	6.03	3.54	2.76	3.1	3.05
	THYRO1000796	0.6	7.73	2.44	2.26	2.95	1.66
	THYRO1000798	1.89	5.82	2.51	2.59	3.57	3.53
50	THYRO1000800	9.26	17.2	24.74	17.74	20.68	21.06
	THYRO1000805	0.49	3.04	1.08	0.72	2.66	1.38
	THYRO1000815	2.54	3.49	9.48	7.61	5.47	7.87
	THYRO1000829	5.55	7.83	10.57	3.78	8.32	10.01
	THYRO1000835	0.96	3.2	1.93	1.07	2.36	1.8
55	THYRO1000843	1.09	11.48	3.56	3.69	4.41	3.62

EP 1 130 094 A2

	THYRO1000846	0.76	5.71	1.32	2.67	1.62	1.26		
5	THYRO1000852	1.59	6.02	5.63	2.8	4.7	3.32		
	THYRO1000855	3.14	5.02	6.63	9.03	15.1	10.07	*	+
	THYRO1000865	1.86	4.3	11.97	10.01	11.47	8.95		
	THYRO1000866	7.47	6.29	12.66	4.49	7.87	6.01		
10	THYRO1000881	5.62	7.3	10.93	15.65	26.64	29.58	*	+
	THYRO1000894	0.33	3.95	1.36	1.75	1.48	1		
	THYRO1000895	0.58	4.43	1.42	1.62	1.46	0.82		
15	THYRO1000916	1.22	5.49	3.43	2.43	3.13	2.29		
	THYRO1000917	16.19	25.26	34.11	30.37	37.42	35.89		
	THYRO1000926	0.78	3.13	1.27	1.76	1.57	0.82		
	THYRO1000934	0.08	3.1	1.34	0.43	1.38	1.46		
20	THYRO1000951	0.52	2.46	1.26	2.33	2.11	1.9		
	THYRO1000952	2.25	3.81	6.01	2.38	2.53	2.24		
	THYRO1000956	0.06	2.55	1.81	1.16	1.5	0.87		
	THYRO1000960	0.5	6.72	2.89	1.85	2.79	1.48		
25	THYRO1000961	1.67	7.77	3.56	4.73	5.26	4.64		
	THYRO1000964	0.42	11.59	0.76	1	1.27	1.06		
	THYRO1000971	1.82	9.9	3.56	3.29	3.33	2.19		
	THYRO1000974	2.87	8.83	7.53	9.87	11.79	8.71		
	THYRO1000975	1.5	2.19	3.8	4.02	3.68	3.68		
	THYRO1000983	6.42	8.31	11.63	12.67	8.49	7.12		
30	THYRO1000984	2.4	2.83	3.03	3.29	2.98	3.26		
	THYRO1000988	1.36	4.14	3.23	3.48	3.68	2.67		
	THYRO1000991	1.22	4.71	2.05	1.76	2.22	3.2		
	THYRO1000999	0.87	9.64	3.26	1.96	3.14	2.26		
35	THYRO1001003	2.97	8.43	4.42	3.1	4.52	3.56		
	THYRO1001015	0.6	6.29	2.04	2.22	1.79	1.66		
	THYRO1001016	1.73	2.26	3.34	2.06	1.85	1.24		
	THYRO1001022	0.9	1.86	0.86	1.68	1.25	1.41		
	THYRO1001031	4.65	3.97	4.55	5.03	7.03	6.16		
40	THYRO1001033	1.18	3.34	2.46	2.86	3.45	2.02		
	THYRO1001062	1.21	5.4	4.14	2.9	4.31	2.62		
	THYRO1001063	0.5	8.74	2.38	2.37	2.09	2.84		
	THYRO1001071	0.12	7.45	0.88	1.33	0.68	0.76		
	THYRO1001080	2.56	6.75	5.11	4.96	4.31	4.78		
45	THYRO1001093	0.77	1.63	3.24	5.11	1.74	1.5		
	THYRO1001100	0.52	1.89	2.05	1.89	1.21	0.78		
	THYRO1001102	2.61	3.6	5.7	4.4	4.95	6.93		
	THYRO1001104	3.67	6.54	6.55	8.77	8.01	11.18		
	THYRO1001109	1.81	6.02	2.68	3.06	2.58	1.99		
50	THYRO1001113	11.41	17.42	32	21.81	26.65	18.72		
	THYRO1001120	1.65	6.22	5.27	4.78	5.8	3.72		
	THYRO1001121	1.57	4.28	4.19	3.92	2.72	3		
	THYRO1001128	1.64	2.77	5.86	3.52	3.19	5.09		
	THYRO1001133	1.14	3.02	7.23	6.54	4.54	4.12		
55	THYRO1001134	2.97	4.78	1.63	3.14	2.83	1.38		
	THYRO1001142	0.3	2.69	0.63	1.3	1.71	0.22		
	THYRO1001173	8.37	12.87	7.72	11.14	9.92	10.62		
	THYRO1001175	3.26	6.63	5.51	3.46	4.62	3.52		
	THYRO1001177	1.36	5.85	5.93	4.66	7.27	7.97		
	THYRO1001189	2.74	6.93	11.42	7.84	7.27	9.94		

EP 1 130 094 A2

	THYRO1001194	1.05	2.62	4.96	4.89	4.57	2.31		
5	THYRO1001204	2.17	3.58	4.27	4.03	4.74	4		
	THYRO1001205	5.76	10.65	20.23	18.54	19.57	20.9		
	THYRO1001213	1.21	4.69	4.44	3.12	3.21	2.33		
	THYRO1001224	3.59	8.25	6.37	9.92	12.69	10.55	*	+
10	THYRO1001237	2.82	6.25	4.99	3.61	4.53	4.46		
	THYRO1001242	9.74	11.65	19.04	20.02	19.98	20.46		
	THYRO1001258	2.08	5.45	3.58	3.33	2.05	2.66		
15	THYRO1001262	0.86	2.64	3.38	2.36	3.61	2.69		
	THYRO1001266	0.15	2.39	1.02	0.97	1.64	0.66		
	THYRO1001271	1.85	4.12	4.12	2.46	2.77	2.97		
	THYRO1001287	7.3	8.3	39.26	30.14	43.68	26.2		
20	THYRO1001290	0.38	3.25	1.14	1.15	1.35	0.36		
	THYRO1001291	0.96	7.17	4.38	4.31	4.97	3.5		
	THYRO1001297	3.05	8.04	6.14	6.85	7.47	9.18		
	THYRO1001302	1.72	5.59	5.17	3.8	3.71	3.5		
25	THYRO1001313	1.61	2.33	2.91	2.91	2.62	1.48		
	THYRO1001320	1.76	2.52	5.31	5.07	5.74	4.83		
	THYRO1001321	2.25	2.65	4.3	2.48	4.23	4.23		
	THYRO1001322	1.34	3.93	3.34	1.75	2.67	2.01		
	THYRO1001327	1.29	6.01	4.18	1.4	3.89	2.49		
30	THYRO1001336	1.89	6.84	6.72	4.62	4.43	4.18		
	THYRO1001347	0.43	4.12	3.35	1.85	2.81	0.65		
	THYRO1001358	2.57	5.74	4.52	4.3	5.75	5.1		
	THYRO1001363	0.8	2.15	1.52	2.09	2.24	2.28		
	THYRO1001365	0.86	3	1.6	2.19	2.6	1.96		
35	THYRO1001374	1.85	4.45	12.86	9.4	13.01	6.21		
	THYRO1001401	1.76	5.33	4.89	5.39	7.86	6.29		
	THYRO1001403	1.26	5.15	3.22	3.22	4.42	3.94		
	THYRO1001405	6.99	12.5	10.86	6.69	8.56	10.63		
	THYRO1001406	15.73	14.87	27.69	21.36	22.77	21.36		
40	THYRO1001411	4.49	5.46	10.08	8.93	12.44	8.12		
	THYRO1001420	11.55	15.25	47.52	42.01	44.49	49.87		
	THYRO1001426	3.42	5.56	8.83	9.32	12.77	11.18		
	THYRO1001430	6.97	6.54	10.84	11.13	11.7	13.81		
45	THYRO1001434	0.68	5.19	2.11	2.08	4.23	1.73		
	THYRO1001456	1.74	6.05	2.63	2.89	2.66	2.4		
	THYRO1001457	1.71	4.72	2.04	2.95	4.7	2.67		
	THYRO1001458	0.95	5.44	6.11	6.13	9.17	7.23		
	THYRO1001459	4.54	5.07	9.42	7.18	9.87	14.21		
50	THYRO1001471	0.91	2.07	1.93	2.36	2.91	1.64		
	THYRO1001478	0.58	3.09	1.34	0.95	2.61	2.75		
	THYRO1001480	5.4	10.53	13.62	14.79	15.94	15.57		
	THYRO1001481	2.95	8.64	7.24	4.91	7.76	7.13		
	THYRO1001487	1.36	5.51	3.52	4.1	2.67	3.48		
	THYRO1001495	2.06	5.57	5.43	5.06	9.4	7.55		
55	THYRO1001498	5.39	8.08	13.42	11.59	16.38	19.6		
	THYRO1001510	1.67	2.88	1.59	1.65	2.57	3.35		
	THYRO1001512	26.7	26.97	110.28	56.03	90.95	68.54		
	THYRO1001519	5.92	7.77	11.05	8.91	5.75	10.38		
	THYRO1001522	2.02	4.7	5.79	4.15	4.69	5.51		
	THYRO1001523	1.83	4.92	3.73	4.38	4.07	4.26		

EP 1 130 094 A2

	THYRO1001526	26.21	28.22	44.73	34.28	47.64	46.52
5	THYRO1001529	1.64	5.27	2.8	2.32	2.42	2.98
	THYRO1001534	1.41	4.01	4.96	5.1	5.9	4.54
	THYRO1001537	7.4	5.17	12.33	5.97	7.42	7.23
	THYRO1001541	2.14	3.88	8.27	7.76	8.7	6.73
10	THYRO1001545	1.26	3.84	2.9	4.95	3.57	3.16
	THYRO1001559	4.52	6.34	8.04	9.06	10.5	10.54 * +
	THYRO1001563	9.49	14.06	15.89	10	15.49	22.09
	THYRO1001570	2.01	8.2	3.85	4.25	5.17	3.41
	THYRO1001573	1.15	5.77	2.22	1.47	2.87	2.67
15	THYRO1001584	2.47	8.54	8.38	5.14	7.81	7.29
	THYRO1001593	4.27	5.67	11.17	9.5	10.93	9.52
	THYRO1001595	3.14	4.53	7.06	5.97	6.35	7.29
	THYRO1001596	4.71	5.48	7.44	6.45	5.86	2.51
	THYRO1001602	1.49	3.26	3.52	4.95	5.22	3.41
20	THYRO1001605	1.58	4.48	3.22	3.2	3.43	2.42
	THYRO1001608	1.87	9.45	5.1	5.04	8.23	4.7
	THYRO1001617	6.06	13.68	11.47	9.75	10.87	9.61
	THYRO1001634	1.87	9.08	3.46	2.93	5.59	2.05
	THYRO1001637	3.51	3.13	9.65	8.72	7.94	9.07
	THYRO1001641	2.57	3.73	5.09	4.03	3.08	2.94
25	THYRO1001656	1.59	2.94	4.16	2.82	5.36	2.33
	THYRO1001658	22.34	29.19	40.11	34.98	33.16	42.01
	THYRO1001661	1.4	5.83	2.31	2.93	3.31	2.05
	THYRO1001671	0.67	7.36	2.68	1.89	1.34	1.8
	THYRO1001672	1.1	9.24	2.1	1.14	1.52	1.66
30	THYRO1001673	1.59	7.6	3.49	2.86	4.74	2.16
	THYRO1001677	1.6	2.27	3.87	3.03	3.54	3.36
	THYRO1001683	12.71	17.66	29.06	24.4	15.4	16.72
	THYRO1001700	1.39	2.52	2.67	2.09	1.58	1.37
	THYRO1001702	11.83	15.98	16.19	15.63	14.35	14.29
35	THYRO1001703	1.63	6.74	4.25	4.72	3.27	4.21
	THYRO1001706	1.7	6.47	3.01	2.96	5.6	3.53
	THYRO1001721	1.84	5.66	3.2	2.73	6.37	2.77
	THYRO1001725	5.3	6.55	9.69	8.97	8.65	8.29
40	THYRO1001730	17.72	20.4	40.1	30.61	26.56	34.8
	THYRO1001738	1.35	3.18	4.65	3.52	2.82	1.78
	THYRO1001743	0.19	2.13	1.85	1.8	1.64	1.06
	THYRO1001745	0.47	2.88	1.55	1.05	1.2	1.27
	THYRO1001746	1.9	6.25	4.04	6.12	4.01	3.88
45	THYRO1001770	15.49	20.38	35.39	41.65	44.42	40.17 * +
	THYRO1001772	1.12	4.88	3.64	4.78	4.24	3.06
	THYRO1001778	3.89	6.68	9.89	14.67	13.47	14.25 * +
	THYRO1001793	3.85	3.77	9.43	10.3	10.42	4.92
	THYRO1001796	1.35	2.28	2.28	3.45	4.22	3.24 * +
50	THYRO1001800	1.82	2.99	2.75	4.17	5.12	2.09
	THYRO1001803	3.42	6.03	5.21	4.31	4.14	3.42
	THYRO1001809	1.6	4.26	3.4	5.9	4.23	3.39
	THYRO1001817	8.69	18.33	24.88	22.11	22.77	25.27
	THYRO1001819	4.68	8.46	9.01	7.84	10.46	6.77
55	THYRO1001828	21.89	24.53	104.32	106.68	121.95	68.55
	THYRO1001854	6.67	6.12	12.45	13.43	15.86	13.31

EP 1 130 094 A2

	THYRO1001895	0.85	1.31	2.52	3.54	4.31	1.28		
5	THYRO1001907	2.16	3.08	3.37	3.9	4.53	2.74		
	TRACH1000006	2.51	5.87	6.63	4.34	3.46	3.22		
	TRACH1000013	1.53	4.65	3.68	2.55	3.33	2.65		
	TRACH1000074	2.65	6.75	6.09	7.5	7.26	4.77		
	TRACH1000095	0.28	5.66	2.23	2.46	1.48	1.11		
10	TRACH1000102	2.42	6.66	4.09	5.79	5.04	3.65		
	TRACH1000108	1.1	1.01	2.05	1.75	2.49	1.09		
	TRACH1000126	0.96	1.75	2.71	1.82	3.79	2.54		
	TRACH1000146	1.3	2.67	2.31	3.02	5.18	3.75		
	TRACH1000160	0.61	4.06	1.5	1.47	1.76	0.72		
	TRACH1000184	4.45	7.16	10.16	7.47	8.73	5.69		
15	VESEN1000004	0.69	5.55	3.19	2.56	2.95	2.02		
	VESEN1000007	0.93	5.32	2.94	2.38	3.45	2.94		
	VESEN1000013	5.96	10.11	16.78	10.76	11.25	13.88		
	VESEN1000028	5.2	7.5	9.88	13.18	11.71	14.08	*	+
	VESEN1000059	1.55	2.88	2.1	3.38	2.82	2.27		
20	VESEN1000100	1.96	3.22	3.35	3.49	4.58	3.59		
	VESEN1000107	0.88	4.84	2.88	3.12	2.9	2.48		
	VESEN1000117	1.63	6.43	2.46	2.16	2.7	1.79		
	VESEN1000122	1.52	5.34	1.24	4.79	4.51	4.5		
	VESEN1000137	0.76	5.47	1.92	1.75	3.33	1.65		
25	VESEN1000195	7.79	7.93	11.67	8.42	7.51	10.27		
	VESEN1000215	1.48	3.03	2.06	2.67	3.84	1.87		
	VESEN1000279	8.71	11.32	18.49	22.93	23.38	34.68	*	+
	VESEN1000363	3.52	6.07	9.99	7.2	9.06	4.59		
30	VESEN1000388	2.55	6.48	3.31	4.17	3.75	6.7		
	VESEN1000394	0.44	7.11	2.33	2.37	2.55	2.36		
	VESEN1000410	1.11	5	1.78	2.36	2.71	3.69		
	VESEN1000411	2.37	4.95	5.08	6.76	7.55	9	*	+
	VESEN1000415	1.54	2.64	4.03	5.57	3.92	5.29		
35	VESEN1000440	7	5.53	7.81	3.79	9.4	12.22		
	VESEN1000452	1.22	3.65	2.33	2.91	3.97	4.11		
	VESEN1000539	191.54	185.28	334.6	389.84	403.89	547.31	*	+
	VESEN1000554	0.67	6.47	1.43	1.47	2.55	1.58		
	VESEN1000557	4.22	7.94	7.73	6.55	9.07	10		
40	VESEN1000575	7.49	9.75	16.33	11.95	11.73	14.8		
	VESEN1000585	1.69	4.49	3.37	2.53	2.93	3.08		
	VESEN1000592	1.58	2.31	1.58	2.02	1.83	1.46		
	VESEN1000658	1.96	3.56	4.45	5.86	3.91	4.91		
	VESEN1000669	8.43	10.02	16.35	15.06	14.17	15.51		
45	VESEN1000743	0.97	3.3	2.52	1.99	3.37	3.21		
	VESEN1000752	37.43	51.51	72.35	49.32	57.03	57.96		
	VESEN1000761	13.48	18.17	19.37	24.6	33.21	31.28	*	+
	VESEN2000039	10.45	15.98	15.56	13.56	18.3	20.1		
50	VESEN2000102	0.4	3.99	1.6	1.21	1.51	1.61		
	VESEN2000164	2.45	3.52	4.8	5.55	4.36	3.66		
	VESEN2000175	0.57	2.64	1.94	3.03	2.05	2.59		
	VESEN2000186	3.77	5.53	6.53	6.68	3.87	2.47		
	VESEN2000199	8.94	13.26	21.75	19.58	24.45	24.12		
55	VESEN2000200	0.5	4.97	2.78	3.03	3.1	1.6		
	VESEN2000204	0.48	12.7	1.02	0.98	1.2	0.33		

EP 1 130 094 A2

	VESEN2000218	6.66	20.26	19.48	21.37	20.75	18.86		
5	VESEN2000230	0.84	7.4	1.45	2.74	1.7	2.41		
	VESEN2000272	2.29	4	8.92	7	8.31	5.88		
	VESEN2000299	1.99	2.97	3.2	3.3	3.77	3.31		
	VESEN2000323	4.51	8.12	8.37	8.91	9.5	9.36		
10	VESEN2000327	3.16	5.8	4.42	3.62	7.66	5.07		
	VESEN2000328	5.44	8.02	11.88	8.73	15.35	14.36		
	VESEN2000330	6.39	15.42	14.7	14.59	27.73	18.86		
	VESEN2000336	0.82	8.97	2.54	3.46	3.83	2.88		
15	VESEN2000354	1.56	8.24	2.48	1.53	2.71	2.1		
	VESEN2000378	7.17	8.87	14.57	13.23	11.14	10.3		
	VESEN2000379	19.87	23.02	44.55	49.13	42.81	32.61		
20	VESEN2000397	0.72	2.38	1.24	1.36	2.06	1.54		
	VESEN2000416	2.83	3.88	4.41	5.74	5.31	5.71	*	+
	VESEN2000420	1.08	3.58	1.94	0.95	1.21	1.13		
	VESEN2000430	0.51	6.68	1.53	2.06	1.79	1.8		
25	VESEN2000448	0.51	6.87	1.73	2.12	2.69	1.5		
	VESEN2000449	2.43	8.07	6.59	8.3	11.31	8.21		
	VESEN2000456	0.74	0.87	2.11	1.54	1.22	0.87		
	VESEN2000562	4.07	3.42	17.42	13.67	22.82	14.47		
	VESEN2000573	0.18	1.75	1.75	1.04	1.21	1.13		
30	VESEN2000604	1.73	3.44	2.24	2.04	1.67	2.15		
	VESEN2000614	4.16	9.02	14.64	13.54	16.27	12.27		
	VESEN2000638	0.48	5.92	1.98	1.33	1.91	1.68		
	VESEN2000641	0.83	3.69	1.34	1.95	2.21	1.43		
	VESEN2000645	2.18	5.29	5.38	5.91	5.73	5.5		
35	Y79AA1000013	2.57	2.7	4.33	3.45	3.8	3.94		
	Y79AA1000030	1.79	4.06	4.52	3.24	3.85	2.47		
	Y79AA1000033	2.87	6	8.4	8.37	10.17	5.83		
	Y79AA1000037	1.38	3.36	5.71	4.84	6.82	4.49		
	Y79AA1000041	1.05	5.16	3.79	4.73	3.65	2.06		
40	Y79AA1000059	1.69	5	4.09	3.88	4.51	2.82		
	Y79AA1000065	24.06	28.99	52.25	82.48	101.48	98.73	**	+
	Y79AA1000081	39.47	49.78	73.62	113.19	114.49	98.22	**	+
	Y79AA1000127	4.08	4.21	5.8	8.42	10.03	7.39	*	+
	Y79AA1000130	2.24	2.48	5.76	6.61	8.1	8.03	*	+
45	Y79AA1000131	507.64	569.21	946.04	769.75	725.35	342.07		
	Y79AA1000134	1.99	4.93	4.21	5.63	4.75	5.38		
	Y79AA1000143	3.58	8.79	4.83	9.98	10.98	11.04	*	+
	Y79AA1000144	4.63	10.79	10.59	11.02	11.62	11		
	Y79AA1000150	18.39	22.18	84.69	93.5	117.62	78.89		
50	Y79AA1000153	183.67	191.4	436.64	423.46	442.52	386.45		
	Y79AA1000166	2.13	2.25	4.15	3.52	4.97	3.6		
	Y79AA1000179	2.58	3.76	4.2	6.85	7.58	3.89		
	Y79AA1000181	1.96	3.92	4.2	4.82	5.66	3.79		
55	Y79AA1000202	22.93	24.47	55.57	91.68	86.86	83.22	**	+
	Y79AA1000207	5.22	7.51	9.82	14.95	16.24	12.62	*	+
	Y79AA1000214	14.94	22.18	33.76	50.43	60.78	41.96	*	+
	Y79AA1000222	11.8	14.89	21.69	49.21	58.01	68.86	**	+
	Y79AA1000226	11.04	14.94	34.41	22.86	33.54	30.03		
	Y79AA1000227	5.95	4.52	7.25	8.98	9.51	9.62	*	+
	Y79AA1000230	1.09	1.49	2.02	2.07	2.88	2.59		

EP 1 130 094 A2

	Y79AA1000231	5.99	9.04	15.81	14.63	23.77	17.1		
5	Y79AA1000239	15.47	20.55	25.65	18.95	24.01	22.11		
	Y79AA1000258	2.64	5.17	6.72	5.87	4.95	5.84		
	Y79AA1000268	2.65	5.48	5.09	4.33	5.76	4.01		
	Y79AA1000269	4.32	7.88	7.86	8	6.86	8.24		
	Y79AA1000270	5.28	8.35	11.58	13.17	17.58	16.23	*	+
10	Y79AA1000280	1.74	4.17	4.9	5.29	3.1	5.27		
	Y79AA1000285	3.44	4.21	5.91	4.01	6.86	5.22		
	Y79AA1000295	0.75	3.06	4.85	4.32	4.23	4.45		
	Y79AA1000307	2.88	3.91	5.06	9.35	7.58	11.25	*	+
	Y79AA1000313	3.11	9.02	9.85	10.61	12.84	13.36		
15	Y79AA1000314	4.23	10.74	9.19	6.93	6.53	7.51		
	Y79AA1000328	4.65	10.05	2.64	7.73	9.28	8.68		
	Y79AA1000334	1.43	4.22	3.55	2.68	2.81	3.46		
	Y79AA1000342	10.65	10.05	26.47	23.7	19.13	28.35		
	Y79AA1000346	7.61	8.17	7.9	20.1	22.06	20.18	**	+
20	Y79AA1000347	6.94	7.96	12.42	18.78	16.47	18.48	**	+
	Y79AA1000349	6.93	9.63	12.67	12.31	11.96	14.75		
	Y79AA1000355	3.17	8.28	8.94	8.84	13.55	8.77		
	Y79AA1000368	5.24	8.39	24.43	22.48	35.67	22.55		
	Y79AA1000388	22.9	32.66	62.37	94.17	128.35	109.08	**	+
25	Y79AA1000392	3.02	6.81	3.76	3.42	2.73	3.78		
	Y79AA1000405	3.98	5.97	8.25	7.14	8.17	9.32		
	Y79AA1000410	6.01	7.87	15.72	13.79	17.05	14.95		
	Y79AA1000420	1.54	4.78	3.13	3.32	3.95	5.1		
	Y79AA1000423	1.38	7.08	5.59	5.22	6.04	10.27		
30	Y79AA1000426	3.61	9.44	8.66	4.24	4.43	5.22		
	Y79AA1000432	0.8	4.79	2.16	1.91	2.01	2.34		
	Y79AA1000453	23.94	30.67	47.79	39.74	50.65	58.24		
	Y79AA1000465	4.12	6.02	6.65	4.77	4.14	7.69		
35	Y79AA1000469	11.59	9.61	18.04	13.82	16.21	17.18		
	Y79AA1000480	1.24	4.37	2.78	3.33	3.57	2.79		
	Y79AA1000502	5.31	7.97	12.58	10.49	11.35	15.26		
	Y79AA1000521	1.24	4.4	4.13	2.51	3.61	2.7		
	Y79AA1000534	3.22	8.13	8.92	11.97	14.41	13.46	*	+
40	Y79AA1000538	3.58	6.95	8.79	9.52	12.12	8.41		
	Y79AA1000539	12.76	14.96	53.11	42.61	68.56	50.97		
	Y79AA1000540	1.32	3.59	1.61	2.54	2.97	3.21		
	Y79AA1000560	160.46	140.99	339.33	380.8	313.21	220.43		
45	Y79AA1000574	1	2.92	1.65	1.98	2.04	1.59		
	Y79AA1000584	2.07	4.55	4.97	4.62	5.39	4.04		
	Y79AA1000589	10.74	13.67	81.43	59.09	95.35	68.5		
	Y79AA1000598	1.43	7.64	2.17	1.85	3.88	3.18		
	Y79AA1000600	2.7	10.02	7.93	13.64	15.64	12.84	*	+
50	Y79AA1000609	1.18	5.16	1.44	2.28	2.77	1.55		
	Y79AA1000618	1.85	10.59	5.76	7.4	9.5	9.37		
	Y79AA1000627	1.91	3.93	4.57	3.27	3.02	2.43		
	Y79AA1000636	5.16	5.7	9.9	15.57	11.52	5.38		
	Y79AA1000649	9.45	10.97	12.73	18.7	11.56	20.54		
	Y79AA1000656	15.32	20.21	96.75	80.17	115.97	82.61		
55	Y79AA1000673	1.02	5.86	2.14	1.39	3.13	2.4		
	Y79AA1000674	11.88	21.96	78.28	59.4	98.22	62.67		

EP 1 130 094 A2

	Y79AA1000678	2.48	8.91	3.88	3.01	4.15	2.45		
5	Y79AA1000682	17.99	53.99	93.7	102.53	110.87	118.22		
	Y79AA1000683	1.87	2.66	3.21	4.27	2.59	2.17		
	Y79AA1000697	21.76	27.52	43.01	21.93	24.76	27.31		
	Y79AA1000700	5.07	7.1	7.08	7.51	6.93	9.97		
10	Y79AA1000702	5.13	14.57	13.31	41.48	56.57	63.15	**	+
	Y79AA1000704	1.34	5.24	1.14	1.5	2.1	1.18		
	Y79AA1000705	1.86	9.7	6.24	6.06	7.98	6.45		
	Y79AA1000717	6.18	12.39	9.42	9.73	11.1	8.7		
	Y79AA1000722	5.61	8.6	8.65	26.26	34.81	34.31	**	+
15	Y79AA1000724	6.42	9.77	18.55	26.57	21.7	11.95		
	Y79AA1000726	0.77	1.24	0.83	1.46	2.01	0.71		
	Y79AA1000734	2.05	4.46	4.92	3.57	3.3	2.94		
	Y79AA1000748	0.88	4.38	1.77	2.14	2.99	1.56		
	Y79AA1000750	4.17	8.47	20.58	18.11	20.02	18.62		
	Y79AA1000752	1.25	5.13	2.33	2.23	3.38	3.38		
20	Y79AA1000774	2.11	6.23	4.24	4.28	5.79	4.21		
	Y79AA1000776	1.2	4.37	1.9	2.13	1.83	2.11		
	Y79AA1000777	4.36	5.84	9.63	10.05	6.99	6.01		
	Y79AA1000778	1.72	3.77	3.79	3.87	4.19	1.44		
	Y79AA1000782	2.08	4.18	3.72	3.53	2.89	2.96		
25	Y79AA1000784	7.04	10.01	7.78	13.87	15.58	14.26	**	+
	Y79AA1000794	0.61	5.21	1.88	2.92	1.69	1.23		
	Y79AA1000800	1.59	5.44	3.82	3.38	2.97	3.39		
	Y79AA1000802	0.64	4.18	1.15	2.52	1.77	2.1		
	Y79AA1000805	2.29	4.03	2.63	2.43	2.11	2.6		
30	Y79AA1000814	2.73	3.9	4.14	4.98	7.09	6.76	*	+
	Y79AA1000823	7.91	9.99	12.07	12.02	12.42	6.56		
	Y79AA1000824	0.98	2.47	1.84	2.75	2.26	0.79		
	Y79AA1000827	1.6	4.02	7.27	6.71	8.91	6.14		
	Y79AA1000831	7.04	10.49	17.32	26.61	30.43	27.82	**	+
35	Y79AA1000833	62.14	67.46	191.76	270.42	308.16	248.21	*	+
	Y79AA1000850	1.69	5.68	2.72	4.92	4.59	4.21		
	Y79AA1000856	3.49	6.78	6.31	9.28	6.01	8.51		
	Y79AA1000862	2.22	2.76	2.44	3.08	2.87	2.59		
	Y79AA1000876	7.46	10.04	17.91	27.36	27.61	25.46	**	+
40	Y79AA1000888	4.59	5.07	28.1	24.51	38.78	22.48		
	Y79AA1000902	4.65	5.74	8.44	12.18	12.32	7.68		
	Y79AA1000935	3.53	5.99	6.69	8.28	10.07	9.18	*	+
	Y79AA1000959	0.74	6.29	4.35	6.71	5.77	6.07		
45	Y79AA1000962	1.22	4.45	3.18	2.9	2.41	1.79		
	Y79AA1000963	18.6	26.86	35.93	31.61	42.17	49.13		
	Y79AA1000966	18.52	19.25	98.18	77.47	116.12	61.1		
	Y79AA1000967	8.62	8.82	33.82	34.47	40.36	29.3		
	Y79AA1000968	3.32	5.67	6.89	8.86	9.4	7.96	*	+
50	Y79AA1000969	0.91	3.18	3.04	2.66	2.91	1.41		
	Y79AA1000976	1.43	4.72	3.02	2.55	3.51	1.43		
	Y79AA1000978	1.99	5.6	7.26	6.9	10.54	5.56		
	Y79AA1000985	9.39	12.84	40.49	38.26	44.3	27.89		
	Y79AA1000989	21.59	22.49	46.19	51.84	58.65	55.19	*	+
55	Y79AA1000991	22.11	22.21	110.42	72.46	96.96	82.23		
	Y79AA1001013	59.2	62.64	140.9	174.85	214.13	201.9	*	+

EP 1 130 094 A2

	Y79AA1001014	2.27	4.16	4.1	4.8	5.2	6.55		
5	Y79AA1001019	3.37	5.89	7.74	9.24	9.02	9.43	*	+
	Y79AA1001020	5.37	7.82	9.43	12.31	11.11	10.86	*	+
	Y79AA1001023	0.83	6.11	2.29	1.22	1.95	1.54		
	Y79AA1001030	4.23	8.79	10.87	11.14	10.72	12.43		
	Y79AA1001035	0.19	2.88	0.03	14.44	8.19	17.16	*	+
10	Y79AA1001041	1.78	2.46	2.36	2.93	2.45	2.78		
	Y79AA1001043	11.65	12.62	15.22	8.64	12.01	14.71		
	Y79AA1001048	1.1	4.78	3.73	4.05	4.52	4.21		
	Y79AA1001056	4.56	7.82	11.04	8.27	7.11	9.94		
	Y79AA1001061	1.53	7.79	5.28	6.13	7.46	6.66		
15	Y79AA1001062	2.62	6.14	5.02	4.44	6.01	4.67		
	Y79AA1001068	3.46	6.39	7.29	6.61	8.69	7.05		
	Y79AA1001073	8.19	13.08	17.46	24.14	22.1	29.81	*	+
	Y79AA1001077	7.1	7.08	17.15	14.69	14.74	17.08		
	Y79AA1001078	3.11	8.34	11.07	5.01	12.15	12.92		
20	Y79AA1001081	3.59	5.61	4.94	9.62	9.98	10.5	**	+
	Y79AA1001088	27.75	38.61	69.33	93.1	88.97	113.04	*	+
	Y79AA1001089	4.64	7.8	11.92	22.67	22.6	27.73	**	+
	Y79AA1001090	1.38	4.15	2.2	3.58	2.83	2.35		
	Y79AA1001105	3.7	5.23	15.81	12.52	22.1	13.35		
	Y79AA1001142	8.53	13.38	15.85	14.28	11.42	22.32		
25	Y79AA1001145	2.22	4.68	5.13	4.97	6.26	5.87		
	Y79AA1001162	2.27	2.91	1.62	1.62	4.56	4		
	Y79AA1001167	0.86	2.76	2.38	1.12	2.35	0.77		
	Y79AA1001176	0.57	3.33	1.14	2.02	1.68	0.88		
	Y79AA1001177	1.21	5.5	2.22	2.35	3.01	1.99		
30	Y79AA1001179	6.81	8.66	16.73	22.82	22.64	20.07	*	+
	Y79AA1001185	1.33	5.3	4.55	3.65	4.49	5.8		
	Y79AA1001201	5.69	11.3	16.13	14.57	15.21	19.38		
	Y79AA1001205	1.87	3.28	2.85	5.87	4.85	4.09	*	+
	Y79AA1001211	1.64	4.75	6.93	4.83	4.36	4.15		
35	Y79AA1001212	3.55	6.93	15.91	13.74	15	11.65		
	Y79AA1001216	52.59	51.46	93.73	76.52	97.53	109.55		
	Y79AA1001228	6.1	11.21	9.34	8.99	12.19	10.24		
	Y79AA1001233	0.68	11.46	2.39	0.92	1.66	1.09		
40	Y79AA1001236	4.46	12.86	9.25	11.4	10.66	13.08		
	Y79AA1001239	4.62	13.93	9.94	11.53	12.15	12.94		
	Y79AA1001240	8.74	8.6	13.75	9.13	6.68	3.01		
	Y79AA1001255	10.37	12.22	22.61	12.47	7.51	6.57		
	Y79AA1001264	3.63	5.15	4.49	7.73	8.59	8.75	**	+
45	Y79AA1001272	10.81	13.63	17.47	21.56	20.67	21.32	*	+
	Y79AA1001281	0.45	4.95	1.89	1.42	1.81	0.95		
	Y79AA1001299	2.49	11.34	9.06	9.9	9.26	9.81		
	Y79AA1001312	2.49	10.36	5.17	2.15	4.77	4.14		
	Y79AA1001319	3.34	11.88	5.27	7.23	6.05	7.15		
50	Y79AA1001323	1.22	1.16	2.09	1.11	1.55	0.89		
	Y79AA1001328	2.04	3.18	3.62	4.66	4.48	4.05	*	+
	Y79AA1001343	154.19	151.55	345.05	304.88	394.54	265.65		
	Y79AA1001351	0.81	2.77	1.67	0.03	1.26	0.96		
	Y79AA1001364	1.65	6.07	4.03	3.39	4.43	3.6		
55	Y79AA1001367	2.16	7.41	2.93	3.09	5.34	3.19		

EP 1 130 094 A2

	Y79AA1001384	0.5	5.14	1.98	0.73	1.15	0.94
5	Y79AA1001391	0.59	3.73	2.88	1.35	1.65	1.2
	Y79AA1001394	3.12	4.66	12.92	10.94	9.56	10.94
	Y79AA1001402	2.77	3.7	5.95	5.65	5.09	4.14
	Y79AA1001410	0.82	2.78	2.33	2.06	2.31	2.25
10	Y79AA1001414	2.76	7.5	7.59	11.08	10.73	10.06 * +
	Y79AA1001426	0.61	4.36	2.61	1.5	1.43	1.82
	Y79AA1001427	14.22	13.44	86.36	59.92	88.36	63.53
10	Y79AA1001430	11.28	16.98	20.98	29.04	34.03	34.38 ** +
	Y79AA1001439	16.22	21.53	33.42	45.02	43.74	43.1 * +
15.	Y79AA1001485	1.65	2.51	4.38	4.85	3.88	3.57
	Y79AA1001493	1.29	2.3	3.43	2.43	2.35	2.46
	Y79AA1001511	4.79	8.57	11.05	9.39	9.11	6.47
15.	Y79AA1001523	2.64	6.57	5.08	8.74	7.37	6.1
	Y79AA1001530	7.46	11.69	22	41.43	36.37	36.07 ** +
	Y79AA1001532	5.12	7.35	6.69	10.49	14.82	12.9 * +
20	Y79AA1001533	1.84	4.89	2.53	4.15	4	4.19
	Y79AA1001541	2.82	5.89	7.54	7.23	5.08	7.34
	Y79AA1001548	4.25	4.84	9.82	10.46	7.37	7.1
	Y79AA1001555	2	2.55	3.65	4.7	5.28	4.25 * +
	Y79AA1001562	7.76	10.11	17.15	14.07	16.16	10.83
25	Y79AA1001581	2	5.05	4.47	5.1	7.01	3.54
	Y79AA1001585	3.18	7.38	10.96	9.72	10.93	8.05
	Y79AA1001592	2.61	7.38	5.97	8.15	8	7.02
	Y79AA1001594	0.76	4.73	3.85	1.96	3.24	1.73
	Y79AA1001603	56.74	70.81	153.14	131.56	112.16	107.66
30	Y79AA1001613	3.74	3.52	14.81	13.12	15.36	10.66
	Y79AA1001630	0.71	2.36	1.73	1.14	2.64	0.67
	Y79AA1001647	1.96	3.57	2.47	4.14	4.32	2.65
	Y79AA1001664	4.67	8.39	11.43	8.96	10.01	8.73
35	Y79AA1001665	1.39	6.4	3.73	4.67	4.71	3.75
	Y79AA1001679	8.92	15.94	20.71	20.53	26.67	25.35
	Y79AA1001692	1.87	5.55	3.95	3.99	3.95	3.51
	Y79AA1001696	1.97	6.49	2.77	1.83	2.63	2.55
	Y79AA1001705	6.09	6.44	10.39	7.62	7.92	7.85
40	Y79AA1001711	16.17	12.34	29.74	13.73	23.83	21
	Y79AA1001717	0.72	2.99	1.29	1.68	3.13	1.14
	Y79AA1001719	2.5	5.79	6.44	6.15	6.07	6.43
	Y79AA1001727	6.87	12.13	14.99	8.73	14.71	8.77
	Y79AA1001750	10.21	13.63	21.67	21.92	32.29	24.33
45	Y79AA1001760	25.24	27.31	122.97	113.56	155.17	83.24
	Y79AA1001777	1.17	3.59	1.6	2.49	1.75	1.28
	Y79AA1001781	0.31	2.3	0.42	1.62	1.84	1.42
	Y79AA1001787	1	3.94	3.54	5.51	5.18	5.15
	Y79AA1001793	16.23	15.19	91.7	60.44	87.21	75.35
50	Y79AA1001795	1.23	3.84	2.24	2.05	2.45	2.8
	Y79AA1001799	4.9	8.35	6.99	10.7	10.72	11.26 * +
	Y79AA1001800	2.25	8.3	10.1	8.49	10.51	9.9
	Y79AA1001801	1.77	6.44	4.87	7.67	5.91	7.33
	Y79AA1001803	0.74	2.15	1.72	1.85	1.68	1.17
55	Y79AA1001805	6.05	6.88	12.15	10.21	8.32	11.15
	Y79AA1001807	3.37	6.33	12.56	11.76	17.8	16.79

EP 1 130 094 A2

	Y79AA1001827	1.7	4.41	3.12	3.43	3.6	2.52
5	Y79AA1001846	1.82	6.52	5.51	6.52	5.09	5.07
	Y79AA1001848	0.86	5.57	2.75	5.98	4.78	5.14
	Y79AA1001853	1.38	6.16	2.76	3.24	4.56	3.63
	Y79AA1001863	0.86	5	2.53	2.93	3.83	3.85
10	Y79AA1001866	2.29	3.2	5.81	3.53	3.98	3.46
	Y79AA1001874	0.12	2.18	-0.21	1.17	0.75	0.51
	Y79AA1001875	9.33	12.67	13.09	11.05	17.79	18.63
	Y79AA1001907	68.02	70.94	96.4	118.34	86.75	104.86
	Y79AA1001908	0.64	8.4	2.29	1.92	2.59	2.31
15	Y79AA1001923	1.61	6.64	3.03	3.86	3.76	3.35
	Y79AA1001927	19.1	22.05	36.94	42.46	45.29	48.81 * +
	Y79AA1001930	4.07	6.65	8.07	7.92	12.42	12.21
	Y79AA1001932	2.84	4.41	8.47	11.51	9.1	8.57
	Y79AA1001933	2.14	3.27	3.69	4.34	7.99	6.65 * +
	Y79AA1001942	1.58	3.45	2.69	2.94	2.13	2.41
20	Y79AA1001963	9.6	9.37	46.06	38.48	49.64	47.27
	Y79AA1001968	18.61	27.73	37.44	42.93	44.16	55.23 * +
	Y79AA1001983	1.81	6.35	4.28	3.97	5.86	4.47
	Y79AA1002000	2.55	5.35	4.55	4.42	3.21	2.83
	Y79AA1002004	13.1	18.87	27.47	23.72	29.45	40.93
25	Y79AA1002008	2.51	3.73	3.79	4.54	2.19	2.85
	Y79AA1002012	1.37	3.22	2.81	3.22	2.29	2.87
	Y79AA1002017	1.34	2.53	2.46	3.51	3.07	2.82
	Y79AA1002022	2.99	4.94	5.93	7.32	7.51	6.01
	Y79AA1002027	2.02	6.33	2.67	2.69	4.03	4.09
30	Y79AA1002050	2.53	8.12	4.22	6.68	6.91	5.11
	Y79AA1002058	13.69	21.8	70.12	59.07	70.89	55.33
	Y79AA1002060	6.38	13.17	20.54	17.14	21.12	24.23
	Y79AA1002062	4.33	5.18	8.15	8.54	6.66	5.51
	Y79AA1002065	33.54	39.97	72.6	49.46	30.04	41.81
35	Y79AA1002067	10.11	11.64	17.24	16.25	9.42	8.13
	Y79AA1002069	0.97	1.79	0.54	1.55	1.44	0.66
	Y79AA1002070	10.16	33.47	44.36	52.16	71.15	73.35 * +
	Y79AA1002074	38.55	74.38	179.6	165.55	282.48	224.96
40	Y79AA1002076	0.48	9.71	2.89	2.86	3.34	1.91
	Y79AA1002083	1.2	7.48	2.03	2.73	1.75	2.06
	Y79AA1002084	1.79	2.59	4.54	3.73	3.73	2.98
	Y79AA1002086	0.96	1.78	1.71	2.77	1.88	1.43
	Y79AA1002087	11.18	14.9	27.67	33.34	30.01	23.08
45	Y79AA1002089	1.18	3.46	2.13	1.46	2.92	3.26
	Y79AA1002093	2.19	5.48	5.25	5.28	5.68	6.17
	Y79AA1002101	1.11	8.58	2.98	6.54	5.58	6.6
	Y79AA1002103	1.47	10.22	3.39	4.43	6.49	4.7
	Y79AA1002115	4.34	9.78	7.37	7.45	7.03	6.95
50	Y79AA1002121	1.55	2.16	2.18	1.67	2.55	2.31
	Y79AA1002125	6.67	7.08	9.29	8.81	6.4	7.6
	Y79AA1002129	1.64	6.23	7.84	5.41	2.2	4.93
	Y79AA1002131	0.9	3.25	0.78	0.77	1.29	1.15
	Y79AA1002139	0.69	5.02	1.04	1.83	1.53	1.34
55	Y79AA1002144	25.99	29.62	51.01	42.61	51.16	43.17
	Y79AA1002177	1.72	5.97	4.33	4.79	3.09	4.73

EP 1130 094 A2

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	Y79AA1002183	10.44	13.89	17.69	27.61	29.67	28.92	**	+
5	Y79AA1002202	3.97	7.15	8.34	18.27	10.12	17.85	*	+
	Y79AA1002204	0.53	0.99	1.56	1.7	2.2	1.54		
	Y79AA1002206	2.63	5.36	7.28	4.35	2.95	1.49		
	Y79AA1002208	4.26	6.54	3.94	6.88	6.3	3.96		
	Y79AA1002209	1.8	6.34	2.88	4.38	3.74	4.57		
10	Y79AA1002210	0.41	4.14	2.09	1.8	2.24	1.65		
	Y79AA1002211	2.25	5.39	3.85	5.71	5.3	4.5		
	Y79AA1002213	1.15	4.13	6.53	7.38	7.54	7.43		
	Y79AA1002215	18.7	18.69	26.61	17.72	15.59	9.62		
	Y79AA1002220	3.78	3.38	2.87	4.89	4.19	4.14	*	+
15	Y79AA1002226	8.54	8.9	9.75	13.06	14.2	4.41		
	Y79AA1002229	1.35	3.88	3.38	2.95	2.79	2.67		
	Y79AA1002234	3.24	6.82	3.94	4.29	7.74	6.88		
	Y79AA1002235	5.6	7.55	6.43	8.78	9.74	9.47	*	+
	Y79AA1002246	0.59	5.06	2.41	3.94	2.54	4.27		
20	Y79AA1002258	0.72	7.26	2.92	3.99	4.19	2.7		
	Y79AA1002279	17.79	19.12	27.8	16.52	19.13	11.5		
	Y79AA1002292	1.68	2.1	3.22	2.96	3.91	2.73		
	Y79AA1002298	0.76	2.52	1.32	2.03	2.77	1.06		
	Y79AA1002307	1.05	4.35	1.79	0.76	1.05	1.2		
25	Y79AA1002309	1.15	4.19	2.3	2.21	1.78	2.55		
	Y79AA1002311	2.84	7.35	3.43	5.71	6.04	5.45		
	Y79AA1002334	1.72	6.54	2.95	4.77	4.19	3.35		
	Y79AA1002351	1.27	5.5	2.89	3.5	3.38	3.06		
	Y79AA1002355	12.83	12.25	28.96	22.94	22.07	21.02		
30	Y79AA1002361	2.22	2.27	3.26	2.47	4.54	1.55		
	Y79AA1002365	0.66	2.04	2.26	1.97	3.51	2.25		
	Y79AA1002373	1.17	3.93	2.42	1.59	1.97	1.43		
	Y79AA1002376	110.81	135.82	249.8	205.99	213.25	191.69		
35	Y79AA1002378	1.9	4.8	4.91	2.2	3.6	3		
	Y79AA1002381	8.65	14.11	19.19	18.84	21.52	17.97		
	Y79AA1002388	7.05	9.99	18.24	15.88	21.51	19.99		
	Y79AA1002399	1.79	4.25	3.74	4.62	4.08	3.47		
	Y79AA1002407	3.05	4.16	3.13	4.66	5.77	4.5	*	+
40	Y79AA1002413	3.21	6.78	8.05	6.46	8.32	6.87		
	Y79AA1002416	1.46	5	2.74	2.49	3.44	3.55		
	Y79AA1002429	5.5	8.15	7.27	8	11.11	8.01		
	Y79AA1002431	0.92	4.43	0.48	0.79	1.78	0.89		
	Y79AA1002433	1.27	5.9	3.24	4.8	3.84	5.58		
45	Y79AA1002445	4.01	5.34	5.76	3.1	4.89	5.41		
	Y79AA1002461	0.63	2.45	1.79	1.19	2.71	1.41		
	Y79AA1002466	39.02	70.71	94.5	91.12	82.27	94.71		
	Y79AA1002471	4.44	6.67	6.08	7.43	8.06	10.49		
50	Y79AA1002472	2.41	6.16	5.99	6.8	8.39	4.06		
	Y79AA1002474	1.93	8.27	4.31	4.89	6.52	7.13		
	Y79AA1002482	3.52	6.66	10.37	9.02	11.81	8.69		
	Y79AA1002487	1.38	4.12	2.46	1.96	3.01	2.56		
	Y79AA1002490	10.37	9.91	16.35	11.11	12.88	16.86		
	Y79AA1002493	1.96	4.07	6.14	6.5	8.9	4.1		
55	ZRV6C1006278	0.61	4.08	2.22	1.81	1.58	2.11		

Table 367

Difference in the expression level of each clone in response to TNF. stimulation or IL-1. stimulation

Before stimulation, IL1 1h, and IL1 7h represent relative levels of expression in the absence of the stimulation, 1 hour after the IL-1. stimulation, and 7 hours after the stimulation, respectively. TNF 1h, TNF 3h, and TNF 7h represent relative levels of expression 1 hour after the TNF. stimulation, 3 hours after the stimulation, and 7 hours after the stimulation, respectively. Correlation coefficients 1 and 2 indicate the correlation coefficients in the calibration curves prepared based on the data for the internal standard in reaction systems A and B, respectively.

Clone	IL1		TNF		Correlation		
	before stimulation	1h	7h	1h	3h	7h	coefficients
	1	2					
NT2RM1000858	5.6	7.6	3.8	4.7	2.1	1.7	0.98 0.94
NT2RM1000462	0.9	0.9	0.5	0.7	0.1	0	1 1
NT2RM1000855	1	1.3	1	1.1	0.4	0.4	1 1
NT2RM1000789	1	0.9	0.4	1	0.4	0.6	0.96 0.98
NT2RM2000306	0.7	1.1	0.3	1.1	0.3	0.1	1 0.98
NT2RM2000514	0.2	0.2	0.6	0.2	0.1	0.2	0.98 0.96
NT2RM2001126	0.5	0	0.4	0.3	0.3	1.2	0.99 0.99
NT2RM2001902	1.3	1.6	0.6	1.3	0.8	0.8	1 1
NT2RM2001738	1.6	1.8	1.5	1.7	0.8	0.9	0.98 1
NT2RM2000582	0.2	0.1	0	0.7	0.1	0.1	0.99 0.99
NT2RM2000773	1.1	1.2	1.4	2	1	0.8	0.95 1
NT2RM2001626	0.4	0.2	0.6	0.7	0.1	0.7	1 1
NT2RM2001643	1.6	3.1	1.2	2.4	0.7	0.8	1 1
NT2RM2001792	0.2	0	0	0.3	0.1	0.1	0.98 0.97
NT2RM2000589	0.2	0.1	0	0.1	0	0	1 0.99
NT2RM2000588	0.6	0.7	0.1	0.8	0.2	0.2	1 1
NT2RM2002109	0	0	0	0.2	0.1	0	0.99 0.99
NT2RM4000284	6.5	9.1	4.8	10.1	3.4	3	1 1
NT2RM4001735	3.8	4.6	2.1	5	1.6	1.4	1 1
NT2RM4000100	0.5	0.6	0.2	0.5	0.3	0.3	0.95 0.95
NT2RM4000417	0.2	0	0	0.2	0.1	0	0.99 0.98
NT2RM4000761	3.2	3.2	2.2	2.6	0.7	0.7	0.95 1
NT2RM4001843	1.5	1.8	1.7	2.8	1.2	0.6	0.98 1
NT2RP1000239	2.1	3.2	1.2	2.1	0.5	0.6	1 0.99
NT2RP1000465	0.9	0.3	0.3	0.9	0.2	0.1	0.97 0.96
NT2RP1000679	0.3	0.3	0.4	0.9	0.2	0.3	0.97 1
NT2RP1001031	1.4	1.4	0.4	1.2	0.1	0.3	1 0.98
NT2RP2001200	2	1.5	0.8	2.2	0.7	0.7	0.99 1
NT2RP2001562	2.7	2.4	0.7	3.6	0.4	1.1	1 0.94
NT2RP2001948	1.1	1.5	0.7	1.8	0.6	0.7	0.97 0.99
NT2RP2002015	1.3	1.7	0.7	1.8	0.6	0.5	0.99 1
NT2RP2003390	2	1.7	1.3	2.3	0.6	0.5	0.99 0.99
NT2RP2003664	0.4	0.1	0.1	0.8	0.1	0	0.99 0.99
NT2RP2005597	1.2	1.4	0.5	2.7	2.2	2.2	0.96 0.99
NT2RP2001469	1.7	1.4	1.2	2	0.6	0.6	1 1
NT2RP2000240	0.9	0.9	0.3	1.4	0.7	0.3	1 1
NT2RP2000610	2.4	2.2	2.1	2.7	1.5	1.6	0.93 0.96

EP 1 130 094 A2

	NT2RP2001276	1	0.4	0.4	0.8	0.2	0.7	0.95	1
5	NT2RP2001817	1.2	0.8	0.5	1.9	0.7	0.7	1	1
	NT2RP2004069	0.6	0.6	0.4	0.8	0.5	0.3	0.93	0.97
	NT2RP2004108	0.3	0.2	0.6	1.1	0.4	0.5	0.96	1
	NT2RP2005391	0.7	0.5	0.1	1.2	0.3	0.3	1	0.99
	NT2RP2006092	1.6	1.2	0.9	2.1	0.6	0.7	0.97	1
10	NT2RP2006134	1.2	1.5	0.7	1.9	1	0	0.91	1
	NT2RP2000818	0.9	0.3	0.3	1.6	0.3	0.3	0.95	1
	NT2RP2000092	1.8	1.8	0.8	2	1	1	0.99	0.98
	NT2RP2000092	1.1	1.1	0.5	1.4	0.6	0.6	0.99	0.97
	NT2RP2001538	2.1	1.9	1.8	2.5	0.6	0.8	0.98	1
15	NT2RP2006476	2.1	2.2	1.4	3.2	1.6	2	0.97	0.98
	NT2RP3000616	0.1	0.1	0	0	0	0	1	1
	NT2RP3000721	2.2	2.8	0.7	2.4	0.4	0.4	1	0.98
	NT2RP3001044	1.5	1.9	0.6	2	0.7	0.4	1	1
	NT2RP3001240	0.8	1	0.8	1.5	0.6	0.7	0.97	0.99
20	NT2RP3001592	0.3	0.8	0.8	1.1	0	0	0.94	0.93
	NT2RP3002448	4.6	4.2	2.5	4.5	0.8	1.2	1	0.98
	NT2RP3002721	1.3	1.6	0.5	1.4	0.3	0.3	1	0.99
	NT2RP3002738	0.1	0	0.1	1.9	0.1	0.1	0.99	1
	NT2RP3002790	1.6	2	0.6	1.7	0.6	0.5	0.98	1
25	NT2RP3002836	1.7	3	0.9	2.4	1.6	0.7	1	1
	NT2RP3003354	0.9	0.7	0.5	0.6	0.4	0.5	0.99	0.92
	NT2RP3003614	0.5	0.4	0	0.3	0.3	0.2	0.99	0.99
	NT2RP3004075	0.8	1.4	0.7	1	0.4	0.4	1	1
	NT2RP3004130	0.3	0.4	0	0.2	0.1	0	0.93	0.96
30	NT2RP3004133	1.9	3.5	0.6	3.8	1	1.3	0.99	1
	NT2RP3004321	0.2	0.2	0	1.4	0.4	0.2	1	0.99
	NT2RP3004406	1.3	0.2	0.2	0.7	0.1	0	1	1
	NT2RP3004552	0.1	0.1	0.1	0.1	0	0	1	1
	NT2RP3004557	1.3	1.1	2.2	2.6	1.5	1.4	0.98	0.94
35	NT2RP3004647	1.2	2.1	0.6	1.2	1	0.5	1	1
	NT2RP3000201	2.3	2.9	0.4	1	1.3	0.5	1	0.98
	NT2RP3000820	1.2	1.6	0.9	1.2	0.6	0.5	1	1
	NT2RP3000818	1.4	1.5	0.7	1.8	0.5	0.7	1	0.99
	NT2RP3001159	1.2	2.5	1.2	1.4	0.6	0.7	0.99	0.99
40	NT2RP3002281	1.6	2	1.2	1.8	1	1.2	0.99	1
	NT2RP3002571	3.9	1.8	1.2	5.2	1.4	0.8	0.99	0.97
	NT2RP3002983	1.4	1.7	0.5	1.4	0.4	0.3	1	1
	NT2RP3003473	0.8	0.9	1	0.7	0.4	0.5	1	0.99
	NT2RP3001976	0.6	1.1	0.1	0.7	0.4	0.1	1	0.99
45	NT2RP3002286	1.4	1.8	1	1.6	0.6	0.5	1	0.99
	NT2RP3002353	7.7	6.4	2.2	8.7	1.1	1.3	0.94	0.99
	NT2RP3004025	1.9	2	1	2.1	1	1	0.96	0.98
	NT2RP3004119	0.8	1.1	0.4	0	0	0.2	1	0.99
	NT2RP3000171	0.7	1.3	0.6	1	0.4	0.3	0.99	1
50	NT2RP3000676	1.2	1.9	0.7	1.1	1.3	0.5	0.99	1
	NT2RP3000921	0.2	0.1	0	0.2	0.1	0	1	0.99
	NT2RP3002015	0.8	0.6	0.4	0.7	0.1	0.1	0.99	0.99
	NT2RP3004294	0	0	0	0.1	0.1	0	1	1
	NT2RP3004345	0.6	0.4	0.2	0.9	0.2	0.5	1	1
55	NT2RP3000148	1.7	2.5	0.8	2	0.8	0.8	1	1

EP 1 130 094 A2

	NT2RP3000232	0.6	0.8	0.4	0.3	0	0	1	0.99
5	NT2RP3001650	2.3	1.5	1.6	1.7	1	1.3	1	1
	NT2RP3002411	0.5	0.4	0.1	0.5	0.2	0.1	1	1
	NT2RP4001001	0.8	1.3	0.7	1	0.7	0.4	0.97	0.97
	NT2RP4001877	1.5	0.9	1.1	1.2	0.5	0.7	1	0.99
	NT2RP4002451	0.7	1	0.6	0.7	0.2	0.3	0.91	0.95
10	NT2RP4000634	1	1	0.3	0.9	0.3	0.4	0.99	1
	NT2RP4002187	0.4	0.4	0.1	0.7	0.3	0.2	1	0.99
	NT2RP4002715	1.5	1.6	0.7	1.5	0.4	0.3	1	0.99
	MAMMA1000986	3.9	4.1	1.9	4.2	1.8	1.4	0.99	1
	MAMMA1001237	0	0	1.6	0.2	0	0	0.99	0.98
15	MAMMA1001978	3.5	3.4	2.3	6	3.4	2.5	0.97	0.98
	MAMMA1002080	0.4	0	0	0.4	0.1	0	1	0.99
	MAMMA1002234	4	4.4	3	7.7	1.9	3	0.97	1
	MAMMA1000614	4.8	1	15.5	5.6	3.9	4.8	0.95	0.93
	MAMMA1000141	7.1	11.5	3.5	14.8	6.5	3.7	1	0.98
20	MAMMA1000706	7.2	9.3	3.9	3.7	2.3	2.6	0.98	0.99
	MAMMA1000788	3	3.8	2.8	8.9	4.8	4.2	0.92	0.98
	MAMMA1000994	0.3	0	0	0.4	0	0	1	1
	MAMMA1001310	4.1	6.1	3.8	8	2.5	3.6	0.99	0.95
	MAMMA1001344	2.7	4.4	2.2	3.2	2.6	2.1	1	0.99
25	MAMMA1001957	2.3	2.7	1.9	1.7	1	1.8	0.99	1
	MAMMA1002070	0.1	0.1	0	0.8	0.4	0.2	1	0.99
	MAMMA1002586	1.7	1.6	1.2	1.3	0.4	0.3	0.94	1
	MAMMA1000102	2.1	2.3	1.4	3.3	1.6	1.6	1	1
	MAMMA1001066	2.8	2.6	1.8	5.3	0.7	1.2	1	0.98
30	MAMMA1001094	2.3	2.9	2	3.3	2.1	2.5	0.96	0.9
	MAMMA1001609	2	3	1.2	2.7	1.7	2.2	0.99	0.97
	PLACE1002547	2	1.7	1.2	4.1	1.2	2	0.95	1
	PLACE1003573	0	0	0	0.1	0	0	1	0.98
35	PLACE1004199	0.1	0.2	0	0	0	0	0.99	0.97
	PLACE1004305	0	0	0	0.3	0	0.2	0.96	0.99
	PLACE1004450	0.9	0.3	0	0.1	0	0	0.98	0.98
	PLACE1005031	0.9	0	0	0.5	0	0	0.98	0.99
	PLACE1007845	0.8	1	0.4	0.4	0.1	0.1	1	0.98
	PLACE1008984	1.4	1.2	0.4	1.9	0.6	0.5	0.98	0.98
40	PLACE1011116	2.6	1.5	1.6	1.6	0.3	0.4	1	1
	PLACE1000986	0.6	0.2	0.2	0.3	0.1	0.1	1	0.98
	PLACE1004492	1.9	1.9	1.5	3.3	1	1	1	0.97
	PLACE1005569	2.6	0.4	0	1.1	0.3	0.1	0.98	0.99
	PLACE1005601	1.7	1.3	1	2.3	0.6	0.3	0.93	1
45	PLACE1006079	0.6	0.3	0	0.1	0.1	0	0.98	0.99
	PLACE1007077	1.1	0	0	0.3	0.1	0	0.97	0.98
	PLACE1008744	0.4	0.1	0.1	1.1	0.1	0	0.98	1
	PLACE1011181	0.6	0.3	0.5	1.6	0.3	0.5	0.98	0.99
	PLACE1005539	0.4	0	0.2	0.3	0.2	0	1	0.93
50	PLACE1008282	1.1	0.7	0.6	1.2	0.4	0.4	0.98	1
	PLACE1010713	0.6	0.7	0	1.4	0.5	0.4	0.99	0.95
	PLACE1010011	1.2	1.4	0.2	2.7	1.5	1.7	1	0.99
	PLACE3000213	1.9	0.2	0.1	0.8	0.1	0	0.99	1
	PLACE1002080	6.7	3.9	0.3	1.7	0.8	0.5	0.95	0.98
	SKNMC1000082	1.3	0.1	1.1	0.7	0	0	1	1

	Y79AA1000127	1.8	1.8	1.1	2.1	0.5	0.6	1	1
5	Y79AA1000226	1.4	0.8	0.6	0.9	0.3	0.4	0.99	0.99
	Y79AA1000776	0.3	0.1	0	1.1	0.3	0.5	0.99	0.99
	Y79AA1000876	1.1	1.5	1.2	1.3	0.5	0.8	0.97	1
10	Y79AA1001056	1.7	1.7	0.8	1.4	0.9	0.7	1	1
	Y79AA1000777	3.1	3.1	1.2	3.8	0.7	0.5	0.98	0.99
	Y79AA1000030	1	1.3	0.2	1.3	0	0.6	0.98	0.96
15	Y79AA1001212	1.5	1.2	1	2	0.8	0.5	1	0.99
	Y79AA1001427	2.3	3	0.6	2	0.8	0.4	1	1
	Y79AA1001530	0.9	0.9	0.5	1.1	0.4	0.4	1	1
20	Y79AA1001592	0.6	0.2	0	0.7	0	0	0.97	1
	Y79AA1001727	0.8	0.4	0.2	0.9	0.2	0.1	1	1
	Y79AA1001803	0.1	0	0	0.2	0.1	0	0.97	0.99
	Y79AA1002373	0	0	0	0	0	0.99	1	
	Y79AA1002376	0.9	0.1	0	1.2	0.1	0.4	0.98	1
	Y79AA1001523	0.5	0.5	0.3	0.6	0.3	0.1	1	0.98
	Y79AA1000888	1.1	1	0.7	1.4	0.7	0.5	1	1
	Y79AA1002129	0.2	0.2	0.1	0.5	0.2	0.2	0.99	1

25 [0285] The present invention has provided a total of 830 novel full length cDNA clones. As has not yet proceeded the isolation of full length cDNA within the human, the invention has a large significance. Those proteins such as secretory proteins, membrane proteins, and proteins associated with signal transduction, glycoprotein, and transcription are known to be associated with many diseases. Those genes and proteins associating with diseases are useful for developing medicines as they can be used as a diagnostic marker, or a target for gene therapy or developing medicines that is capable of regulating their expression and activity. Especially, the cDNA clones encoding a secretion protein are extremely important for medicinal industry since the protein itself is expected to be effective as a medicine, and also the gene may have potential to be associating with many diseases. Moreover, those proteins such as membrane proteins, and proteins associated with signal transduction, glycoprotein, transcription, and diseases, and the genes encoding the proteins may be used as a disease marker. These cDNA clones are also important for medicinal industry as they may be effective for treating diseases through the regulation of the expression and activity of their encoded proteins.

40 Table 368
The names of the representative sequences of the clusters (groups) and the corresponding SEQ IDs.

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	HRIFA013589a : 1879	HRIFA029440a : 2285
	HRIFA013620a : 1880	HRIFA029460a : 2286
	HRIFA013668a : 1881	HRIFA029467a : 2287
	HRIFA013726a : 1882	HRIFA029508a : 2288
40	HRIFA013744a : 1883	HRIFA029511a : 2289
	HRIFA013899a : 1884	HRIFA029577a : 2290
	HRIFA013911a : 1885	HRIFA029602a : 2291
	HRIFA013919a : 1886	HRIFA029649a : 2292
45	HRIFA013932a : 1887	HRIFA029715a : 2293
	HRIFA013980a : 1888	HRIFA029730a : 2294
	HRIFA014006a : 1889	HRIFA029779a : 2295
	HRIFA014024a : 1890	HRIFA029792a : 2296
	HRIFA014056a : 1891	HRIFA029802a : 2297
50	HRIFA014111a : 1892	HRIFA029866a : 2298
	HRIFA014133a : 1893	HRIFA029932a : 2299
	HRIFA014178a : 1894	HRIFA030025a : 2300
	HRIFA014185a : 1895	HRIFA030045a : 2301
	HRIFA014303a : 1896	HRIFA030097a : 2302
55	HRIFA014336a : 1897	HRIFA030103a : 2303

	HRIFA014396a : 1898	HRIFA030106a : 2304
5	HRIFA014397a : 1899	HRIFA030147a : 2305
	HRIFA014417a : 1900	HRIFA030203a : 2306
	HRIFA014465a : 1901	HRIFA030237a : 2307
	HRIFA014467a : 1902	HRIFA030248a : 2308
	HRIFA014482a : 1903	HRIFA030250a : 2309
10	HRIFA014500a : 1904	HRIFA030264a : 2310
	HRIFA014561a : 1905	HRIFA030342a : 2311
	HRIFA014568a : 1906	HRIFA030370a : 2312
	HRIFA014590a : 1907	HRIFA030371a : 2313
	HRIFA014598a : 1908	HRIFA030381a : 2314
15	HRIFA014620a : 1909	HRIFA030385a : 2315
	HRIFA014621a : 1910	HRIFA030394a : 2316
	HRIFA014688a : 1911	HRIFA030408a : 2317
	HRIFA014692a : 1912	HRIFA030411a : 2318
	HRIFA014702a : 1913	HRIFA030448a : 2319
20	HRIFA014819a : 1914	HRIFA030456a : 2320
	HRIFA014868a : 1915	HRIFA030461a : 2321
	HRIFA014951a : 1916	HRIFA030472a : 2322
	HRIFA014953a : 1917	HRIFA030509a : 2323
	HRIFA014967a : 1918	HRIFA030511a : 2324
25	HRIFA015063a : 1919	HRIFA030545a : 2325
	HRIFA015070a : 1920	HRIFA030566a : 2326
	HRIFA015122a : 1921	HRIFA030599a : 2327
	HRIFA015129a : 1922	HRIFA030629a : 2328
	HRIFA015219a : 1923	HRIFA030642a : 2329
30	HRIFA015236a : 1924	HRIFA030662a : 2330
	HRIFA015246a : 1925	HRIFA030839a : 2331
	HRIFA015351a : 1926	HRIFA030981a : 2332
	HRIFA015409a : 1927	HRIFA031062a : 2333
	HRIFA015423a : 1928	HRIFA031075a : 2334
35	HRIFA015443a : 1929	HRIFA031091a : 2335
	HRIFA015453a : 1930	HRIFA031126a : 2336
	HRIFA015471a : 1931	HRIFA031249a : 2337
	HRIFA015486a : 1932	HRIFA031336a : 2338
	HRIFA015506a : 1933	HRIFA031350a : 2339
40	HRIFA015536a : 1934	HRIFA031395a : 2340
	HRIFA015547a : 1935	HRIFA031397a : 2341
	HRIFA015568a : 1936	HRIFA031438a : 2342
	HRIFA015671a : 1937	HRIFA031472a : 2343
	HRIFA015682a : 1938	HRIFA031510a : 2344
45	HRIFA015756a : 1939	HRIFA031672a : 2345
	HRIFA015764a : 1940	HRIFA031869a : 2346
	HRIFA015802a : 1941	HRIFA031871a : 2347
	HRIFA015811a : 1942	HRIFA031895a : 2348
50	HRIFA015902a : 1943	HRIFA031935a : 2349
	HRIFA015947a : 1944	HRIFA031986a : 2350
	HRIFA015995a : 1945	HRIFA032009a : 2351
	HRIFA016070a : 1946	HRIFA032011a : 2352
	HRIFA016129a : 1947	HRIFA032066a : 2353
55	HRIFA016214a : 1948	HRIFA032067a : 2354
	HRIFA016240a : 1949	HRIFA032070a : 2355

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	HRIFA016255a : 1950	HRIFA032073a : 2356
	HRIFA016290a : 1951	HRIFA032079a : 2357
	HRIFA016430a : 1952	HRIFA032097a : 2358
	HRIFA016599a : 1953	HRIFA032161a : 2359
	HRIFA016623a : 1954	HRIFA032186a : 2360
10	HRIFA016639a : 1955	HRIFA032224a : 2361
	HRIFA016654a : 1956	HRIFA032257a : 2362
	HRIFA016669a : 1957	HRIFA032271a : 2363
	HRIFA016758a : 1958	HRIFA032274a : 2364
	HRIFA016838a : 1959	HRIFA032275a : 2365
15	HRIFA016963a : 1960	HRIFA032360a : 2366
	HRIFA017031a : 1961	HRIFA032389a : 2367
	HRIFA017146a : 1962	HRIFA032433a : 2368
	HRIFA017190a : 1963	HRIFA032453a : 2369
20	HRIFA017257a : 1964	HRIFA032478a : 2370
	HRIFA017295a : 1965	HRIFA032506a : 2371
	HRIFA017312a : 1966	HRIFA032511a : 2372
	HRIFA017456a : 1967	HRIFA032530a : 2373
25	HRIFA017457a : 1968	HRIFA032587a : 2374
	HRIFA017509a : 1969	HRIFA032605a : 2375
	HRIFA017594a : 1970	HRIFA032642a : 2376
	HRIFA017643a : 1971	HRIFA032696a : 2377
	HRIFA017670a : 1972	HRIFA032730a : 2378
30	HRIFA017703a : 1973	HRIFA032820a : 2379
	HRIFA017729a : 1974	HRIFA032984a : 2380
	HRIFA017791a : 1975	HRIFA033349a : 2381
	HRIFA017801a : 1976	HRIFA033718a : 2382
35	HRIFA017818a : 1977	HRIFA034010a : 2383
	<u>HRIFA017836a : 1978</u>	

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Table 369

The names of the internal sequences that are used in the selection of the clones from the representative sequences, and the corresponding SEQ IDs.

5	AA533598 : 2384	HRIFA036799a : 2463
10	AI051329 : 2385	HRIFA037138a : 2464
	HRIFA000595a : 2386	HRIFA037776a : 2465
	HRIFA000667a : 2387	HRIFA037838a : 2466
	HRIFA000878a : 2388	HRIRA000001a : 2467
15	HRIFA001269a : 2389	HRIRA000041a : 2468
	HRIFA001283a : 2390	HRIRA000058a : 2469
	HRIFA002000a : 2391	HRIRA000260a : 2470
	HRIFA002196a : 2392	HRIRA000490a : 2471
	HRIFA003583a : 2393	HRIRA000522a : 2472
20	HRIFA005077a : 2394	HRIRA000553a : 2473
	HRIFA005781a : 2395	HRIRA000563a : 2474
	HRIFA006216a : 2396	HRIRA000640a : 2475
	HRIFA006468a : 2397	HRIRA000725a : 2476
	HRIFA006822a : 2398	HRIRA000998a : 2477
25	HRIFA007048a : 2399	HRIRA001053a : 2478
	HRIFA007661a : 2400	HRIRA001314a : 2479

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HRIFA007777a : 2401	HRIRAA001443a : 2480
HRIFA007997a : 2402	HRIRAA001473a : 2481
HRIFA008312a : 2403	HRIRAA001648a : 2482
HRIFA009250a : 2404	HRIRAA001690a : 2483
HRIFA009495a : 2405	HRIRAA001726a : 2484
HRIFA009607a : 2406	HRIRAA001884a : 2485
HRIFA009923a : 2407	HRIRAA002098a : 2486
HRIFA009978a : 2408	HRIRAA002100a : 2487
HRIFA010730a : 2409	HRIRAA002155a : 2488
HRIFA011029a : 2410	HRIRAA002307a : 2489
HRIFA011416a : 2411	HRIRAA002442a : 2490
HRIFA011461a : 2412	HRIRAA002446a : 2491
HRIFA012670a : 2413	HRIRAA002479a : 2492
HRIFA012717a : 2414	HRIRAA002945a : 2493
HRIFA012802a : 2415	HRIRAA003028a : 2494
HRIFA013357a : 2416	HRIRAA003108a : 2495
HRIFA013484a : 2417	HRIRAA003139a : 2496
HRIFA015333a : 2418	HRIRAA003819a : 2497
HRIFA015375a : 2419	HRIRAA004049a : 2498
HRIFA015663a : 2420	HRIRAA004286a : 2499
HRIFA016287a : 2421	HRIRAA004583a : 2500
HRIFA016302a : 2422	HRIRAA004691a : 2501
HRIFA016782a : 2423	HRIRAA004783a : 2502
HRIFA018555a : 2424	HRIRAA005152a : 2503
HRIFA019338a : 2425	HRIRAA005221a : 2504
HRIFA020315a : 2426	HRIRAA005227a : 2505
HRIFA020806a : 2427	HRIRAA005305a : 2506
HRIFA022264a : 2428	HRIRAA005563a : 2507
HRIFA022923a : 2429	HRIRAA006263a : 2508
HRIFA023027a : 2430	HRIRAA006324a : 2509
HRIFA023218a : 2431	HRIRAA006517a : 2510
HRIFA023363a : 2432	HRIRAA006580a : 2511
HRIFA023434a : 2433	HRIRAA007665a : 2512
HRIFA023444a : 2434	HRIRAA007680a : 2513
HRIFA023551a : 2435	HRIRAA008129a : 2514
HRIFA023558a : 2436	HRIRAA008152a : 2515
HRIFA023641a : 2437	HRIRAA008276a : 2516
HRIFA023798a : 2438	HRIRAA008329a : 2517
HRIFA024330a : 2439	HRIRAA008854a : 2518
HRIFA024338a : 2440	HRIRAA008896a : 2519
HRIFA024384a : 2441	HRIRAA008958a : 2520
HRIFA024644a : 2442	HRIRAA009551a : 2521
HRIFA025170a : 2443	HRIRAA009828a : 2522
HRIFA025496a : 2444	HRIRAA010472a : 2523
HRIFA025565a : 2445	HRIRAA012442a : 2524
HRIFA025651a : 2446	HRIRAA012921a : 2525
HRIFA026224a : 2447	HRIRAA013325a : 2526
HRIFA026729a : 2448	HRIRAA013644a : 2527
HRIFA026925a : 2449	HRIRAA013675a : 2528
HRIFA028501a : 2450	HRIRAA013702a : 2529
HRIFA029454a : 2451	HRIRAA013757a : 2530
HRIFA030181a : 2452	HRIRAA013951a : 2531

5 HRIFA032701a : 2453 HRIR014256a : 2532
 HRIFA032801a : 2454 HRIR014380a : 2533
 HRIFA033384a : 2455 HRIR015831a : 2534
 HRIFA033682a : 2456 HRIR015904a : 2535
 HRIFA033930a : 2457 HRIR016124a : 2536
 HRIFA034817a : 2458 HRIR017071a : 2537
 HRIFA035409a : 2459 HRIR018191a : 2538
 HRIFA035542a : 2460 HRIR020304a : 2539
 HRIFA035577a : 2461 HRIR000579a : 2540
 HRIFA036630a : 2462

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[0286] The internal sequences include EST, HRIFA(the representative sequence of the 5'-end), and HRIR0 (the representative sequence of the 3'-end).

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Table 370

clone	the name of full-length nucleotide sequences	SEQ ID NO of the full-length nucleotide sequences	SEQ ID NO of the deduced amino acid sequences
	HEMBA1000006 nnnnnnnnnnnn	C-HEMBA1000006 C-nnnnnnnnnnnn	2547 nnnn
15	HEMBA1000121 HEMBA1000128 HEMBA1000275 HEMBA1000300	C-HEMBA1000121 C-HEMBA1000128 C-HEMBA1000275 C-HEMBA1000300	2551 2553 2555 2557
20	HEMBA1000349 HEMBA1000443 HEMBA1000590 HEMBA1000634	C-HEMBA1000349 C-HEMBA1000443 C-HEMBA1000590 C-HEMBA1000634	2558 2560 2562 2564
25	HEMBA1000713 HEMBA1000745 HEMBA1000907 HEMBA1000940	C-HEMBA1000713 C-HEMBA1000745 C-HEMBA1000907 C-HEMBA1000940	2566 2568 2570 2572
30	HEMBA1000962 HEMBA1001221 HEMBA1001228 HEMBA1001297	C-HEMBA1000962 C-HEMBA1001221 C-HEMBA1001228 C-HEMBA1001297	2574 2576 2578 2580
35	HEMBA1001390 HEMBA1001563 HEMBA1001621 nnnnnnnnnnnn	C-HEMBA1001390 C-HEMBA1001563 C-HEMBA1001621 C-nnnnnnnnnnnn	2581 2583 2584 nnnn
40	HEMBA1001878 HEMBA1002131 HEMBA1002163 HEMBA1002164	C-HEMBA1001878 C-HEMBA1002131 C-HEMBA1002163 C-HEMBA1002164	2588 2590 2592 2594
45	HEMBA1002167 HEMBA1002178 nnnnnnnnnnnn	C-HEMBA1002167 C-HEMBA1002178 C-nnnnnnnnnnnn	2596 2598 nnnn

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EP 1 130 094 A2

	HEMBA1002195	C-HEMBA1002195	2602	2603
5	HEMBA1002227	C-HEMBA1002227	2604	2605
	HEMBA1002239	C-HEMBA1002239	2606	
	HEMBA1002316	C-HEMBA1002316	2607	2608
	HEMBA1002420	C-HEMBA1002420	2609	2610
10	HEMBA1002421	C-HEMBA1002421	2611	2612
	HEMBA1002524	C-HEMBA1002524	2613	2614
	HEMBA1002551	C-HEMBA1002551	2615	2616
	HEMBA1002767	C-HEMBA1002767	2617	2618
	HEMBA1002992	C-HEMBA1002992	2619	2620
15	HEMBA1003047	C-HEMBA1003047	2621	2622
	HEMBA1003072	C-HEMBA1003072	2623	2624
	HEMBA1003101	C-HEMBA1003101	2625	2626
	HEMBA1003230	C-HEMBA1003230	2627	2628
	HEMBA1003294	C-HEMBA1003294	2629	
	HEMBA1003315	C-HEMBA1003315	2630	2631
20	HEMBA1003392	C-HEMBA1003392	2632	2633
	HEMBA1003399	C-HEMBA1003399	2634	2635
	HEMBA1003487	C-HEMBA1003487	2636	2637
	HEMBA1003530	C-HEMBA1003530	2638	2639
	HEMBA1003602	C-HEMBA1003602	2640	2641
25	HEMBA1003732	C-HEMBA1003732	2642	2643
	HEMBA1003945	C-HEMBA1003945	2644	2645
	HEMBA1004110	C-HEMBA1004110	2646	2647
	HEMBA1004250	C-HEMBA1004250	2648	2649
	HEMBA1004391	C-HEMBA1004391	2650	2651
30	HEMBA1004444	C-HEMBA1004444	2652	2653
	HEMBA1004454	C-HEMBA1004454	2654	2655
	HEMBA1004505	C-HEMBA1004505	2656	2657
	HEMBA1004797	C-HEMBA1004797	2658	2659
	HEMBA1004982	C-HEMBA1004982	2660	2661
35	HEMBA1005070	C-HEMBA1005070	2662	2663
	HEMBA1005084	C-HEMBA1005084	2664	2665
	HEMBA1005145	C-HEMBA1005145	2666	2667
	HEMBA1005430	C-HEMBA1005430	2668	2669
	HEMBA1005449	C-HEMBA1005449	2670	2671
40	HEMBA1005489	C-HEMBA1005489	2672	2673
	HEMBA1005522	C-HEMBA1005522	2674	2675
	HEMBA1005545	C-HEMBA1005545	2676	2677
	HEMBA1005698	C-HEMBA1005698	2678	2679
	HEMBA1005913	C-HEMBA1005913	2680	
45	HEMBA1005929	C-HEMBA1005929	2681	2682
	HEMBA1005945	C-HEMBA1005945	2683	2684
	HEMBA1006016	C-HEMBA1006016	2685	
	HEMBA1006171	C-HEMBA1006171	2686	2687
	HEMBA1006299	C-HEMBA1006299	2688	2689
50	HEMBA1006311	C-HEMBA1006311	2690	2691
	HEMBA1006335	C-HEMBA1006335	2692	2693
	HEMBA1006430	C-HEMBA1006430	2694	2695
	HEMBA1006482	C-HEMBA1006482	2696	2697
55	HEMBA1006572	C-HEMBA1006572	2698	2699
	HEMBA1006707	C-HEMBA1006707	2700	2701

EP 1 130 094 A2

	HEMBA1006724	C-HEMBA1006724	2702	2703
5	HEMBA1006902	C-HEMBA1006902	2704	2705
	HEMBA1006916	C-HEMBA1006916	2706	2707
	HEMBA1006960	C-HEMBA1006960	2708	2709
	HEMBA1007013	C-HEMBA1007013	2710	2711
	HEMBA1007057	C-HEMBA1007057	2712	2713
10	HEMBA1007241	C-HEMBA1007241	2714	
	HEMBA1007291	C-HEMBA1007291	2715	2716
	HEMBA1007332	C-HEMBA1007332	2717	
	HEMBB1000276	C-HEMBB1000276	2718	
	HEMBB1000447	C-HEMBB1000447	2719	2720
15	HEMBB1000642	C-HEMBB1000642	2721	
	HEMBB1000668	C-HEMBB1000668	2722	2723
	HEMBB1000679	C-HEMBB1000679	2724	2725
	HEMBB1000881	C-HEMBB1000881	2726	2727
	HEMBB1000905	C-HEMBB1000905	2728	2729
20	HEMBB1001026	C-HEMBB1001026	2730	2731
	HEMBB1001048	C-HEMBB1001048	2732	2733
	HEMBB1001200	C-HEMBB1001200	2734	
	HEMBB1001407	C-HEMBB1001407	2735	2736
	HEMBB1001530	C-HEMBB1001530	2737	2738
25	HEMBB1001573	C-HEMBB1001573	2739	2740
	nnnnnnnnnnnn	C-nnnnnnnnnnnn	nnnn	nnnn
	HEMBB1001847	C-HEMBB1001847	2743	2744
	HEMBB1001978	C-HEMBB1001978	2745	2746
	HEMBB1002162	C-HEMBB1002162	2747	2748
30	HEMBB1002228	C-HEMBB1002228	2749	
	HEMBB1002245	C-HEMBB1002245	2750	2751
	HEMBB1002427	C-HEMBB1002427	2752	2753
	HEMBB1002465	C-HEMBB1002465	2754	2755
	HEMBB1002663	C-HEMBB1002663	2756	2757
35	HEMBB1002693	C-HEMBB1002693	2758	2759
	MAMMA1000046	C-MAMMA1000046	2760	
	MAMMA1000118	C-MAMMA1000118	2761	2762
	nnnnnnnnnnnn	C-nnnnnnnnnnnn	nnnn	nnnn
	MAMMA1000449	C-MAMMA1000449	2765	
40	MAMMA1000457	C-MAMMA1000457	2766	2767
	MAMMA1000591	C-MAMMA1000591	2768	2769
	MAMMA1000681	C-MAMMA1000681	2770	2771
	MAMMA1001043	C-MAMMA1001043	2772	2773
	MAMMA1001893	C-MAMMA1001893	2774	2775
45	NT2RM2000241	C-NT2RM2000241	2776	2777
	NT2RM2000306	C-NT2RM2000306	2778	2779
	NT2RM2000410	C-NT2RM2000410	2780	2781
	NT2RM2000423	C-NT2RM2000423	2782	2783
	NT2RM2000497	C-NT2RM2000497	2784	2785
50	NT2RM2000514	C-NT2RM2000514	2786	2787
	NT2RM2000622	C-NT2RM2000622	2788	2789
	NT2RM2001126	C-NT2RM2001126	2790	2791
	NT2RM2001902	C-NT2RM2001902	2792	2793
55	NT2RM2001939	C-NT2RM2001939	2794	2795
	NT2RM2001941	C-NT2RM2001941	2796	2797

EP 1 130 094 A2

	NT2RM4000198	C-NT2RM4000198	2798	2799
5	NT2RM4000284	C-NT2RM4000284	2800	2801
	NT2RM4000295	C-NT2RM4000295	2802	2803
	NT2RM4000326	C-NT2RM4000326	2804	2805
	NT2RM4000444	C-NT2RM4000444	2806	2807
	NT2RM4000587	C-NT2RM4000587	2808	2809
	NT2RM4000648	C-NT2RM4000648	2810	2811
10	NT2RM4000997	C-NT2RM4000997	2812	2813
	NT2RM4001321	C-NT2RM4001321	2814	2815
	NT2RM4001325	C-NT2RM4001325	2816	2817
	NT2RM4001735	C-NT2RM4001735	2818	2819
	NT2RM4002352	C-NT2RM4002352	2820	2821
15	NT2RP1000002	C-NT2RP1000002	2822	2823
	NT2RP1000050	C-NT2RP1000050	2824	2825
	NT2RP1000181	C-NT2RP1000181	2826	2827
	NT2RP1000261	C-NT2RP1000261	2828	2829
20	NT2RP1000300	C-NT2RP1000300	2830	2831
	NT2RP1000325	C-NT2RP1000325	2832	2833
	NT2RP1000448	C-NT2RP1000448	2834	2835
	NT2RP1000551	C-NT2RP1000551	2836	2837
	NT2RP1000579	C-NT2RP1000579	2838	2839
25	NT2RP1000613	C-NT2RP1000613	2840	2841
	NT2RP1000903	C-NT2RP1000903	2842	2843
	NT2RP1000981	C-NT2RP1000981	2844	2845
	NT2RP1001004	C-NT2RP1001004	2846	2847
	NT2RP1001020	C-NT2RP1001020	2848	2849
30	NT2RP1001563	C-NT2RP1001563	2850	2851
	NT2RP2000394	C-NT2RP2000394	2852	2853
	NT2RP2000479	C-NT2RP2000479	2854	2855
	NT2RP2000514	C-NT2RP2000514	2856	2857
35	NT2RP2000533	C-NT2RP2000533	2858	2859
	NT2RP2000649	C-NT2RP2000649	2860	2861
	NT2RP2000663	C-NT2RP2000663	2862	2863
	NT2RP2000694	C-NT2RP2000694	2864	2865
	NT2RP2000903	C-NT2RP2000903	2866	2867
	NT2RP2001480	C-NT2RP2001480	2868	2869
40	NT2RP2001495	C-NT2RP2001495	2870	2871
	NT2RP2001514	C-NT2RP2001514	2872	2873
	NT2RP2001529	C-NT2RP2001529	2874	2875
	NT2RP2001769	C-NT2RP2001769	2876	2877
45	NT2RP2001878	C-NT2RP2001878	2878	2879
	NT2RP2001903	C-NT2RP2001903	2880	2881
	NT2RP2001915	C-NT2RP2001915	2882	2883
	NT2RP2001956	C-NT2RP2001956	2884	2885
50	NT2RP2002063	C-NT2RP2002063	2886	2887
	NT2RP2002188	C-NT2RP2002188	2888	2889
	NT2RP2002232	C-NT2RP2002232	2890	2891
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EP 1 130 094 A2

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EP 1 130 094 A2

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EP 1 130 094 A2

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	OVARC1000439	C-OVARC1000439	3152	3153
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EP 1 130 094 A2

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EP 1 130 094 A2

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	THYRO1000580	C-THYRO1000580	3494	3495
	THYRO1000584	C-THYRO1000584	3496	3497
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50	THYRO1000795	C-THYRO1000795	3500	3501
	THYRO1000846	C-THYRO1000846	3502	3503
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55	THYRO1000999	C-THYRO1000999	3508	
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EP 1 130 094 A2

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	THYRO1001523	C-THYRO1001523	3537	3538
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	Y79AA1000426	C-Y79AA1000426	3557	3558
	Y79AA1000521	C-Y79AA1000521	3559	3560
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	Y79AA1001328	C-Y79AA1001328	3585	3586
	Y79AA1001430	C-Y79AA1001430	3587	3588
	Y79AA1002022	C-Y79AA1002022	3589	3590
45	BNGH41000020	C-BNGH41000020	3595	3596
	BNGH41000091	C-BNGH41000091	3597	3598
	HEMBA1000462	C-HEMBA1000462	3599	3600
	HEMBA1000477	C-HEMBA1000477	3601	3602
50	HEMBA1000671	C-HEMBA1000671	3603	3604
	HEMBA1000732	C-HEMBA1000732	3605	3606
	HEMBA1000835	C-HEMBA1000835	3607	3608
	HEMBA1000875	C-HEMBA1000875	3609	
	HEMBA1001184	C-HEMBA1001184	3610	
55	HEMBA1001272	C-HEMBA1001272	3611	
	HEMBA1001296	C-HEMBA1001296	3612	

EP 1 130 094 A2

	HEMBA1002048	C-HEMBA1002048	3613	3614
5	HEMBA1002985	C-HEMBA1002985	3615	3616
	HEMBA1003120	C-HEMBA1003120	3617	3618
	HEMBA1003497	C-HEMBA1003497	3619	3620
	HEMBA1004007	C-HEMBA1004007	3621	
	HEMBA1004085	C-HEMBA1004085	3622	3623
10	HEMBA1004785	C-HEMBA1004785	3624	3625
	HEMBA1004952	C-HEMBA1004952	3626	
	HEMBA1004971	C-HEMBA1004971	3627	
	HEMBA1005230	C-HEMBA1005230	3628	
	HEMBA1005246	C-HEMBA1005246	3629	3630
15	HEMBA1005267	C-HEMBA1005267	3631	3632
	HEMBA1006276	C-HEMBA1006276	3633	
	HEMBA1006357	C-HEMBA1006357	3634	3635
	HEMBA1006517	C-HEMBA1006517	3636	3637
	HEMBA1006544	C-HEMBA1006544	3638	3639
20	HEMBA1006749	C-HEMBA1006749	3640	3641
	HEMBA1006770	C-HEMBA1006770	3642	3643
	HEMBA1006912	C-HEMBA1006912	3644	
	HEMBA1007063	C-HEMBA1007063	3645	3646
	HEMBB1000106	C-HEMBB1000106	3647	3648
25	HEMBB1000407	C-HEMBB1000407	3649	3650
	HEMBB1000542	C-HEMBB1000542	3651	3652
	HEMBB1001547	C-HEMBB1001547	3653	3654
	HEMBB1001959	C-HEMBB1001959	3655	3656
	HEMBB1002039	C-HEMBB1002039	3657	
30	HEMBB1002041	C-HEMBB1002041	3658	3659
	HEMBB1002051	C-HEMBB1002051	3660	3661
	HEMBB1002120	C-HEMBB1002120	3662	3663
	HEMBB1002302	C-HEMBB1002302	3664	3665
	HEMBB1002661	C-HEMBB1002661	3666	3667
35	MAMMA1000106	C-MAMMA1000106	3668	3669
	MAMMA1000141	C-MAMMA1000141	3670	3671
	MAMMA1000204	C-MAMMA1000204	3672	3673
	MAMMA1000226	C-MAMMA1000226	3674	3675
	MAMMA1000403	C-MAMMA1000403	3676	3677
40	MAMMA1000473	C-MAMMA1000473	3678	3679
	MAMMA1000496	C-MAMMA1000496	3680	3681
	MAMMA1000528	C-MAMMA1000528	3682	
	MAMMA1000614	C-MAMMA1000614	3683	3684
	MAMMA1000652	C-MAMMA1000652	3685	
45	MAMMA1000706	C-MAMMA1000706	3686	3687
	MAMMA1000788	C-MAMMA1000788	3688	3689
	MAMMA1000810	C-MAMMA1000810	3690	3691
	MAMMA1000814	C-MAMMA1000814	3692	3693
	MAMMA1000881	C-MAMMA1000881	3694	3695
50	MAMMA1000986	C-MAMMA1000986	3696	3697
	MAMMA1000994	C-MAMMA1000994	3698	3699
	MAMMA1001141	C-MAMMA1001141	3700	3701
	MAMMA1001150	C-MAMMA1001150	3702	3703
55	MAMMA1001237	C-MAMMA1001237	3704	3705
	MAMMA1001284	C-MAMMA1001284	3706	3707

EP 1 130 094 A2

	MAMMA1001310	C-MAMMA1001310	3708	3709
5	MAMMA1001344	C-MAMMA1001344	3710	3711
	MAMMA1001418	C-MAMMA1001418	3712	3713
	MAMMA1001532	C-MAMMA1001532	3714	3715
	MAMMA1001615	C-MAMMA1001615	3716	3717
10	MAMMA1001623	C-MAMMA1001623	3718	3719
	MAMMA1001634	C-MAMMA1001634	3720	3721
	MAMMA1001957	C-MAMMA1001957	3722	3723
	MAMMA1001978	C-MAMMA1001978	3724	3725
15	MAMMA1002070	C-MAMMA1002070	3726	3727
	MAMMA1002080	C-MAMMA1002080	3728	3729
	MAMMA1002087	C-MAMMA1002087	3730	3731
	MAMMA1002095	C-MAMMA1002095	3732	3733
	MAMMA1002128	C-MAMMA1002128	3734	3735
20	MAMMA1002142	C-MAMMA1002142	3736	3737
	MAMMA1002165	C-MAMMA1002165	3738	3739
	MAMMA1002205	C-MAMMA1002205	3740	
	MAMMA1002234	C-MAMMA1002234	3741	3742
	MAMMA1002586	C-MAMMA1002586	3743	3744
	MAMMA1002633	C-MAMMA1002633	3745	3746
	MAMMA1003126	C-MAMMA1003126	3747	3748
25	NT2RM1000580	C-NT2RM1000580	3749	3750
	NT2RM1000858	C-NT2RM1000858	3751	3752
	NT2RM2000565	C-NT2RM2000565	3753	3754
	NT2RM2000582	C-NT2RM2000582	3755	
	NT2RM2000589	C-NT2RM2000589	3756	3757
30	NT2RM2000632	C-NT2RM2000632	3758	3759
	NT2RM2000773	C-NT2RM2000773	3760	
	NT2RM2001558	C-NT2RM2001558	3761	3762
	NT2RM2001626	C-NT2RM2001626	3763	3764
	NT2RM2001643	C-NT2RM2001643	3765	3766
35	NT2RM2001738	C-NT2RM2001738	3767	3768
	NT2RM2001792	C-NT2RM2001792	3769	3770
	NT2RM2001818	C-NT2RM2001818	3771	3772
	NT2RM4000100	C-NT2RM4000100	3773	3774
40	NT2RM4000115	C-NT2RM4000115	3775	3776
	NT2RM4000417	C-NT2RM4000417	3777	3778
	NT2RM4000593	C-NT2RM4000593	3779	3780
	NT2RM4000761	C-NT2RM4000761	3781	3782
	NT2RM4000965	C-NT2RM4000965	3783	3784
45	NT2RM4001377	C-NT2RM4001377	3785	3786
	NT2RM4001768	C-NT2RM4001768	3787	3788
	NT2RM4001843	C-NT2RM4001843	3789	3790
	NT2RP1000239	C-NT2RP1000239	3791	3792
	NT2RP1000465	C-NT2RP1000465	3793	3794
50	NT2RP1000468	C-NT2RP1000468	3795	3796
	NT2RP1000679	C-NT2RP1000679	3797	3798
	NT2RP1000740	C-NT2RP1000740	3799	3800
	NT2RP1001031	C-NT2RP1001031	3801	3802
	NT2RP2000178	C-NT2RP2000178	3803	3804
55	NT2RP2000240	C-NT2RP2000240	3805	
	NT2RP2000447	C-NT2RP2000447	3806	3807

EP 1 130 094 A2

5	NT2RP2000610	C-NT2RP2000610	3808	3809
	NT2RP2000616	C-NT2RP2000616	3810	3811
	NT2RP2000712	C-NT2RP2000712	3812	3813
	NT2RP2000739	C-NT2RP2000739	3814	3815
	NT2RP2000818	C-NT2RP2000818	3816	3817
10	NT2RP2001200	C-NT2RP2001200	3818	3819
	NT2RP2001223	C-NT2RP2001223	3820	3821
	NT2RP2001276	C-NT2RP2001276	3822	3823
	NT2RP2001388	C-NT2RP2001388	3824	3825
	NT2RP2001469	C-NT2RP2001469	3826	3827
15	NT2RP2001562	C-NT2RP2001562	3828	3829
	NT2RP2001662	C-NT2RP2001662	3830	3831
	NT2RP2001755	C-NT2RP2001755	3832	3833
	NT2RP2001817	C-NT2RP2001817	3834	3835
	NT2RP2001948	C-NT2RP2001948	3836	3837
20	NT2RP2002015	C-NT2RP2002015	3838	3839
	NT2RP2003390	C-NT2RP2003390	3840	3841
	NT2RP2003664	C-NT2RP2003664	3842	3843
	NT2RP2003940	C-NT2RP2003940	3844	3845
	NT2RP2004069	C-NT2RP2004069	3846	3847
	NT2RP2004108	C-NT2RP2004108	3848	3849
25	nnnnnnnnnnnn	C-nnnnnnnnnnnnn	3850	3851
	NT2RP2005069	C-NT2RP2005069	3852	3853
	NT2RP2005378	C-NT2RP2005378	3854	3855
	NT2RP2005391	C-NT2RP2005391	3856	3857
	NT2RP2005597	C-NT2RP2005597	3858	3859
30	NT2RP2005666	C-NT2RP2005666	3860	3861
	NT2RP2006004	C-NT2RP2006004	3862	3863
	NT2RP2006092	C-NT2RP2006092	3864	3865
	NT2RP2006134	C-NT2RP2006134	3866	3867
35	NT2RP3000011	C-NT2RP3000011	3868	3869
	NT2RP3000022	C-NT2RP3000022	3870	3871
	NT2RP3000171	C-NT2RP3000171	3872	3873
	NT2RP3000304	C-NT2RP3000304	3874	3875
	NT2RP3000378	C-NT2RP3000378	3876	3877
40	NT2RP3000444	C-NT2RP3000444	3878	3879
	NT2RP3000645	C-NT2RP3000645	3880	3881
	NT2RP3000676	C-NT2RP3000676	3882	3883
	NT2RP3000677	C-NT2RP3000677	3884	3885
	NT2RP3000789	C-NT2RP3000789	3886	3887
45	NT2RP3000818	C-NT2RP3000818	3888	3889
	NT2RP3000838	C-NT2RP3000838	3890	3891
	NT2RP3000921	C-NT2RP3000921	3892	3893
	NT2RP3001159	C-NT2RP3001159	3894	3895
	NT2RP3001271	C-NT2RP3001271	3896	3897
50	NT2RP3001542	C-NT2RP3001542	3898	3899
	NT2RP3001685	C-NT2RP3001685	3900	3901
	NT2RP3001976	C-NT2RP3001976	3902	3903
	NT2RP3002015	C-NT2RP3002015	3904	3905
55	NT2RP3002281	C-NT2RP3002281	3906	3907
	NT2RP3002286	C-NT2RP3002286	3908	3909
	NT2RP3002324	C-NT2RP3002324	3910	3911

EP 1 130 094 A2

	NT2RP3002353	C-NT2RP3002353	3912	3913
5	NT2RP3002571	C-NT2RP3002571	3914	3915
	NT2RP3002664	C-NT2RP3002664	3916	3917
	NT2RP3002737	C-NT2RP3002737	3918	3919
	NT2RP3002887	C-NT2RP3002887	3920	3921
10	NT2RP3002900	C-NT2RP3002900	3922	3923
	NT2RP3002983	C-NT2RP3002983	3924	3925
	NT2RP3003473	C-NT2RP3003473	3926	3927
	NT2RP3003532	C-NT2RP3003532	3928	3929
15	NT2RP3004025	C-NT2RP3004025	3930	3931
	NT2RP3004067	C-NT2RP3004067	3932	3933
	NT2RP3004119	C-NT2RP3004119	3934	3935
	NT2RP3004294	C-NT2RP3004294	3936	3937
20	NT2RP3004345	C-NT2RP3004345	3938	3939
	NT2RP4000634	C-NT2RP4000634	3940	3941
	NT2RP4001001	C-NT2RP4001001	3942	3943
	NT2RP4001877	C-NT2RP4001877	3944	3945
25	NT2RP4001879	C-NT2RP4001879	3946	3947
	NT2RP4002187	C-NT2RP4002187	3948	3949
	NT2RP4002451	C-NT2RP4002451	3950	3951
	NT2RP4002750	C-NT2RP4002750	3952	3953
30	OVARC1000003	C-OVARC1000003	3954	3955
	OVARC1000313	C-OVARC1000313	3956	3957
	OVARC1000331	C-OVARC1000331	3958	3959
	OVARC1000553	C-OVARC1000553	3960	3961
	OVARC1000873	C-OVARC1000873	3962	3963
35	OVARC1000995	C-OVARC1000995	3964	
	OVARC1001260	C-OVARC1001260	3965	
	OVARC1001336	C-OVARC1001336	3966	3967
	OVARC1001570	C-OVARC1001570	3968	3969
40	OVARC1001607	C-OVARC1001607	3970	3971
	OVARC1001833	C-OVARC1001833	3972	3973
45	OVARC1001952	C-OVARC1001952	3974	3975
	PLACE1000986	C-PLACE1000986	3976	
	PLACE1003407	C-PLACE1003407	3977	3978
	PLACE1004078	C-PLACE1004078	3979	3980
50	PLACE1004492	C-PLACE1004492	3981	3982
	PLACE1005539	C-PLACE1005539	3983	3984
	PLACE1005569	C-PLACE1005569	3985	3986
	PLACE1005601	C-PLACE1005601	3987	
	PLACE1005745	C-PLACE1005745	3988	3989
55	PLACE1005815	C-PLACE1005815	3990	3991
	PLACE1005927	C-PLACE1005927	3992	3993
	PLACE1006071	C-PLACE1006071	3994	3995
	PLACE1006073	C-PLACE1006073	3996	3997
	PLACE1006079	C-PLACE1006079	3998	3999
	PLACE1006786	C-PLACE1006786	4000	
	PLACE1007077	C-PLACE1007077	4001	4002
	PLACE1007971	C-PLACE1007971	4003	
	PLACE1008282	C-PLACE1008282	4004	4005
	PLACE1008359	C-PLACE1008359	4006	4007
	PLACE1008744	C-PLACE1008744	4008	4009

EP 1 130 094 A2

	PLACE1010445	C-PLACE1010445	4010	4011
	PLACE1010713	C-PLACE1010713	4012	4013
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	PLACE1011181	C-PLACE1011181	4016	4017
	PLACE1011364	C-PLACE1011364	4018	4019
10	PLACE3000181	C-PLACE3000181	4020	4021
	SKNMC1000014	C-SKNMC1000014	4022	4023
	SKNMC1000082	C-SKNMC1000082	4024	4025
	THYRO1000964	C-THYRO1000964	4026	4027
	THYRO1001242	C-THYRO1001242	4028	4029
	THYRO1001608	C-THYRO1001608	4030	4031
15	THYRO1001641	C-THYRO1001641	4032	4033
	THYRO1001770	C-THYRO1001770	4034	4035
	Y79AA1000030	C-Y79AA1000030	4036	4037
	Y79AA1001212	C-Y79AA1001212	4038	4039
	Y79AA1001426	C-Y79AA1001426	4040	4041
20	Y79AA1001427	C-Y79AA1001427	4042	4043
	Y79AA1001523	C-Y79AA1001523	4044	4045
	Y79AA1001530	C-Y79AA1001530	4046	4047
	Y79AA1001592	C-Y79AA1001592	4048	4049
	Y79AA1001727	C-Y79AA1001727	4050	4051
25	Y79AA1001787	C-Y79AA1001787	4052	4053
	Y79AA1001793	C-Y79AA1001793	4054	4055
	Y79AA1001795	C-Y79AA1001795	4056	4057
	Y79AA1001799	C-Y79AA1001799	4058	4059
	Y79AA1001803	C-Y79AA1001803	4060	4061
30	Y79AA1001863	C-Y79AA1001863	4062	4063
	Y79AA1002058	C-Y79AA1002058	4064	4065
	Y79AA1002121	C-Y79AA1002121	4066	4067
	Y79AA1002213	C-Y79AA1002213	4068	4069
35	Y79AA1002373	C-Y79AA1002373	4070	4071
	Y79AA1002376	C-Y79AA1002376	4072	4073
	Y79AA1002378	C-Y79AA1002378	4074	4075
	Y79AA1002381	C-Y79AA1002381	4076	4077
	BNGH41000087	C-BNGH41000087	4078	4079
40	HEMBA1001886	C-HEMBA1001886	4080	4081
	HEMBA1004067	C-HEMBA1004067	4082	4083
	HEMBA1007226	C-HEMBA1007226	4084	4085
	HEMBB1000309	C-HEMBB1000309	4086	4087
	HEMBB1000567	C-HEMBB1000567	4088	4089
45	MAMMA1000102	C-MAMMA1000102	4090	4091
	MAMMA1001066	C-MAMMA1001066	4092	4093
	MAMMA1001094	C-MAMMA1001094	4094	4095
	MAMMA1001609	C-MAMMA1001609	4096	4097
	MAMMA1001901	C-MAMMA1001901	4098	
50	MAMMA1002091	C-MAMMA1002091	4099	4100
	NT2RM1000462	C-NT2RM1000462	4101	4102
	NT2RM1000542	C-NT2RM1000542	4103	4104
	NT2RM1000789	C-NT2RM1000789	4105	4106
	NT2RM1000855	C-NT2RM1000855	4107	4108
55	NT2RM1000899	C-NT2RM1000899	4109	4110

5	NT2RP2000092	C-NT2RP2000092	4111	4112
	NT2RP2001538	C-NT2RP2001538	4113	4114
	NT2RP2001921	C-NT2RP2001921	4115	4116
	NT2RP2003138	C-NT2RP2003138	4117	4118
10	NT2RP2003302	C-NT2RP2003302	4119	4120
	NT2RP2003950	C-NT2RP2003950	4121	4122
	NT2RP2005535	C-NT2RP2005535	4123	4124
15	NT2RP2005774	C-NT2RP2005774	4125	4126
	NT2RP3000148	C-NT2RP3000148	4127	4128
	NT2RP3000232	C-NT2RP3000232	4129	4130
20	NT2RP3000427	C-NT2RP3000427	4131	
	NT2RP3000652	C-NT2RP3000652	4132	4133
	NT2RP3001650	C-NT2RP3001650	4134	4135
	NT2RP3002409	C-NT2RP3002409	4136	
25	NT2RP3002411	C-NT2RP3002411	4137	4138
	NT2RP3003448	C-NT2RP3003448	4139	
	NT2RP4002715	C-NT2RP4002715	4140	4141
	OVARC1000307	C-OVARC1000307	4142	4143
	PLACE1000907	C-PLACE1000907	4144	4145
30	PLACE1007081	C-PLACE1007081	4146	4147
	PLACE1010011	C-PLACE1010011	4148	4149
	PLACE3000213	C-PLACE3000213	4150	4151
	PLACE4000354	C-PLACE4000354	4152	4153
35	PLACE4000455	C-PLACE4000455	4154	
	THYRO1000776	C-THYRO1000776	4155	4156
	THYRO1001593	C-THYRO1001593	4157	4158
	Y79AA1000750	C-Y79AA1000750	4159	4160
40	Y79AA1000888	C-Y79AA1000888	4161	4162
	Y79AA1002129	C-Y79AA1002129	4163	4164
	Y79AA1002334	C-Y79AA1002334	4165	4166
	MAMMA1002224	C-MAMMA1002224	4167	
45	NT2RP1000271	C-NT2RP1000271	4168	4169
	NT2RP3000481	C-NT2RP3000481	4170	4171
	NT2RP3004481	C-NT2RP3004481	4172	4173
	HEMBA1006658	C-HEMBA1006658	4174	4175
	NT2RP2006099	C-NT2RP2006099	4176	4177
	NT2RP2006580	C-NT2RP2006580	4178	4179

Homology search result 1

50 [0287] The result of the homology search in the SwissProt using the representative sequences of the 5'-ends.

55 Indicated are from the top,
the name of the representative sequence of the cluster,
definition of the top hit data,
the P-value: the length of the sequence used for comparison (nucleotide):similarity (%),
the organism of which the top hit data is obtained,
the Accession No. of the top hit data.

[0288] Homology search results of the representative sequences of the 5'-end cluster to the data in SwissProt database are shown only for the representative sequences of the cluster from which clones were selected based on the homology search results.

[0289] The P-value is the score which is determined by taking into account the statistic probability of occurrence between the two sequences, and generally low score reflects high similarity. (Altschul, S.F., Gish, W., Miller, W., Myers, E.W. & Lipman, D.J. (1990) "Basic local alignment search tool." J. Mol. Biol. 215:403-410; Gish, W. & States, D.J. (1993) "Identification of protein coding regions by database similarity search." Nature Genet. 3:266-272).

HRIFA000016a

10 GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1.8 PRECURSOR (GRP 1.8).

9.2e-05:178:32

PHASEOLUS VULGARIS (KIDNEY BEAN) (FRENCH BEAN).

P10496

HRIFA000071a

15 CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).

5.8e-05:194:29

PLASMODIUM SIMIUM.

Q03110

HRIFA000116a

20 HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III.

6.2e-06:83:27

CAENORHABDITIS ELEGANS.

P34679

HRIFA000123a

25 PATHOGENESIS-RELATED PROTEIN 1 PRECURSOR (PR-1).

6.2e-08:89:34

ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).

P33154

HRIFA000264a

30 PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.

1.4e-06:231:34

GALLUS GALLUS (CHICKEN).

P02457

HRIFA000327a

35 ATP-BINDING CASSETTE TRANSPORTER 1.

2.0e-16:238:31

MUS MUSCULUS (MOUSE).

P41233

HRIFA000415a

40 PROLINE-RICH PROTEIN MP-2 PRECURSOR.

3.6e-06:120:35

MUS MUSCULUS (MOUSE).

P05142

HRIFA000432a

50 PUTATIVE GENERAL NEGATIVE REGULATOR OF TRANSCRIPTION C16C9.04C.

2.2e-21:86:52

SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).

Q09818

HRIFA000446a

894
55 HYPOTHETICAL 64.8 KD PROTEIN IN GDI1-COX15 INTERGENIC REGION.

2.5e-09:138:34
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P40085

5 HRIFA000553a
CARTILAGE MATRIX PROTEIN PRECURSOR (MATRILIN-1).
1.7e-27:117:48
GALLUS GALLUS (CHICKEN).
P05099

10 HRIFA000564a
ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN (STOMATIN) (PROTEIN 7.2B).
2.9e-28:163:38
MUS MUSCULUS (MOUSE).
P54116

15 HRIFA000631a
ZINC FINGER PROTEIN 140.
8.2e-45:155:47
HOMO SAPIENS (HUMAN).
P52738

20 HRIFA000683a
FIBRILLIN 1 PRECURSOR.
4.8e-18:77:46
HOMO SAPIENS (HUMAN).
P35555

25 HRIFA000695a
"SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEP-TIDE IB-6" PEPTIDE P-H].
4.0e-06:105:33
HOMO SAPIENS (HUMAN).
P04280

30 HRIFA000776a
FIBRILLIN 2 PRECURSOR.
1.6e-42:214:44
HOMO SAPIENS (HUMAN).
P35556

35 HRIFA000814a
ZINC FINGER PROTEIN 133.
4.4e-16:49:87
HOMO SAPIENS (HUMAN).
P52736

40 HRIFA000845a
PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.
6.0e-06:172:34
MUS MUSCULUS (MOUSE).
P11087

45 HRIFA001099a
CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-5 (FRAGMENT).
0.92:38:34
HOMO SAPIENS (HUMAN).
P18849

- 5 HRIFA001132a
AGRIN PRECURSOR.
1.3e-26:239:32
GALLUS GALLUS (CHICKEN).
P31696
- 10 HRIFA001138a
CARTILAGE OLIGOMERIC MATRIX PROTEIN PRECURSOR (COMP).
5.9e-114:147:83
HOMO SAPIENS (HUMAN).
P49747
- 15 HRIFA001200a
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (P135 PROTEIN) (IER 2.9/ER2.6).
0.035:119:34
BOVINE HERPESVIRUS TYPE 1 (STRAIN JURA).
P29128
- 20 HRIFA001337a
LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR (LDL RECEPTOR).
2.4e-17:98:42
CRICETULUS GRISEUS (CHINESE HAMSTER).
P35950
- 25 HRIFA001341a
NEUROFILAMENT TRIPLET L PROTEIN (68 KD NEUROFILAMENT PROTEIN) (NF-L)
(NF68).
1.2e-102:248:87
RATTUS NORVEGICUS (RAT).
P19527
- 30 HRIFA001413a
BACTENECIN 7 PRECURSOR (BAC7) (PR-59).
0.0032:33:63
35 BOS TAURUS (BOVINE).
P19661
- 35 HRIFA001439a
B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).
0.00031:34:61
HOMO SAPIENS (HUMAN).
P20931
- 40 HRIFA001489a
PROBABLE G PROTEIN-COUPLED RECEPTOR APJ.
8.4e-65:105:72
HOMO SAPIENS (HUMAN).
P35414
- 45 HRIFA001558a
HISTIDINE-RICH GLYCOPROTEIN PRECURSOR.
0.0048:80:31
PLASMODIUM LOPHURAE.
P04929
- 50 HRIFA001712a
PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).
2.5e-19:169:31

THERMOMONOSPORA CURVATA.
P49695

- 5 HRIFA001720a
ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).
1.4e-94:273:64
HOMO SAPIENS (HUMAN).
Q03923
- 10 HRIFA001866a
EARLY ANTIGEN PROTEIN D (EA-D).
0.10:93:34
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03191
- 15 HRIFA001942a
"PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE 1 PRECURSOR (EC 1.14.11.4) (LYSYL HYDROXYLASE 1) (LH1)." 4.7e-12:140:30
GALLUS GALLUS (CHICKEN).
P24802
- 20 HRIFA001971a
HYPOTHETICAL 46.3 KD PROTEIN IN PTA1-CDC24 INTERGENIC REGION.
2.5e-10:86:30
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P39727
- 25 HRIFA001972a
LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN).
0.10:100:34
MUS MUSCULUS (MOUSE).
P19137
- 30 HRIFA001975a
ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7).
6.5e-30:243:33
MUS MUSCULUS (MOUSE).
P21836
- 35 HRIFA001984a
"PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE 1 PRECURSOR (EC 1.14.11.4) (LYSYL HYDROXYLASE 1) (LH1)." 1.2e-11:140:30
GALLUS GALLUS (CHICKEN).
P24802
- 40 HRIFA002063a
GNS1 PROTEIN.
1.3e-05:127:30
SACCHAROMYCES CEREVISIAE (BAKERS YEAST).
P25358
- 45 HRIFA002102a
MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).
2.9e-07:241:30
HOMO SAPIENS (HUMAN).
Q02817

- 5 HRIFA002284a
ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP33).
3.8e-05:104:34
RATTUS NORVEGICUS (RAT).
P04474
- 10 HRIFA002309a
PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).
1.5e-08:110:37
THERMOMONOSPORA CURVATA.
P49695
- 15 HRIFA002384a
GAP JUNCTION ALPHA-6 PROTEIN (CONNEXIN 45) (CX45).
1.8e-31:94:42
HOMO SAPIENS (HUMAN).
P36383
- 20 HRIFA002503a
N-ACETYLGLUCOSAMINE SYNTHASE (EC 2.4.1.90) (N-ACETYLGLUCOSAMINE (BETA 1→4)GALACTOSYL-TRANSFERASE) (EC 2.4.1.38) (LACTOSE SYNTHASE A PROTEIN (EC 2.4.1.22)) (GALACTOSYLTRANSFERASE) (GT).
6.1e-92:246:67
MUS MUSCULUS (MOUSE).
P15535
- 25 HRIFA002689a
TRANSCRIPTION FACTOR GATA-6 (GATA BINDING FACTOR-6) (DNA BINDING PROTEIN GATA-GT2).
0.38:49:34
RATTUS NORVEGICUS (RAT).
P46153
- 30 HRIFA002694a
ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR.
4.7e-05:93:37
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
P40602
- 35 HRIFA002743a
BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (EC 3.4.24.-) (BMP-1).
1.2e-23:216:31
HOMO SAPIENS (HUMAN).
P13497
- 40 HRIFA002762a
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
5.1e-09:129:41
MUS MUSCULUS (MOUSE).
P05142
- 45 HRIFA002766a
FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN).
1.8e-12:139:34
HOMO SAPIENS (HUMAN).
Q06828
- 50 HRIFA002787a
PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR.

- 1.6e-10:124:37
HOMO SAPIENS (HUMAN).
P08123
- 5 HRIFA002805a
ZINC FINGER PROTEIN 140.
3.6e-23:43:74
HOMO SAPIENS (HUMAN).
P52738
- 10 HRIFA002891a
"FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90)." 2.0e-41:239:39
MUS MUSCULUS (MOUSE).
Q08878
- 15 HRIFA002919a
BEM46 PROTEIN (FRAGMENT). 1.0e-12:171:32
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
P54069
- 20 HRIFA002980a
LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR (LRP) (ALPHA-2-MAC-ROGLOBULIN RECEPTOR) (A2MR). 8.7e-32:202:37
GALLUS GALLUS (CHICKEN).
P98157
- 25 HRIFA003055a
PROLINE-RICH PROTEIN MP-2 PRECURSOR. 3.4e-08:175:29
MUS MUSCULUS (MOUSE).
P05142
- 30 HRIFA003063a
B-CELL LYMPHOMA 6 PROTEIN HOMOLOG. 2.8e-15:123:34
MUS MUSCULUS (MOUSE).
P41183
- 35 HRIFA003093a
PROLINE-RICH PROTEIN MP-2 PRECURSOR. 1.3e-11:142:37
MUS MUSCULUS (MOUSE).
P05142
- 40 HRIFA003340a
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (ALPHA-0 PROTEIN). 2.3e-05:200:31
HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).
P08393
- 45 HRIFA003357a
GLUCOSE REPRESSION MEDIATOR PROTEIN. 0.0023:190:26
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P14922

- 5 HRIFA003402a
COLLAGEN ALPHA 1(II) CHAIN (FRAGMENTS).
3.6e-05:194:27
BOS TAURUS (BOVINE).
P02459
- 10 HRIFA003504a
CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).
1.4e-08:150:33
DROSOPHILA MELANOGASTER (FRUIT FLY).
P33450
- 15 HRIFA003592a
CD9 ANTIGEN.
0.0053:24:70
BOS TAURUS (BOVINE).
P30932
- 20 HRIFA003635a
"MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ISOFORM 1 (EC 3.2.1.113) (MAN(9)-ALPHA-MANNOSIDASE)." 5.3e-45:239:43
- 25 DROSOPHILA MELANOGASTER (FRUIT FLY).
P53624
- 30 HRIFA003640a
PROCYCLIC FORM SPECIFIC POLYPEPTIDE A-BETA PRECURSOR (PROCYCLIN) (PARP A-BETA).
0.00018:28:64
TRYPANOSOMA BRUCEI BRUCEI.
P09791
- 35 HRIFA003883a
TRANSCRIPTIONAL REPRESSOR PROTEIN YY1 (YIN AND YANG 1) (YY-1) (DELTA TRANSCRIPTION FACTOR) (NF-E1) (UCR-MOTIF DNA-BINDING PROTEIN).
1.0:57:35
MUS MUSCULUS (MOUSE).
Q00899
- 40 HRIFA003892a
MULTIDRUG RESISTANCE PROTEIN 2 (MULTIDRUG-EFFLUX TRANSPORTER 2).
6.5e-08:144:25
- 45 BACILLUS SUBTILIS.
P39843
- 50 HRIFA003946a
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
1.4e-06:85:37
MUS MUSCULUS (MOUSE).
P05142
- 55 HRIFA004006a
ZINC FINGER PROTEIN 140.
6.2e-20:83:66
HOMO SAPIENS (HUMAN).
P52738

- 5 HRIFA004034a
 B-CELL LYMPHOMA 3-ENCODED PROTEIN (BCL-3 PROTEIN).
 1.4e-15:192:32
 HOMO SAPIENS (HUMAN).
 P20749
- 10 HRIFA004112a
 CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).
 7.2e-26:193:37
 DROSOPHILA MELANOGASTER (FRUIT FLY).
 P33450
- 15 HRIFA004162a
 ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN (STOMATIN) (PROTEIN 7.2B).
 3.6e-10:117:29
 MUS MUSCULUS (MOUSE).
 P54116
- 20 HRIFA004401a
 LACTOSE OPERON REPRESSOR.
 1.1e-07:36:86
 ESCHERICHIA COLI.
 P03023
- 25 HRIFA004426a
 ATRIAL GLAND-SPECIFIC ANTIGEN PRECURSOR (AGSA).
 5.1e-11:85:41
 APLYSIA CALIFORNICA (CALIFORNIA SEA HARE).
 P15287
- 30 HRIFA004490a
 BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE) (ACID BETA-GALACTOSIDASE).
 5.3e-19:101:44
 MUS MUSCULUS (MOUSE).
 P23780
- 35 HRIFA004523a
 GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).
 2.6e-36:180:43
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 P43636
- 40 HRIFA004663a
 T-CELL-SPECIFIC TRANSCRIPTION FACTOR 1 (TCF-1) (T-CELL FACTOR 1) (TRANSCRIPTION FACTOR-7).
 1.2e-40:112:75
 MUS MUSCULUS (MOUSE).
 Q00417
- 45 HRIFA004696a
 PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.
 1.1e-62:145:84
 CANIS FAMILIARIS (DOG).
 P38377
- 50 HRIFA004714a
 HYPOTHETICAL 36.7 KD PROTEIN AH6.2 IN CHROMOSOME II.
 2.3e-50:127:54
 CAENORHABDITIS ELEGANS.

Q09201

- 5 HRIFA004745a
MITOCHONDRIAL RNA SPLICING PROTEIN MSR4.
5.0e-17:107:43
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P23500
- 10 HRIFA004780a
EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).
7.2e-07:142:30
ZEA MAYS (MAIZE).
P14918
- 15 HRIFA004919a
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1.8 PRECURSOR (GRP 1.8).
1.5e-25:156:46
PHASEOLUS VULGARIS (KIDNEY BEAN) (FRENCH BEAN).
P10496
- 20 HRIFA005072a
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN (CLONE W10-1) (FRAGMENT).
8.3e-05:24:62
LYCOPERSICON ESCULENTUM (TOMATO).
Q01157
- 25 HRIFA005102a
A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.
2.5e-07:188:31
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P32323
- 30 HRIFA005184a
CYTOCHROME B5.
3.4e-11:117:29
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P40312
- 35 HRIFA005214a
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (VMW118 PROTEIN).
5.9e-05:141:33
HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HG52).
P28284
- 40 HRIFA005231a
ORM1 PROTEIN.
1.7e-18:137:35
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53224
- 45 HRIFA005240a
ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).
6.3e-81:194:70
HOMO SAPIENS (HUMAN).
Q03923
- 50 HRIFA005255a
HYPOTHETICAL 57.1 KD PROTEIN IN MAP2-TEL1 INTERGENIC REGION.

- 1.5e-07:202:24
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 P38176
- 5 HRIFA005271a
 MITOCHONDRIAL PHOSPHATE CARRIER PROTEIN PRECURSOR.
 1.2e-55:86:81
 HOMO SAPIENS (HUMAN).
 Q00325
- 10 HRIFA005296a
 INSULIN PROMOTER FACTOR 1 (IPF-1) (ISLET/DUODENUM HOMEobox-1) (IDX-1) (SOMATOSTATIN
 TRANSACTIVATING FACTOR-1) (STF-1) (PANCREAS/DUODENUM HOMEobox-1) (GLUCOSE SENSITIVE
 FACTOR) (GSF).
 0.82:90:34
 HOMO SAPIENS (HUMAN).
 P52945
- 15 HRIFA005300a
 SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
 1.6e-07:178:30
 XENOPUS LAEVIS (AFRICAN CLAWED FROG).
 P17437
- 20 HRIFA005369a
 EBNA-1 NUCLEAR PROTEIN.
 2.3e-07:101:39
 EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
 P03211
- 25 HRIFA005372a
 CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN B) (NF-YB) (CAAT-
 BOX DNA BINDING PROTEIN SUBUNIT B).
 1.1e-14:97:38
 PETROMYZON MARINUS (SEA LAMPREY).
 P25210
- 30 HRIFA005392a
 SYNDECAN-2 PRECURSOR (FIBROGLYCAN) (HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN)
 (HSPG) (SYND2).
 1.3e-50:126:84
 HOMO SAPIENS (HUMAN).
 P34741
- 35 HRIFA005409a
 HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 (CAT-1) (CAT1) (SYSTEM Y+ BASIC AMINO ACID
 TRANSPORTER) (ECOTROPIC RETROVIRAL LEUKEMIA RECEPTOR HOMOLOG) (ERR) (ECOTROPIC RET-
 ROVIRUS RECEPTOR HOMOLOG).
 7.1e-66:197:64
 HOMO SAPIENS (HUMAN).
 P30825
- 40 HRIFA005420a
 INTERFERON-RELATED PROTEIN PC4 (TPA INDUCED SEQUENCE 7) (TIS7 PROTEIN).
 1.5e-33:221:41
 MUS MUSCULUS (MOUSE).
 P19182

- 5 HRIFA005438a
SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR (EC 1.3.5.1) (FP)
(FLAVOPROTEIN SUBUNIT OF COMPLEX II).
6.4e-71:175:68
HOMO SAPIENS (HUMAN).
P31040
- 10 HRIFA005462a
CARBONIC ANHYDRASE VI (EC 4.2.1.1) (SALIVARY) (CARBONATE DEHYDRATASE VI).
1.4e-19:137:37
OVIS ARIES (SHEEP).
P08060
- 15 HRIFA005500a
EBNA-1 NUCLEAR PROTEIN.
0.00042:54:50
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211
- 20 HRIFA005540a
CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-6 (FRAGMENT).
0.12:47:29
HOMO SAPIENS (HUMAN).
P18850
- 25 HRIFA005644a
VACUOLAR ATP SYNTHASE SUBUNIT AC45 PRECURSOR (EC 3.6.1.34) (V-ATPASE AC45 SUBUNIT).
1.2e-102:233:87
BOS TAURUS (BOVINE).
P40682
- 30 HRIFA005702a
CELL SURFACE GLYCOPROTEIN MUC18 PRECURSOR (MELANOMA-ASSOCIATED ANTIGEN MUC18)
(MELANOMA-ASSOCIATED ANTIGEN A32) (S-ENDO 1 ENDOTHELIAL- ASSOCIATED ANTIGEN) (CD146 AN-
TIGEN) (MELANOMA ADHESION MOLECULE).
8.7e-05:174:28
HOMO SAPIENS (HUMAN).
P43121
- 35 HRIFA005720a
F-SPONDIN PRECURSOR.
8.9e-12:155:31
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P35447
- 40 HRIFA005728a
SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-).
1.7e-05:126:29
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P08458
- 45 HRIFA005732a
PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).
4.4e-26:159:38
THERMOMONOSPORA CURVATA.
P49695
- 50 HRIFA005760a

EP 1 130 094 A2

FUCOSYLGlycoprotein ALPHA-N-ACETYLGLACTOSAMINYLTRANSFERASE (EC 2.4.1.40) (HISTO-BLOOD GROUP A TRANSFERASE) (A TRANSFERASE) / FUCOSYLGlycoprotein 3-ALPHA-GALACTOSYLTRANSFERASE (EC 2.4.1.37) (HISTO-BLOOD GROUP B TRANSFERASE) (B TRANSFERASE) (NAGAT).

3.8e-15:53:54

5 HOMO SAPIENS (HUMAN).

P16442

HRIFA005781a

ESTRADIOL 17 BETA-DEHYDROGENASE 3 (EC 1.1.1.62) (17-BETA-HSD 3) (TESTICULAR 17-BETA-HYDROXYSTEROID DEHYDROGENASE).

10 5.2e-47:228:47

HOMO SAPIENS (HUMAN).

P37058

15 HRIFA005944a

PROCOLLAGEN ALPHA 1(II) CHAIN PRECURSOR [CONTAINS: CHONDROCALCIN].

2.5e-06:142:35

MUS MUSCULUS (MOUSE).

P28481

20 HRIFA006183a

ZINC FINGER PROTEIN 136.

1.3e-42:129:62

HOMO SAPIENS (HUMAN).

25 P52737

HRIFA006250a

HOMEOTIC GENE REGULATOR (BRAHMA PROTEIN).

0.0038:75:37

30 DROSOPHILA MELANOGASTER (FRUIT FLY).

P25439

HRIFA006298a

EBNA-1 NUCLEAR PROTEIN.

35 1.4e-05:80:42

EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).

P03211

40 HRIFA006448a

SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).

8.5e-05:183:28

XENOPUS LAEVIS (AFRICAN CLAWED FROG).

P17437

45 HRIFA006494a

AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1) (TRANSIENT AXONAL GLYCOPROTEIN 1).

1.2e-18:201:33

HOMO SAPIENS (HUMAN).

Q02246

50 HRIFA006510a

CORNICHON PROTEIN.

6.0e-53:144:66

DROSOPHILA MELANOGASTER (FRUIT FLY).

55 P49858

HRIFA006566a

CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN B) (NF-YB) (CAAT-

5 BOX DNA BINDING PROTEIN SUBUNIT B).
 6.6e-15:97:38
 PETROMYZON MARINUS (SEA LAMPREY).
 P25210

10 HRIFA006572a
 PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.
 7.2e-05:158:29
 MUS MUSCULUS (MOUSE).
 P11087

15 HRIFA006586a
 HYPOTHETICAL 53.3 KD PROTEIN IN HXT8-CAN1 INTERGENIC REGION.
 1.3e-13:219:26
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 P39981

20 HRIFA006596a
 POTENTIAL CAAX PRENYL PROTEASE 1 (EC 3.4.24.-) (PRENYL PROTEIN- SPECIFIC ENDOPROTEASE 1)
 (PPSEP 1).
 7.2e-22:241:32
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
 Q10071

25 HRIFA006609a
 PANCREATIC HORMONE PRECURSOR (PANCREATIC POLYPEPTIDE) (PP).
 0.61:28:46
 "GALLUS GALLUS (CHICKEN), AND MELEAGRIS GALLOPAVO (COMMON TURKEY)." .
 P01306

30 HRIFA006633a
 COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR.
 7.8e-07:170:34
 HOMO SAPIENS (HUMAN).
 Q07092

35 HRIFA006642a
 AMALGAM PROTEIN PRECURSOR.
 1.5e-09:185:28
 DROSOPHILA MELANOGLASTER (FRUIT FLY).
 P15364

40 HRIFA006649a
 ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).
 1.7e-50:166:50
 HOMO SAPIENS (HUMAN).
 Q03923

45 HRIFA006667a
 ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).
 6.8e-45:180:43
 HOMO SAPIENS (HUMAN).
 Q03923

50 HRIFA006730a
 SYG1 PROTEIN.
 1.8e-14:164:35
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P40528

HRIFA006798a

SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).

5 0.22:149:34

XENOPUS LAEVIS (AFRICAN CLAWED FROG).

P17437

HRIFA006926a

10 SYNAPTAGMIN IV.

3.6e-19:168:38

RATTUS NORVEGICUS (RAT).

P50232

HRIFA007013a

MIC1 PROTEIN.

15 1.4e-13:115:38

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P53258

HRIFA007032a

20 CCAAT DISPLACEMENT PROTEIN (HOMEobox PROTEIN CLOX) (CLOX-1) (FRAGMENT).

0.00013:92:35

CANIS FAMILIARIS (DOG).

25 P39881

HRIFA007068a

EBNA-1 NUCLEAR PROTEIN.

30 7.0e-10:145:38

EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).

P03211

HRIFA007152a

35 TRANSCRIPTION FACTOR SOX-4.

0.90:47:44

HOMO SAPIENS (HUMAN).

Q06945

HRIFA007219a

40 THROMBOSPONDIN 3 PRECURSOR.

1.3e-105:209:88

HOMO SAPIENS (HUMAN).

P49746

HRIFA007228a

45 HYPOTHETICAL 53.3 KD PROTEIN IN HXT8-CAN1 INTERGENIC REGION.

2.3e-11:174:24

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P39981

50

HRIFA007243a

PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38).

3.0e-18:163:36

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

55 P39986

HRIFA007244a

EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).

4.2e-05:81:33

NICOTIANA TABACUM (COMMON TOBACCO).

P13983

5 HRIFA007256a

DEATH-ASSOCIATED PROTEIN KINASE 1 (EC 2.7.1.-) (DAP KINASE 1).

2.3e-77:186:75

HOMO SAPIENS (HUMAN).

P53355

10 HRIFA007262a

PAIRED AMPHIPATHIC HELIX PROTEIN.

1.3e-06:152:26

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P22579

15 HRIFA007352a

5'-TG-3'INTERACTING FACTOR (HOMEobox PROTEIN TGIF).

4.2e-36:146:57

20 HOMO SAPIENS (HUMAN).

Q15583

25 HRIFA007424a

F-SPONDIN PRECURSOR.

8.9e-34:84:89

RATTUS NORVEGICUS (RAT).

P35446

30 HRIFA007435a

PROTEIN KINASE CEK1 (EC 2.7.1.-).

1.0e-37:159:53

SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).

P38938

35 HRIFA007463a

HST1 PROTEIN (HOMOLOGOUS TO SIR2 PROTEIN 1).

4.8e-32:85:48

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P53685

40 HRIFA007493a

UBIQUITIN-CONJUGATING ENZYME E2-28.4 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN).

1.2e-47:171:56

45 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P33296

50 HRIFA007512a

EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).

8.0e-07:173:28

NICOTIANA TABACUM (COMMON TOBACCO).

P13983

55 HRIFA007532a

"CALPAIN P94, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEUTRAL PROTEINASE) (CANP) (P94 PROTEIN) (MUSCLE-SPECIFIC CALCIUM-ACTIVATED NEUTRAL PROTEASE 3 LARGE SUBUNIT)."

1.8e-10:110:37

HOMO SAPIENS (HUMAN).
P20807

5 HRIFA007547a
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (P135 PROTEIN) (IER 2.9/ER2.6).
0.068:51:45
BOVINE HERPESVIRUS TYPE 1 (STRAIN K22).
P29836

10 HRIFA007565a
COLLAGEN ALPHA 1(X) CHAIN PRECURSOR.
5.1e-08:121:37
HOMO SAPIENS (HUMAN).
Q03692

15 HRIFA007571a
ORM1 PROTEIN.
5.8e-17:106:36
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53224

20 HRIFA007659a
HYPOTHETICAL 51.5 KD PROTEIN D2024.3 IN CHROMOSOME IV.
2.5e-47:213:41
25 CAENORHABDITIS ELEGANS.
P49191

HRIFA007722a
HYPOTHETICAL 24.5 KD PROTEIN IN SAP185-BCK1 INTERGENIC REGION.
30 7.7e-13:146:32
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P40857

35 HRIFA007728a
EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).
9.1e-05:124:31
NICOTIANA TABACUM (COMMON TOBACCO).
P13983

40 HRIFA007745a
ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7) (ACHE).
7.0e-15:109:36
45 TORPEDO CALIFORNICA (PACIFIC ELECTRIC RAY).
P04058

HRIFA007829a
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN (CLONE W10-1) (FRAGMENT).
0.00045:16:68
50 LYCOPERSICON ESCULENTUM (TOMATO).
Q01157

HRIFA007909a
COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).
6.1e-06:173:34
55 BOS TAURUS (BOVINE).
P02453

HRIFA007985a

T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11).

0.00079:97:37

ORYCTOLAGUS CUNICULUS (RABBIT).

P06333

5

HRIFA008000a

"DIHYDROPYRIDINE-SENSITIVE L-TYPE, CALCIUM CHANNEL ALPHA-2/DELTA SUBUNITS PRECURSOR."

1.6e-37:165:42

ORYCTOLAGUS CUNICULUS (RABBIT).

10

P13806

HRIFA008174a

COLLAGEN 1(X) CHAIN PRECURSOR.

4.5e-05:215:28

15

BOS TAURUS (BOVINE).

P23206

20

HRIFA008186a

ESTRADIOL 17 BETA-DEHYDROGENASE 3 (EC 1.1.1.62) (17-BETA-HSD 3) (TESTICULAR 17-BETA-HYDROXYSTEROID DEHYDROGENASE).

2.1e-25:118:46

HOMO SAPIENS (HUMAN).

P37058

25

HRIFA008200a

ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT).

7.9e-17:139:36

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

30

P32802

35

HRIFA008212a

A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.

0.035:135:28

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P32323

40

HRIFA008252a

PROLINE-RICH PROTEIN MP-2 PRECURSOR.

0.00015:128:32

MUS MUSCULUS (MOUSE).

P05142

45

HRIFA008284a

NEURAL CELL ADHESION MOLECULE L1 PRECURSOR (N-CAM L1).

3.9e-18:153:30

HOMO SAPIENS (HUMAN).

P32004

50

HRIFA008314a

HYPOTHETICAL 149.7 KD PROTEIN IN IRE1-KSP1 INTERGENIC REGION.

2.1e-18:99:47

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P38800

55

HRIFA008362a

PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR (EC 2.3.1.43) (LECITHIN-CHOLESTEROL ACYLTRANSFERASE) (PHOSPHOLIPID-CHOLESTEROL ACYLTRANSFERASE) (FRAGMENT).

EP 1 130 094 A2

- 9.1e-42:135:57
GALLUS GALLUS (CHICKEN).
P53760
- 5 HRIFA008426a
HOMEODOMAIN PROTEIN AKR (AVIAN KNOTTED-RELATED PROTEIN).
1.3e-08:104:45
GALLUS GALLUS (CHICKEN).
Q90655
- 10 HRIFA008459a
CARBON CATABOLITE DEREPRESSING PROTEIN KINASE (EC 2.7.1.-).
5.5e-15:96:40
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P06782
- 15 HRIFA008483a
PROBABLE LONG-CHAIN FATTY ACID TRANSPORT PROTEIN.
7.4e-26:154:41
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P38225
- 20 HRIFA008547a
ZINC FINGER PROTEIN 136.
7.2e-57:228:50
HOMO SAPIENS (HUMAN).
P52737
- 25 HRIFA008596a
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
1.6e-05:97:35
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437
- 30 HRIFA008611a
NPL1 PROTEIN (SEC63 PROTEIN).
8.1e-15:113:38
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P14906
- 35 HRIFA008661a
GALACTOSE-PROTON SYMPORT (GALACTOSE TRANSPORTER).
2.7e-16:184:29
ESCHERICHIA COLI.
P37021
- 40 HRIFA008717a
SERINE/THREONINE-PROTEIN KINASE NRK1 (EC 2.7.1.-) (N-RICH KINASE 1).
6.9e-32:198:41
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P38692
- 45 HRIFA008784a
HYPOTHETICAL 26.3 KD PROTEIN IN OYE2-GND1 INTERGENIC REGION.
2.2e-16:93:47
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P38869

- 5 HRIFA008790a
HYPOTHETICAL 15.7 KD PROTEIN IN NUP85-SSC1 INTERGENIC REGION.
4.2e-08:121:32
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P47111
- 10 HRIFA008976a
ACROSIN PRECURSOR (EC 3.4.21.10).
0.31:20:70
HOMO SAPIENS (HUMAN).
P10323
- 15 HRIFA008981a
ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).
1.0e-84:126:74
HOMO SAPIENS (HUMAN).
Q03923
- 20 HRIFA008989a
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (AL-PHA-0 PROTEIN).
1.2e-05:134:33
HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).
P08393
- 25 HRIFA009071 a
CELLULAR TUMOR ANTIGEN P53 (PHOSPHOPROTEIN P53).
0.14:104:31
HOMO SAPIENS (HUMAN).
P04637
- 30 HRIFA009101a
ZINC FINGER PROTEIN 136.
6.5e-47:126:67
HOMO SAPIENS (HUMAN).
P52737
- 35 HRIFA009123a
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
0.010:127:35
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437
- 40 HRIFA009136a
REGULATORY PROTEIN E2.
0.032:100:37
HUMAN PAPILLOMAVIRUS TYPE 25.
P36787
- 45 HRIFA009171a
BUTYROPHILIN PRECURSOR (BT).
1.6e-15:168:31
BOS TAURUS (BOVINE).
P18892
- 50 HRIFA009220a
HYPOTHETICAL 43.7 KD PROTEIN C24B11.08C IN CHROMOSOME I.
2.2e-48:268:41

EP 1 130 094 A2

SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).

Q09895

HRIFA009339a

PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR.

0.63:57:35

MUS MUSCULUS (MOUSE).

Q01149

10 HRIFA009451a

METALLOPROTEINASE INHIBITOR 1 PRECURSOR (TIMP-1) (ERYTHROID POTENTIATING ACTIVITY) (EPA) (TISSUE INHIBITOR OF METALLOPROTEINASES) (FIBROBLAST COLLAGENASE INHIBITOR) (COLLAGENASE INHIBITOR).

1.7e-57:163:73

15 HOMO SAPIENS (HUMAN).

P01033

HRIFA009482a

BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE) (ACID BETA-GALACTOSIDASE).

20 7.7e-25:86:59

MUS MUSCULUS (MOUSE).

P23780

HRIFA009578a

25 HYPOTHETICAL 24.5 KD PROTEIN IN SAP185-BCK1 INTERGENIC REGION.

8.8e-10:199:26

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P40857

30 HRIFA009762a

CCAAT DISPLACEMENT PROTEIN (CDP) (CDP2) (FRAGMENT).

0.17:116:32

RATTUS NORVEGICUS (RAT).

P53565

35 HRIFA009783a

HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I.

6.2e-48:231:48

40 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).

Q09782

HRIFA009825a

ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR.

4.0e-06:70:38

45 ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).

P40602

HRIFA009852a

50 "NEURAL CELL ADHESION MOLECULE 1, LARGE ISOFORM PRECURSOR (N-CAM 180) [CONTAINS: N-CAM 140]."

4.0e-07:198:27

XENOPUS LAEVIS (AFRICAN CLAWED FROG).

P16170

55 HRIFA009881a

EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).

1.5e-11:106:35

SORGHUM VULGARE (SORGHUM).

P24152

- 5 HRIFA009983a
G-BOX BINDING FACTOR (GBF).
3.8e-10:156:30
DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).
P36417
- 10 HRIFA010005a
"M PROTEIN, SEROTYPE 49 PRECURSOR."
1.6e-05:183:27
STREPTOCOCCUS PYOGENES.
P16947
- 15 HRIFA010078a
HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.
4.7e-05:194:31
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53214
- 20 HRIFA010085a
ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).
2.9e-92:243:69
HOMO SAPIENS (HUMAN).
Q03923
- 25 HRIFA010090a
N-ACETYLGLUCOSAMINE-6-SULFATASE PRECURSOR (EC 3.1.6.14) (G6S) (GLUCOSAMINE-6-SULFATASE).
6.7e-16:78:51
HOMO SAPIENS (HUMAN).
P15586
- 30 HRIFA010130a
DOLICHYL-PHOSPHATE-MANNOSE--PROTEIN MANNOSYLTRANSFERASE 4 (EC 2.4.1.109).
5.6e-13:99:34
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P46971
- 35 HRIFA010152a
"ADENYLATE CYCLASE, TYPE V (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (CA(2+)-INHIBITABLE ADENYLYL CYCLASE)." .
2.3e-05:73:43
CANIS FAMILIARIS (DOG).
P30803
- 40 HRIFA010176a
HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B).
0.066:105:31
MUS MUSCULUS (MOUSE).
P35583
- 45 HRIFA010301a
ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR.
1.1e-09:120:34
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
P40602

- 5 HRIFA010319a
DOPAMINE-BETA-MONOXYGENASE PRECURSOR (EC 1.14.17.1) (DOPAMINE BETA- HYDROXYLASE)
(DBH).
4.8e-23:185:32
- 10 RATTUS NORVEGICUS (RAT).
Q05754
- 15 HRIFA010361a
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
2.6e-08:136:32
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437
- 20 HRIFA010394a
HYPOTHETICAL 51.5 KD PROTEIN D2024.3 IN CHROMOSOME IV.
3.3e-36:144:47
CAENORHABDITIS ELEGANS.
P49191
- 25 HRIFA010425a
A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.
1.9e-09:199:29
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P32323
- 30 HRIFA010460a
TRANSCRIPTIONAL ACTIVATOR FE65.
2.3e-27:101:54
RATTUS NORVEGICUS (RAT).
P46933
- 35 HRIFA010466a
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
5.3e-07:123:34
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437
- 40 HRIFA010490a
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (EARLY PROTEIN 0) (EP0).
0.0031:118:30
PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).
P29129
- 45 HRIFA010736a
PROTEIN Q300.
0.018:14:85
MUS MUSCULUS (MOUSE).
Q02722
- 50 HRIFA010790a
RENAL SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN 2 (SODIUM/PHOSPHATE COTRANSPORTER 2) (NA(+)/PI COTRANSPORTER 2) (RENAL SODIUM-PHOSPHATE TRANSPORT PROTEIN 2) (RENAL NA+-DEPENDENT PHOSPHATE COTRANSPORTER 2).
1.6e-82:197:72
- 55 HOMO SAPIENS (HUMAN).
Q06495
- HRIFA010799a

- PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.
1.7e-05:220:30
GALLUS GALLUS (CHICKEN).
P02457
- 5 HRIFA010859a
ALPHA-2C-1 ADRENERGIC RECEPTOR (ALPHA-2C-1 ADRENOCEPTOR) (SUBTYPE C4).
0.063:134:33
- 10 HOMO SAPIENS (HUMAN).
P18825
- HRIFA010891a
HYPOTHETICAL 22.7 KD PROTEIN IN PAS1-MST1 INTERGENIC REGION.
0.044:28:64
- 15 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P36015
- HRIFA010975a
TYROSINE-PROTEIN KINASE SYK (EC 2.7.1.112) (SPLEEN TYROSINE KINASE).
8.5e-113:144:86
- 20 HOMO SAPIENS (HUMAN).
P43405
- HRIFA010988a
GASTRIN PRECURSOR.
0.084:59:37
- 25 HOMO SAPIENS (HUMAN).
P01350
- HRIFA011016a
PROTEIN DISULFIDE ISOMERASE-RELATED PROTEIN PRECURSOR (ERP72) (CALCIUM-BINDING PROTEIN 2) (CABP2).
3.1e-15:127:37
- 30 RATTUS NORVEGICUS (RAT).
P38659
- HRIFA011105a
SALIVARY GLUE PROTEIN SGS-7 PRECURSOR.
0.97:41:43
- 40 DROSOPHILA MELANOGASTER (FRUIT FLY).
P02841
- HRIFA011128a
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN (CLONE W10-1) (FRAGMENT).
0.0046:30:63
- 45 LYCOPERSICON ESCULENTUM (TOMATO).
Q01157
- HRIFA011179a
PROBABLE SERINE/THREONINE-PROTEIN KINASE YKL101W (EC 2.7.1.-).
1.1e-20:127:42
- 50 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P34244
- HRIFA011197a
DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (THYMOCYTE-ACTIVATING MOLECULE) (THAM).
5.8e-26:169:40
- 55 MUS MUSCULUS (MOUSE).

P28843

HRIFA011449a

GALACTOSYLTRANSFERASE ASSOCIATED PROTEIN KINASE P58/GTA (EC 2.7.1.-).

5 1.9e-26:109:53

MUS MUSCULUS (MOUSE).

P24788

HRIFA011484a

10 D(4) DOPAMINE RECEPTOR (D(2C) DOPAMINE RECEPTOR).

0.00055:115:33

HOMO SAPIENS (HUMAN).

P21917

HRIFA011512a

POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L2 (SNF2-ALPHA).

0.00024:139:25

HOMO SAPIENS (HUMAN).

P51531

HRIFA011580a

20 VITELLOGENIN II PRECURSOR (MAJOR VITELLOGENIN) [CONTAINS: LIPOVITELLIN I (LV) PHOSVITIN (PV)

LIPOVITELLIN II (LVII) YGP40].

4.0e-08:182:32

25 GALLUS GALLUS (CHICKEN).

P02845

HRIFA011659a

30 VON WILLEBRAND FACTOR PRECURSOR.

9.8e-17:210:25

HOMO SAPIENS (HUMAN).

P04275

HRIFA011820a

35 ZINC FINGER PROTEIN 136.

1.9e-10:42:73

HOMO SAPIENS (HUMAN).

P52737

HRIFA011926a

40 TRANSCRIPTIONAL REGULATORY PROTEIN ALGP (ALGINATE REGULATORY PROTEIN ALGR3).

1.0:149:22

PSEUDOMONAS AERUGINOSA.

P15276

45 HRIFA011947a

ZINC FINGER PROTEIN 136.

1.3e-80:180:72

HOMO SAPIENS (HUMAN).

50 P52737

HRIFA012069a

A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.

0.0027:205:28

55 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P32323

HRIFA012151a

EP 1 130 094 A2

NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 1 PRECURSOR.
0.00028:72:37

RATTUS NORVEGICUS (RAT).
Q07008

5

HRIFA012167a
HYPOTHETICAL SYMPORTER IN GLTS-SELC INTERGENIC REGION.

6.4e-09:145:28
ESCHERICHIA COLI.

10

P31435

HRIFA012278a
ZINC FINGER PROTEIN 140.

3.1e-14:88:52
HOMO SAPIENS (HUMAN).

P52738

15

HRIFA012354a
"SODIUM CHANNEL PROTEIN, BRAIN II ALPHA SUBUNIT."

20

2.1e-05:120:32
RATTUS NORVEGICUS (RAT).

P04775

HRIFA012427a

25

PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.

6.3e-08:250:28

MUS MUSCULUS (MOUSE).
P11087

30

HRIFA012436a
INTESTINAL MEMBRANE A4 PROTEIN (DIFFERENTIATION-DEPENDENT PROTEIN A4).

4.7e-09:95:31

HOMO SAPIENS (HUMAN).
Q04941

35

HRIFA012515a
SODIUM/GLUCOSE COTRANSPORTER 1 (NA(+)/GLUCOSE COTRANSPORTER 1) (HIGH AFFINITY SODIUM-GLUCOSE COTRANSPORTER).

40

3.5e-06:181:27
ORYCTOLAGUS CUNICULUS (RABBIT).

P11170

HRIFA012584a

45
MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (72 KD MITOCHONDRIAL OUTER MEMBRANE PROTEIN) (MITOCHONDRIAL IMPORT RECEPTOR FOR THE ADP/ATP CARRIER) (TRANSLOCASE OF OUTER MEMBRANE TOM70).

4.9e-14:136:29

NEUROSPORA CRASSA.
P23231

50

HRIFA012625a
"HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT (FCER1) (IGE FC RECEPTOR, BETA-SUBUNIT)."

9.6e-12:103:40

55

RATTUS NORVEGICUS (RAT).
P13386

HRIFA012692a

- BLOOM'S SYNDROME PROTEIN.
6.3e-26:203:34
HOMO SAPIENS (HUMAN).
P54132
- 5 HRIFA012702a
EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).
1.9e-07:153:30
ZEA MAYS (MAIZE).
P14918
- 10 HRIFA012737a
LEUCOCYTE ANTIGEN CD97 PRECURSOR.
1.6e-09:170:24
15 HOMO SAPIENS (HUMAN).
P48960
- 15 HRIFA012795a
VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV2.1 (DRK1).
20 3.0e-34:189:39
RATTUS NORVEGICUS (RAT).
P15387
- 25 HRIFA012885a
HYPOTHETICAL 30.6 KD PROTEIN IN SCP160-SMC3 INTERGENIC REGION PRECURSOR.
2.9e-21:159:40
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P47032
- 30 HRIFA012914a
ENV POLYPROTEIN PRECURSOR (COAT POLYPROTEIN) [CONTAINS: OUTER MEMBRANE PROTEIN GP70
TRANSMEMBRANE PROTEIN P20E].
3.4e-29:134:47
35 BABOON ENDOGENOUS VIRUS (STRAIN M7).
P10269
- 35 HRIFA012969a
ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-
FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT).
40 1.2e-30:228:32
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P32802
- 45 HRIFA012990a
PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38).
7.4e-20:181:33
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P39986
- 50 HRIFA013092a
OUTER MEMBRANE PROTEIN H.8 PRECURSOR.
0.0039:51:39
55 NEISSERIA GONORRHOEAE.
P11910
- 55 HRIFA013103a
N-ACETYLGLUCOSAMINE SYNTHASE (EC 2.4.1.90) (N-ACETYLGLUCOSAMINE (BETA 1→4)GALACTOSYL-
TRANSFERASE) (EC 2.4.1.38) (LACTOSE SYNTHASE A PROTEIN (EC 2.4.1.22)) (GALACTOSYLTRANS-

FERASE) (GT).

0.25:50:34

MUS MUSCULUS (MOUSE).

P15535

5

HRIFA013135a

CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (SLAYER PROTEIN 1).

1.6e-05:214:28

CLOSTRIDIUM THERMOCELLUM.

10

Q06852

15

HRIFA013235a

PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSOR.

1.9e-05:113:40

20

HOMO SAPIENS (HUMAN).

P02461

HRIFA013254a

COMPLEMENT C4 PRECURSOR [CONTAINS: C4A ANAPHYLATOXIN].

25

3.8e-13:123:41

MUS MUSCULUS (MOUSE).

P01029

30

HRIFA013265a

CATHEPSIN L PRECURSOR (EC 3.4.22.15) (MAJOR EXCRETED PROTEIN) (MEP).

7.0e-107:225:86

HOMO SAPIENS (HUMAN).

P07711

35

HRIFA013276a

5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) (ECTO-NUCLEOTIDASE) (5'-NT) (CD73 ANTIGEN).

2.2e-117:270:85

HOMO SAPIENS (HUMAN).

P21589

40

HRIFA013279a

CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).

4.9e-05:127:37

PLASMODIUM VIVAX.

P08677

45

HRIFA013376a

MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (72 KD MITOCHONDRIAL OUTER MEMBRANE PROTEIN) (MITOCHONDRIAL IMPORT RECEPTOR FOR THE ADP/ATP CARRIER) (TRANSLOCASE OF OUTER MEMBRANE TOM70).

8.0e-23:230:31

NEUROSPORA CRASSA.

P23231

50

HRIFA013477a

OX-2 MEMBRANE GLYCOPROTEIN PRECURSOR (FRAGMENT).

5.8e-87:197:87

HOMO SAPIENS (HUMAN).

P41217

55

HRIFA013586a

ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DIAZEPAM BINDING INHIBITOR) (MA-DBI).

3.8e-31:93:64
 BOS TAURUS (BOVINE).
 P07106

5 HRIFA013589a
 T-CELL SURFACE PROTEIN TACTILE PRECURSOR (CD96 ANTIGEN).
 5.0e-06:95:35
 HOMO SAPIENS (HUMAN).
 P40200

10 HRIFA013620a
 "HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT (FCER1) (IGE FC RECEPTOR, BETA-SUBUNIT)." 7.1e-08:95:37
 MUS MUSCULUS (MOUSE).
 P20490

15 HRIFA013726a
 SERINE/THREONINE-PROTEIN KINASE STE20 (EC 2.7.1.-).
 20 1.5e-33:99:50
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 Q03497

25 HRIFA013744a
 ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DIAZEPAM BINDING INHIBITOR) (MA-DBI).
 7.5e-15:105:38
 BOS TAURUS (BOVINE).
 P07106

30 HRIFA013911a
 BIOTINIDASE PRECURSOR (EC 3.5.1.12).
 7.8e-37:104:46
 HOMO SAPIENS (HUMAN).
 P43251

35 HRIFA013919a
 MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).
 40 1.2e-10:170:32
 HOMO SAPIENS (HUMAN).
 Q02817

45 HRIFA013932a
 "SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEP-TIDE IB-6" PEPTIDE P-H].
 2.6e-05:168:34
 HOMO SAPIENS (HUMAN).
 P04280

50 HRIFA013980a
 TRANSCRIPTION REGULATORY PROTEIN SNF5 (SWI/SNF COMPLEX COMPONENT SNF5) (TRANSCRIPTION FACTOR TYE4).
 0.00036:157:27
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 P18480

55 HRIFA014006a
 T-CELL SURFACE GLYCOPROTEIN YE1/48 (T LYMPHOCYTE ANTIGEN A1) (LY49-A ANTIGEN).

9.4e-16:185:28

MUS MUSCULUS (MOUSE).
P20937

5 HRIFA014024a

TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (P135 PROTEIN) (IER 2.9/ER2.6).

0.0013:102:44

BOVINE HERPESVIRUS TYPE 1 (STRAIN JURA).

P29128

10

HRIFA014056a

PROTEIN Q300.

5.1e-05:24:70

MUS MUSCULUS (MOUSE).
Q02722

15

HRIFA014111a

TOLL PROTEIN PRECURSOR.

5.5e-08:203:27

20 DROSOPHILA MELANOGASTER (FRUIT FLY).
P08953

25

HRIFA014133a

PROLINE-RICH PROTEIN MP-2 PRECURSOR.

1.6e-06:143:33

MUS MUSCULUS (MOUSE).
P05142

30

HRIFA014185a

LEUCOCYTE ANTIGEN CD97 PRECURSOR.

6.0e-14:192:30

HOMO SAPIENS (HUMAN).
P48960

35

HRIFA014336a

"GELSOLIN PRECURSOR, PLASMA (ACTIN-DEPOLYMERIZING FACTOR) (ADF) (BREVIN) (FRAGMENT)."

2.8e-70:198:58

SUS SCROFA (PIG).

P20305

40

HRIFA014396a

CREB-BINDING PROTEIN.

2.6e-07:101:34

MUS MUSCULUS (MOUSE).
P45481

45

HRIFA014397a

GENERAL NEGATIVE REGULATOR OF TRANSCRIPTION SUBUNIT 1.

5.2e-05:147:30

50 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P25655

55

HRIFA014465a

HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME III.

2.8e-11:166:30

CAENORHABDITIS ELEGANS.

P30638

- 5 HRIFA014500a
 HYPOTHETICAL 71.4 KD PROTEIN IN NMD3-ENO2 INTERGENIC REGION.
 1.0e-14:149:35
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 P38862
- 10 HRIFA014561a
 PROBABLE G PROTEIN-COUPLED RECEPTOR GPR1.
 4.1e-70:156:89
 10 HOMO SAPIENS (HUMAN).
 P46091
- 15 HRIFA014568a
 AMINOPEPTIDASE N (EC 3.4.11.2) (MICROSOMAL AMINOPEPTIDASE).
 2.4e-40:196:44
 RATTUS NORVEGICUS (RAT).
 P15684
- 20 HRIFA014590a
 ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).
 0.18:26:30
 GALLUS GALLUS (CHICKEN).
 P14093
- 25 HRIFA014598a
 SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
 4.9e-05:124:29
 XENOPUS LAEVIS (AFRICAN CLAWED FROG).
 P17437
- 30 HRIFA014620a
 ENL PROTEIN.
 0.58:170:30
 30 HOMO SAPIENS (HUMAN).
 Q03111
- 35 HRIFA014621a
 PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN PRECURSOR.
 2.7e-50:150:74
 40 HOMO SAPIENS (HUMAN).
 P11462
- 45 HRIFA014688a
 INTEGRIN BETA-6 SUBUNIT PRECURSOR.
 6.9e-31:189:39
 HOMO SAPIENS (HUMAN).
 P18564
- 50 HRIFA014702a
 PROLINE-RICH PROTEIN MP-2 PRECURSOR.
 6.4e-05:89:40
 MUS MUSCULUS (MOUSE).
 P05142
- 55 HRIFA014819a
 MICROFIBRIL-ASSOCIATED GLYCOPROTEIN 4.
 7.8e-26:117:46
 HOMO SAPIENS (HUMAN).

P55083

HRIFA014868a

SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.

8.9e-08:195:29

DROSOPHILA ERECTA (FRUIT FLY).

P13730

HRIFA014951a

PLASMINOGEN (EC 3.4.21.7) (FRAGMENT).

4.1e-23:132:39

EQUUS CABALLUS (HORSE).

P80010

HRIFA014967a

CHLORINE CHANNEL PROTEIN P64.

2.0e-52:142:76

BOS TAURUS (BOVINE).

P35526

HRIFA015063a

ZINC FINGER PROTEIN 136.

6.6e-53:229:48

HOMO SAPIENS (HUMAN).

P52737

HRIFA015070a

SERINE/THREONINE-PROTEIN KINASE NRK1 (EC 2.7.1.-) (N-RICH KINASE 1).

9.3e-24:143:41

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P38692

HRIFA015122a

REGULATORY PROTEIN E2.

0.45:129:30

HUMAN PAPILLOMAVIRUS TYPE 5.

P06921

HRIFA015219a

FIBRILLIN 1 PRECURSOR (MP340).

9.9e-09:132:32

BOS TAURUS (BOVINE).

P98133

HRIFA015246a

PREGNANCY-SPECIFIC BETA-1-GLYCOPROTEIN 4 PRECURSOR (PSBG-4).

2.4e-33:184:46

HOMO SAPIENS (HUMAN).

Q00888

HRIFA015351a

PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP).

0.0021:122:30

RATTUS NORVEGICUS (RAT).

P03994

HRIFA015423a

B-CELL LYMPHOMA 3-ENCODED PROTEIN (BCL-3 PROTEIN).

- 1.2e-11:148:35
HOMO SAPIENS (HUMAN).
P20749
- 5 HRIFA015453a
RAC-FAMILY SERINE/THREONINE KINASE HOMOLOG (EC 2.7.1.-).
6.8e-11:91:37
DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).
P54644
- 10 HRIFA015486a
BETA-2-GLYCOPROTEIN I PRECURSOR (APOLIPOPROTEIN H) (APO-H) (ACTIVATED PROTEIN C-BINDING PROTEIN) (APC INHIBITOR).
2.0e-22:208:27
MUS MUSCULUS (MOUSE).
Q01339
- 15 HRIFA015506a
COLORECTAL MUTANT CANCER PROTEIN (MCC PROTEIN).
1.3e-12:73:50
HOMO SAPIENS (HUMAN).
P23508
- 20 HRIFA015536a
CHLORINE CHANNEL PROTEIN P64.
1.2e-49:115:79
BOS TAURUS (BOVINE).
P35526
- 25 HRIFA015547a
BEM46 PROTEIN (FRAGMENT).
1.4e-33:137:49
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
P54069
- 30 HRIFA015568a
HYPOTHETICAL 35.8 KD PROTEIN C12G12.12 IN CHROMOSOME I.
2.4e-16:152:34
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q09875
- 35 HRIFA015756a
EBNA-2 NUCLEAR PROTEIN.
2.9e-15:28:75
45 EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P12978
- 40 HRIFA015802a
PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP).
0.0035:122:30
RATTUS NORVEGICUS (RAT).
P03994
- 45 HRIFA015811a
GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).
6.2e-39:171:43
55 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P43636

- 5 HRIFA015902a
A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.
0.0075:161:29
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P32323
- 10 HRIFA015947a
ZINC FINGER Y-CHROMOSOMAL PROTEIN 1.
0.035:98:28
MUS MUSCULUS (MOUSE).
P10925
- 15 HRIFA015995a
PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSOR.
6.2e-08:221:37
HOMO SAPIENS (HUMAN).
P02461
- 20 HRIFA016070a
"COMPLEMENT C1Q SUBCOMPONENT, A CHAIN PRECURSOR."
1.0e-18:179:35
HOMO SAPIENS (HUMAN).
P02745
- 25 HRIFA016214a
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
4.0e-05:96:42
MUS MUSCULUS (MOUSE).
P05142
- 30 HRIFA016240a
HYPOTHETICAL 65.3 KD PROTEIN IN PRE3-SAG1 INTERGENIC REGION.
8.5e-05:103:33
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P47082
- 35 HRIFA016255a
EBNA-1 NUCLEAR PROTEIN.
4.5e-09:219:33
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211
- 40 HRIFA016290a
COAGULATION FACTOR V PRECURSOR (ACTIVATED PROTEIN C COFACTOR).
6.7e-21:182:41
HOMO SAPIENS (HUMAN).
P12259
- 45 HRIFA016430a
ER LUMEN PROTEIN RETAINING RECEPTOR 1 (KDEL RECEPTOR 1).
7.1e-50:120:86
HOMO SAPIENS (HUMAN).
P24390
- 50 HRIFA016599a
MEIOTIC RECOMBINATION PROTEIN REC104.
0.57:73:31
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P33323

HRIFA016639a

5 "GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)."

8.0e-06:206:23

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P08640

HRIFA016654a

HEME-REGULATED EUKARYOTIC INITIATION FACTOR EIF-2-ALPHA KINASE (EC 2.7.1.-) (HRI).

1.1e-78:181:86

ORYCTOLAGUS CUNICULUS (RABBIT).

P33279

HRIFA016669a

ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR.

1.4e-08:87:36

ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).

P40602

HRIFA016758a

GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).

9.5e-17:158:40

25 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P43636

HRIFA016963a

FMRFAMIDE-RELATED NEUROPEPTIDES PRECURSOR.

30 6.2e-08:131:32

LYMNAEA STAGNALIS (GREAT POND SNAIL).

P42565

HRIFA017031a

35 MYOSIN HEAVY CHAIN KINASE A (EC 2.7.1.129) (MHCK A).

2.6e-11:152:34

DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).

P42527

HRIFA017146a

40 D(4) DOPAMINE RECEPTOR (D(2C) DOPAMINE RECEPTOR).

0.0014:78:37

HOMO SAPIENS (HUMAN).

P21917

45 HRIFA017190a

FLI-1 ONCOGENE (ERGB TRANSCRIPTION FACTOR).

0.0026:89:30

HOMO SAPIENS (HUMAN).

50 Q01543

HRIFA017257a

55 "GELSOLIN PRECURSOR, PLASMA (ACTIN-DEPOLYMERIZING FACTOR) (ADF) (BREVIN) (AGEL)."

2.5e-79:261:57

HOMO SAPIENS (HUMAN).

P06396

HRIFA017295a

- "ALPHA-1,6-MANNOSYL-GLYCOPROTEIN BETA-1,2-N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.143) (N-GLYCOSYL-OLIGOSACCHARIDE-GLYCOPROTEIN N-ACETYLGLUCOSAMINYLTRANSFERASE II) (BETA-1,2-N-ACETYLGLUCOSAMINYLTRANSFERASE II) (GNT-II) (GLCNAC-T II)." 3.4e-20:66:78
- 5 HOMO SAPIENS (HUMAN).
Q10469
- HRIFA017312a
C4B-BINDING PROTEIN ALPHA CHAIN PRECURSOR (PROLINE-RICH PROTEIN) (PRP).
10 2.7e-19:221:33
HOMO SAPIENS (HUMAN).
P04003
- HRIFA017456a
15 LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN).
0.11:94:35
MUS MUSCULUS (MOUSE).
P19137
- HRIFA017457a
SYNAPTAGMIN II.
20 7.2e-07:98:35
MUS MUSCULUS (MOUSE).
P46097
- 25 HRIFA017643a
NOV PROTEIN HOMOLOG PRECURSOR (NOVH).
2.2e-07:81:41
HOMO SAPIENS (HUMAN).
30 P48745
- HRIFA017670a
TRANS-GOLGI NETWORK INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR.
35 4.9e-06:172:27
RATTUS NORVEGICUS (RAT).
P19814
- HRIFA017703a
PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).
40 1.9e-16:129:34
THERMOMONOSPORA CURVATA.
P49695
- HRIFA017791a
45 MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).
0.012:71:38
HOMO SAPIENS (HUMAN).
Q02817
- HRIFA017801a
50 PROLINE-RICH PROTEIN MP-2 PRECURSOR.
4.5e-07:86:39
MUS MUSCULUS (MOUSE).
P05142
- 55 HRIFA017818a
ATP SYNTHASE C CHAIN (EC 3.6.1.34) (LIPID-BINDING PROTEIN).
1.0:32:40

STREPTOMYCES LIVIDANS.
P50014

HRIFA017836a

"TETRACYCLINE RESISTANCE PROTEIN, CLASS H (TETA(H))."

1.3e-08:113:31

PASTEURELLA MULTOCIDA.

P51564

HRIFA017855a

ORM1 PROTEIN.

1.7e-18:137:35

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P53224

HRIFA017921a

TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (ALPHA-0 PROTEIN).

2.0e-09:182:35

HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).

P08393

HRIFA018092a

"DIACYLGLYCEROL CHOLINEPHOSPHOTRANSFERASE (EC 2.7.8.2) (SN-1,2-DIACYLGLYCEROL CHOLINEPHOSPHOTRANSFERASE) (CHOPT)."

2.1e-20:119:42

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P17898

HRIFA018131a

ORM1 PROTEIN.

2.6e-20:137:37

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P53224

HRIFA018134a

SERINE/THREONINE-PROTEIN KINASE CTR1 (EC 2.7.1.37).

1.1e-11:147:32

ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).

Q05609

HRIFA018238a

NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 1 PRECURSOR (MOTCH PROTEIN).

8.6e-06:74:44

45 MUS MUSCULUS (MOUSE).

Q01705

HRIFA018262a

PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).

6.4e-10:71:38

THERMOMONOSPORA CURVATA.

P49695

HRIFA018287a

HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.

1.5e-06:214:32

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P53214

- 5 HRIFA018447a
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
0.00065:133:33
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437
- 10 HRIFA018580a
COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).
2.1e-18:109:41
CRICETULUS GRISEUS (CHINESE HAMSTER).
P49020
- 15 HRIFA018666a
PROTEIN-TYROSINE PHOSPHATASE DLAR PRECURSOR (EC 3.1.3.48) (PROTEIN-TYROSINE-PHOSPHATE PHOSPHOHYDROLASE).
1.7e-06:191:28
DROSOPHILA MELANOGASTER (FRUIT FLY).
P16621
- 20 HRIFA018688a
PHLB PROTEIN PRECURSOR.
1.9e-06:110:35
SERRATIA LIQUEFACIENS.
P18954
- 25 HRIFA018754a
"GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)." 1.8e-06:195:27
30 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P08640
- 35 HRIFA018794a
MSP1 PROTEIN HOMOLOG.
3.2e-06:93:25
CAENORHABDITIS ELEGANS.
P54815
- 40 HRIFA018827a
HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME III.
3.1e-17:180:28
CAENORHABDITIS ELEGANS.
P30638
- 45 HRIFA018870a
HYPOTHETICAL 35.6 KD PROTEIN IN SPC1-ILV3 INTERGENIC REGION.
4.7e-09:70:37
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P47088
- 50 HRIFA018904a
MYOTONIN-PROTEIN KINASE (EC 2.7.1.-) (MYOTONIC DISTROPHY PROTEIN KINASE) (MDPK) (DM-KI-NASE) (DMK) (DMPK) (MT-PK).
5.5e-12:142:32
55 HOMO SAPIENS (HUMAN).
Q09013
- HRIFA018931a

- ZINC FINGER PROTEIN 140.
2.9e-10:47:74
HOMO SAPIENS (HUMAN).
P52738
- 5 HRIFA018993a
HYPOTHETICAL 21.5 KD PROTEIN IN SEC15-SAP4 INTERGENIC REGION.
1.2e-13:117:34
- 10 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53073
- HRIFA019105a
DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR (EC 3.4.24.-).
7.5e-22:203:32
- 15 DROSOPHILA MELANOGASTER (FRUIT FLY).
P25723
- HRIFA019136a
"MYRISTOYLATED ALANINE-RICH C-KINASE SUBSTRATE (MARCKS) (PROTEIN KINASE C SUBSTRATE,
20 80 KD PROTEIN, LIGHT CHAIN) (PKCSL) (80K-L PROTEIN)."
1.0e-25:74:81
- HOMO SAPIENS (HUMAN).
P29966
- 25 HRIFA019175a
PROTEIN KINASE WIS1 (EC 2.7.1.-).
1.3e-14:84:39
- SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
P33886
- 30 HRIFA019262a
ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).
2.5e-55:188:50
- HOMO SAPIENS (HUMAN).
Q03923
- 35 HRIFA019412a
CATHEPSIN E PRECURSOR (EC 3.4.23.34).
1.4e-09:121:33
- 40 CAVIA PORCELLUS (GUINEA PIG).
P25796
- HRIFA019437a
REGULATORY PROTEIN E2.
45 0.26:77:37
- HUMAN PAPILLOMAVIRUS TYPE 14.
P36783
- 50 HRIFA019466a
EBNA-1 NUCLEAR PROTEIN.
2.7e-19:130:43
- EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211
- 55 HRIFA019490a
TRANSCRIPTION REGULATORY PROTEIN SNF5 (SWI/SNF COMPLEX COMPONENT SNF5) (TRANSCRIPTION FACTOR TYE4).
1.1e-09:132:34

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P18480

5 HRIFA019498a
VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN SHAL (SHAL2).
5.6e-05:87:36
DROSOPHILA MELANOGASTER (FRUIT FLY).
P17971

10 HRIFA019532a
EBNA-1 NUCLEAR PROTEIN.
1.8e-05:67:49
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211

15 HRIFA019651a
ACIDIC PHOSPHOPROTEIN PRECURSOR (50 KD ANTIGEN).
6.1e-05:31:64
PLASMODIUM CHABAUDI.

20 Q02752

HRIFA019867a
RENAL SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN 2 (SODIUM/PHOSPHATE COTRANSPORTER 2) (NA(+)/PI COTRANSPORTER 2) (RENAL SODIUM-PHOSPHATE TRANSPORT PROTEIN 2) (RENAL NA+-DEPENDENT PHOSPHATE COTRANSPORTER 2).
8.2e-34:103:71
RATTUS NORVEGICUS (RAT).
Q06496

30 HRIFA019869a
SERINE/THREONINE-PROTEIN KINASE FUSED (EC 2.7.1.-).
7.2e-29:83:49
DROSOPHILA MELANOGASTER (FRUIT FLY).
P23647

35 HRIFA019958a
REPRESSOR PROTEIN CI (FRAGMENT).
0.99:45:37
BACTERIOPHAGE 434.

40 P16117

HRIFA020144a
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
2.8e-06:176:30
45 XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437

50 HRIFA020184a
NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE 1).
1.9e-10:102:37
DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).
P18160

55 HRIFA020272a
MUSCARINIC ACETYLCHOLINE RECEPTOR M3.
5.5e-91:211:85
HOMO SAPIENS (HUMAN).
P20309

EP 1 130 094 A2

- 5 HRIFA020335a
PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-).
5.0e-104:275:72
HOMO SAPIENS (HUMAN).
P27448
- 10 HRIFA020349a
BRITTLE-1 PROTEIN PRECURSOR.
6.0e-30:214:35
ZEA MAYS (MAIZE).
P29518
- 15 HRIFA020453a
PROTEIN TRANSPORT PROTEIN SEC22 (PROTEIN SLY2).
2.5e-08:132:28
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P22214
- 20 HRIFA020693a
TUMOR SUPPRESSOR PROTEIN DCC PRECURSOR (COLORECTAL CANCER SUPPRESSOR).
3.9e-09:96:35
HOMO SAPIENS (HUMAN).
P43146
- 25 HRIFA020707a
PROCYCLIC FORM SPECIFIC POLYPEPTIDE B-ALPHA PRECURSOR (PROCYCLIN) (PARP B-ALPHA) (PS-SA-1).
3.4e-09:95:33
TRYPANOSOMA BRUCEI BRUCEI.
Q06084
- 30 HRIFA020748a
EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).
3.2e-09:210:28
NICOTIANA TABACUM (COMMON TOBACCO).
P13983
- 35 HRIFA020862a
MODIFIER 3 PROTEIN (M33).
5.6e-26:76:61
MUS MUSCULUS (MOUSE).
P30658
- 40 HRIFA020883a
PROTEIN Q300.
0.00054:21:66
MUS MUSCULUS (MOUSE).
Q02722
- 45 HRIFA021007a
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (ALPHA-0 PROTEIN).
0.092:73:36
HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).
P08393
- 50 HRIFA021040a
TRANSCRIPTION FACTOR GATA-4 (GATA BINDING FACTOR-4).

0.98:63:39
HOMO SAPIENS (HUMAN).
P43694

5 HRIFA021061a
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
2.8e-09:162:31
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437

10 HRIFA021213a
OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG.
2.0e-38:96:72
CAENORHABDITIS ELEGANS.
P46975

15 HRIFA021224a
RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17).
2.8e-06:55:52
RATTUS NORVEGICUS (RAT).
Q02975

20 HRIFA021398a
COAGULATION FACTOR VII PRECURSOR (EC 3.4.21.21).
2.5e-17:78:51
ORYCTOLAGUS CUNICULUS (RABBIT).
P98139

25 HRIFA021445a
PRE-B-CELL LEUKEMIA TRANSCRIPTION FACTOR-1 (HOMEobox PROTEIN PBX1) (HOMEobox PROTEIN PRL).
0.38:146:31
HOMO SAPIENS (HUMAN).
P40424

30 HRIFA021494a
EBNA-1 NUCLEAR PROTEIN.
6.8e-07:116:41
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211

35 HRIFA021499a
CARTILAGE MATRIX PROTEIN PRECURSOR (MATRILIN-1).
7.1e-34:159:50
GALLUS GALLUS (CHICKEN).
P05099

40 HRIFA021543a
ANTITHROMBIN-III PRECURSOR (ATIII) (FRAGMENT).
0.0087:50:40
GALLUS GALLUS (CHICKEN).
Q03352

45 HRIFA021620a
PLATELET FACTOR 4 (PF-4).
0.019:65:27
SUS SCROFA (PIG).
P30034

- 5 HRIFA021637a
CARTILAGE MATRIX PROTEIN PRECURSOR (MATRILIN-1).
6.0e-37:147:53
GALLUS GALLUS (CHICKEN).
P05099
- 10 HRIFA021651a
CARG-BINDING FACTOR-A (CBF-A).
2.6e-11:170:30
MUS MUSCULUS (MOUSE).
Q99020
- 15 HRIFA021754a
CARTILAGE MATRIX PROTEIN PRECURSOR (MATRILIN-1).
1.2e-37:137:51
GALLUS GALLUS (CHICKEN).
P05099
- 20 HRIFA021781a
DNA-REPAIR PROTEIN COMPLEMENTING XP-D CELLS (XERODERMA PIGMENTOSUM GROUP D COMPLEMENTING PROTEIN) (DNA EXCISION REPAIR PROTEIN ERCC-2).
7.1e-19:199:31
HOMO SAPIENS (HUMAN).
P18074
- 25 HRIFA021787a
PROTEIN Q300.
0.051:13:84
MUS MUSCULUS (MOUSE).
Q02722
- 30 HRIFA021794a
RAC-FAMILY SERINE/THREONINE KINASE HOMOLOG (EC 2.7.1.-).
1.6e-07:90:32
35 DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).
P54644
- 35 HRIFA021855a
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
8.6e-06:163:30
40 XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437
- 45 HRIFA021906a
S-ANTIGEN PROTEIN PRECURSOR.
2.1e-09:226:28
PLASMODIUM FALCIPARUM (ISOLATE V1).
P09593
- 50 HRIFA022055a
BETA-LYTIC METALLOENDOPEPTIDASE PRECURSOR (EC 3.4.24.32) (BETA-LYTIC PROTEASE).
0.63:118:31
55 ACHROMOBACTER LYTICUS.
P27458
- 55 HRIFA022065a
BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR.
9.7e-24:235:34

HOMO SAPIENS (HUMAN).
P16279

5 HRIFA022139a
HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I.
2.1e-57:232:52
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q09782

10 HRIFA022156a
"GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT PW212 PRECURSOR."
1.4e-07:133:35
TRITICUM AESTIVUM (WHEAT).
P08489

15 HRIFA022166a
EXCISION REPAIR PROTEIN ERCC-6 (COCKAYNE SYNDROME PROTEIN CSB).
3.5e-28:194:35
HOMO SAPIENS (HUMAN).
Q03468

20 HRIFA022177a
PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).
2.2e-12:137:32
25 THERMOMONOSPORA CURVATA.
P49695

30 HRIFA022182a
SERINE/THREONINE-PROTEIN KINASE MAK (EC 2.7.1.-) (MALE GERM CELL-ASSOCIATED KINASE).
1.2e-47:121:79
RATTUS NORVEGICUS (RAT).
P20793

35 HRIFA022203a
COLLAGEN ALPHA 1 (III) CHAIN.
1.1e-05:211:33
BOS TAURUS (BOVINE).
P04258

40 HRIFA022227a
POTENTIAL CAAX PRENYL PROTEASE 1 (EC 3.4.24.-) (PRENYL PROTEIN- SPECIFIC ENDOPROTEASE 1)
(PPSEP 1).
3.2e-31:229:36
45 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q10071

50 HRIFA022234a
CARBOXYPEPTIDASE KEX1 PRECURSOR (EC 3.4.16.6) (CARBOXYPEPTIDASE D).
1.8e-08:110:30
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P09620

55 HRIFA022249a
ZINC FINGER PROTEIN 133.
1.1e-34:84:48
HOMO SAPIENS (HUMAN).
P52736

EP 1 130 094 A2

HRIFA022265a
CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE IV CATALYTIC CHAIN (EC 2.7.1.123) (CAM KINASE-GR) (CAMK IV) [CONTAINS: CALSPERMIN].
5 5.1e-26:188:40
RATTUS NORVEGICUS (RAT).
P13234

HRIFA022328a
SCO1 PROTEIN PRECURSOR.
10 5.4e-25:84:45
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P23833

HRIFA022335a
15 TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (ALPHA-0 PROTEIN).
0.21:121:29
HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).
P08393

20 HRIFA022348a
AGAMOUS PROTEIN.
1.0:40:42
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
25 P17839

HRIFA022411a
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (ALPHA-0 PROTEIN).
30 0.00059:111:35
HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).
P08393

HRIFA022423a
35 HYPOTHETICAL 24.5 KD PROTEIN IN SAP185-BCK1 INTERGENIC REGION.
2.5e-15:106:42
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P40857

40 HRIFA022462a
RETINOIC ACID RECEPTOR RXR-BETA.
0.0010:124:33
HOMO SAPIENS (HUMAN).
P28702

45 HRIFA022493a
ALPHA-2A ADRENERGIC RECEPTOR (ALPHA-2A ADRENOCEPTOR) (ALPHA-2AAR).
0.0018:130:34
MUS MUSCULUS (MOUSE).
50 Q01338

HRIFA022528a
EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).
55 3.2e-23:230:28
ZEA MAYS (MAIZE).
P14918

HRIFA022546a

NINAC SHORT PROTEIN (EC 2.7.1.-).
 8.5e-42:209:43
 DROSOPHILA MELANOGASTER (FRUIT FLY).
 P10677

5 HRIFA022564a
 ZINC FINGER PROTEIN 140.
 7.9e-23:116:51
 HOMO SAPIENS (HUMAN).
 10 P52738

HRIFA022616a
 LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR (LRP) (ALPHA-2-MAC-
 ROGLOBULIN RECEPTOR) (A2MR) (APOLIPOPROTEIN E RECEPTOR) (APOER) (CD91).
 15 7.4e-36:172:43
 HOMO SAPIENS (HUMAN).
 Q07954

20 HRIFA022671a
 PAIRED AMPHIPATHIC HELIX PROTEIN.
 2.0e-26:186:36
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 P22579

25 HRIFA022691a
 FIBRINOGEN-LIKE PROTEIN A PRECURSOR (FREP-A).
 1.4e-44:229:41
 PARASTICHOPUS PARVIMENSIS (SEA CUCUMBER).
 P19477

30 HRIFA022702a
 PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.
 1.1e-08:146:38
 GALLUS GALLUS (CHICKEN).
 35 P02457

HRIFA022707a
 GC-RICH SEQUENCE DNA-BINDING FACTOR (GCF) (TRANSCRIPTION FACTOR 9) (TCF-9).
 7.0e-40:229:37
 40 HOMO SAPIENS (HUMAN).
 P16383

HRIFA022714a
 "AMELOGENIN, CLASS I PRECURSOR."
 45 0.62:96:31
 BOS TAURUS (BOVINE).
 P02817

HRIFA022728a
 ACROSIN PRECURSOR (EC 3.4.21.10) (53 KD FUCOSE-BINDING PROTEIN).
 50 1.7e-06:28:64
 SUS SCROFA (PIG).
 P08001

HRIFA022729a
 "ALPHA-1,6-MANNOSYL-GLYCOPROTEIN BETA-1,2-N-ACETYLGLUCOSAMINYLTRANSFERASE (EC
 55 2.4.1.143) (N-GLYCOSYL-OLIGOSACCHARIDE-GLYCOPROTEIN N-ACETYLGLUCOSAMINYLTRANS-
 FERASE II) (BETA-1,2-N-ACETYLGLUCOSAMINYLTRANSFERASE II) (GNT-II) (GLCNAC-T II)."'

- 7.7e-29:69:84
HOMO SAPIENS (HUMAN).
Q10469
- 5 HRIFA022737a
TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (GMEM) (JI) (MIOTEND-
INOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN) (GP 150-225).
6.7e-19:170:37
GALLUS GALLUS (CHICKEN).
10 P10039
- HRIFA022776a
PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).
4.0e-20:199:31
- 15 MEDICAGO SATIVA (ALFALFA).
P38661
- HRIFA022782a
CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).
20 3.7e-09:184:36
PLASMODIUM CYNOMOLGI (STRAIN BEROK).
P08672
- HRIFA022865a
25 COLLAGEN ALPHA 1(III) CHAIN.
2.5e-09:169:33
BOS TAURUS (BOVINE).
P04258
- 30 HRIFA022875a
BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN).
9.1e-14:115:33
BOS TAURUS (BOVINE).
P21793
- 35 HRIFA022890a
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
1.8e-10:237:30
40 XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437
- HRIFA022895a
ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).
2.4e-106:283:67
- 45 45 HOMO SAPIENS (HUMAN).
Q03923
- HRIFA022985a
50 PROCYCCLIC FORM SPECIFIC POLYPEPTIDE B-ALPHA PRECURSOR (PROCYCLIN) (PARP B-ALPHA) (PS-
SA-1).
3.0e-10:33:72
TRYPANOSOMA BRUCEI BRUCEI.
Q06084
- 55 HRIFA023007a
MHC CLASS II REGULATORY FACTOR RFX1 (RFX) (ENHANCER FACTOR C) (EF-C).
1.1e-27:66:54
HOMO SAPIENS (HUMAN).

P22670

HRIFA023048a

COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).

5 2.2e-07:221:33

RATTUS NORVEGICUS (RAT).

P02454

HRIFA023069a

10 BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR
(HSPG) (PERLECAN) (PLC).

3.4e-08:149:31

HOMO SAPIENS (HUMAN).

P98160

15

HRIFA023129a

HISTIDINE-RICH GLYCOPROTEIN PRECURSOR.

4.2e-06:37:51

PLASMODIUM LOPHURAE.

20 P04929

HRIFA023154a

GLYCOPROTEIN X PRECURSOR.

8.2e-05:140:27

25 EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).

P28968

30

HRIFA023212a

A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.

8.3e-10:249:32

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P32323

35

HRIFA023227a

GALACTOSE-PROTON SYMPORT (GALACTOSE TRANSPORTER).

9.2e-15:180:30

ESCHERICHIA COLI.

P37021

40

HRIFA023257a

PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.

2.4e-118:229:88

RATTUS NORVEGICUS (RAT).

P38378

45

HRIFA023304a

PROBABLE CALCIUM-TRANSPORTING ATPASE 3 (EC 3.6.1.38) (ENDOPLASMIC RETICULUM CA2+-AT-
PASE).

1.3e-23:222:29

50 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P39524

55

HRIFA023434a

VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.6 (RCK2) (KV2).

0.00018:157:30

RATTUS NORVEGICUS (RAT).

P17659

- 5 HRIFA023464a
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 2 PRECURSOR.
1.0e-11:75:46
ORYZA SATIVA (RICE).
P29834
- 10 HRIFA023489a
HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I.
4.4e-09:230:23
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q10297
- 15 HRIFA023634a
EBNA-1 NUCLEAR PROTEIN.
1.8e-08:113:45
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211
- 20 HRIFA023767a
CYTOCHROME B5.
1.1e-12:92:38
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P40312
- 25 HRIFA023894a
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
3.6e-05:80:40
MUS MUSCULUS (MOUSE).
P05142
- 30 HRIFA023923a
CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1).
4.2e-76:128:85
HOMO SAPIENS (HUMAN).
P00395
- 35 HRIFA024088a
NEURON-SPECIFIC X11 PROTEIN (FRAGMENT).
1.1e-05:118:32
MUS MUSCULUS (MOUSE).
P98084
- 40 HRIFA024132a
VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.9.
6.5e-40:136:61
HOMO SAPIENS (HUMAN).
P51787
- 45 HRIFA024185a
ETS-DOMAIN TRANSCRIPTION FACTOR ERF.
0.55:128:29
HOMO SAPIENS (HUMAN).
P50548
- 50 HRIFA024197a
MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (72 KD MITOCHONDRIAL OUTER MEMBRANE PROTEIN) (MITOCHONDRIAL IMPORT RECEPTOR FOR THE ADP/ATP (CARRIER) (TRANSLOCASE OF OUTER MEMBRANE TOM70).

7.5e-09:93:34
NEUROSPORA CRASSA.
P23231

5 HRIFA024218a
PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.
6.7e-06:180:36
HOMO SAPIENS (HUMAN).
P02452

10 HRIFA024255a
HYPOTHETICAL 116.3 KD PROTEIN C26F1.09 IN CHROMOSOME I.
4.8e-23:172:33
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q10496

15 HRIFA024305a
CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-6 (FRAGMENT).
0.047:47:29
20 HOMO SAPIENS (HUMAN).
P18850

25 HRIFA024392a
TRANSMEMBRANE PROTEIN SEX PRECURSOR.
6.7e-24:119:43
HOMO SAPIENS (HUMAN).
P51805

30 HRIFA024423a
COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).
2.1e-18:109:41
CRICETULUS GRISEUS (CHINESE HAMSTER).
P49020

35 HRIFA024473a
COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).
3.3e-05:106:41
BOS TAURUS (BOVINE).
P02453

40 HRIFA024482a
PISTIL-SPECIFIC EXTENSIN-LIKE PROTEIN PRECURSOR (PELP).
1.2e-07:99:31
45 NICOTIANA TABACUM (COMMON TOBACCO).
Q03211

50 HRIFA024504a
ESTRADIOL 17 BETA-DEHYDROGENASE 3 (EC 1.1.1.62) (17-BETA-HSD 3) (TESTICULAR 17-BETA-HY-
DROXYSTEROID DEHYDROGENASE).
2.6e-43:205:49
HOMO SAPIENS (HUMAN).
P37058

55 HRIFA024543a
GLYCOPROTEIN X PRECURSOR.
1.5e-06:257:28
EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).
P28968

- 5 HRIFA024718a
 BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE) (ACID BETA-GALACTOSIDASE).
 5.3e-45:168:52
 MUS MUSCULUS (MOUSE).
 P23780
- 10 HRIFA024767a
 SODIUM CHANNEL PROTEIN (NA+ CHANNEL).
 7.4e-30:221:31
 10 ELECTROPHORUS ELECTRICUS (ELECTRIC EEL).
 P02719
- 15 HRIFA024884a
 HYPOTHETICAL 13.6 KD PROTEIN IN SPT4-ROM1 INTERGENIC REGION.
 0.0089:23:65
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 P53245
- 20 HRIFA024893a
 REGULATORY PROTEIN E2.
 0.0021:167:31
 HUMAN PAPILLOMAVIRUS TYPE 8.
 P06422
- 25 HRIFA024937a
 GNS1 PROTEIN.
 1.0e-15:173:33
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 P25358
- 30 HRIFA024978a
 MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).
 0.00019:150:32
 HOMO SAPIENS (HUMAN).
 Q02817
- 35 HRIFA024994a
 EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).
 5.3e-22:145:46
 40 NICOTIANA TABACUM (COMMON TOBACCO).
 P13983
- 45 HRIFA025033a
 TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (VMW118 PROTEIN).
 0.50:215:29
 HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HG52).
 P28284
- 50 HRIFA025046a
 PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38).
 1.7e-41:104:48
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 P39986
- 55 HRIFA025250a
 "PROTEIN KINASE C, BRAIN ISOZYME (EC 2.7.1.-) (PKC) (DPKC53E(BR))."
 7.4e-17:126:34
 DROSOPHILA MELANOGASTER (FRUIT FLY).

P05130

HRIFA025261a
 MYOSIN I ALPHA (MMI-ALPHA).

5 2.3e-64:141:84
 MUS MUSCULUS (MOUSE).
 P46735

10 HRIFA025290a
 EBNA-1 NUCLEAR PROTEIN.
 0.016:79:40
 EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
 P03211

15 HRIFA025327a
 PROLINE-RICH PROTEIN MP-2 PRECURSOR.
 2.3e-06:104:37
 MUS MUSCULUS (MOUSE).
 P05142

20 HRIFA025353a
 GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 2 PRECURSOR.
 1.0e-11:75:46
 ORYZA SATIVA (RICE).
 P29834

25 HRIFA025479a
 PROTEASE DEGS PRECURSOR (EC 3.4.21.-).
 3.0e-05:112:33
 30 ESCHERICHIA COLI.
 P31137

35 HRIFA025488a
 PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSOR (FRAGMENTS).
 9.5e-05:104:40
 MUS MUSCULUS (MOUSE).
 P08121

40 HRIFA025492a
 SERINE/THREONINE-SPECIFIC PROTEIN KINASE MINIBRAIN HOMOLOG (EC 2.7.1.-) (HP86) (DYRK).
 1.8e-53:159:69
 HOMO SAPIENS (HUMAN).
 Q13627

45 HRIFA025636a
 MITOCHONDRIAL RESPIRATORY CHAIN COMPLEXES ASSEMBLY PROTEIN RCA1 (EC 3.4.24.-) (TAT-BIND-
 ING HOMOLOG 12).
 4.7e-32:81:66
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 P40341

50 HRIFA025695a
 PEREGRIN (BR140 PROTEIN).
 3.1e-40:227:43
 HOMO SAPIENS (HUMAN).
 P55201

HRIFA025703a

CELL SURFACE ANTIGEN 114/A10 PRECURSOR.

1.8e-08:71:42

MUS MUSCULUS (MOUSE).

P19467

5

HRIFA025706a

GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).

1.2e-28:111:44

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

10

P43636

HRIFA025766a

CYTOCHROME B5.

4.2e-13:133:33

15

ORYCTOLAGUS CUNICULUS (RABBIT).

P00169

HRIFA025771a

HYPOTHETICAL 22.2 KD PROTEIN IN NSR1-TIF4631 INTERGENIC REGION.

20

6.7e-10:129:31

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P53288

25

HRIFA025778a

A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.

1.5e-05:212:30

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P32323

30

HRIFA025800a

HYPOTHETICAL 37.4 KD PROTEIN IN IRR1-TIM44 INTERGENIC REGION.

3.7e-18:165:33

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P40544

35

HRIFA025904a

COMPLEMENT RECEPTOR TYPE 1 PRECURSOR (C3B/C4B RECEPTOR) (CD35 ANTIGEN).

2.6e-05:211:28

HOMO SAPIENS (HUMAN).

40

P17927

HRIFA025907a

INTERFERON GAMMA UP-REGULATED I-5111 PROTEIN PRECURSOR (IGUPI-5111).

2.1e-38:176:38

45

HOMO SAPIENS (HUMAN).

Q06323

50

HRIFA025913a

DOLICHYL-PHOSPHATE-MANNOSE--PROTEIN MANNOSYLTRANSFERASE 4 (EC 2.4.1.109).

2.5e-32:185:37

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P46971

55

HRIFA025936a

TRANSCRIPTIONAL ACTIVATOR FE65.

3.4e-09:43:46

RATTUS NORVEGICUS (RAT).

P46933

- 5 HRIFA025966a
SYNAPTOTAGMIN III.
4.5e-05:93:33
RATTUS NORVEGICUS (RAT).
P40748
- 10 HRIFA025978a
"GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT DX5 PRECURSOR."
3.5e-06:224:28
TRITICUM AESTIVUM (WHEAT).
P10388
- 15 HRIFA026089a
BUTYROPHILIN PRECURSOR (BT).
1.1e-12:146:29
BOS TAURUS (BOVINE).
P18892
- 20 HRIFA026121a
FAS ANTIGEN LIGAND (APOPTOSIS ANTIGEN LIGAND) (APTL).
9.7e-06:72:43
HOMO SAPIENS (HUMAN).
P48023
- 25 HRIFA026242a
HYPOTHETICAL 73.0 KD PROTEIN IN CLA4-MID1 INTERGENIC REGION.
7.4e-09:188:26
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P48566
- 30 HRIFA026265a
DNA BINDING PROTEIN S1FA.
0.67:43:37
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
P42551
- 35 HRIFA026303a
SALIVARY PROLINE-RICH PROTEIN PO PRECURSOR (ALLELE S).
0.014:88:32
HOMO SAPIENS (HUMAN).
P10163
- 40 HRIFA026316a
EBNA-2 NUCLEAR PROTEIN.
1.5e-07:82:35
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P12978
- 45 HRIFA026351a
FLI-1 ONCOGENE (ERGB TRANSCRIPTION FACTOR).
0.019:89:31
HOMO SAPIENS (HUMAN).
Q01543
- 50 HRIFA026364a
PROBABLE G PROTEIN-COUPLED RECEPTOR EDG-1.
8.3e-40:167:49
RATTUS NORVEGICUS (RAT).

P48303

- 5 HRIFA026382a
T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11).
6.2e-10:135:38
ORYCTOLAGUS CUNICULUS (RABBIT).
P06333
- 10 HRIFA026465a
COLLAGEN ALPHA 1(IX) CHAIN PRECURSOR (FRAGMENTS).
8.6e-07:158:35
GALLUS GALLUS (CHICKEN).
P12106
- 15 HRIFA026496a
ZINC FINGER PROTEIN 140.
5.9e-24:122:52
HOMO SAPIENS (HUMAN).
P52738
- 20 HRIFA026519a
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
1.3e-08:130:36
MUS MUSCULUS (MOUSE).
P05142
- 25 HRIFA026564a
GLYCOPROTEIN X PRECURSOR
1.8e-10:225:25
30 EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).
P28968
- 35 HRIFA026576a
"ADP,ATP CARRIER PROTEIN, HEART/SKELETAL MUSCLE ISOFORM T1 (ADP/ATP TRANSLOCASE 1) (AD-
ENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1)." 1.7e-09:116:34
HOMO SAPIENS (HUMAN).
P12235
- 40 HRIFA026615a
REGULATORY PROTEIN E2.
0.0024:132:31
HUMAN PAPILLOMAVIRUS TYPE 9.
P36780
- 45 HRIFA026618a
PROTEIN Q300.
1.2e-05:27:66
MUS MUSCULUS (MOUSE).
50 Q02722
- 55 HRIFA026659a
SERINE/THREONINE-PROTEIN KINASE SGK (EC 2.7.1.-) (SERUM/GLUCOCORTICOID-REGULATED KI-
NASE).
2.0e-10:81:45
RATTUS NORVEGICUS (RAT).
Q06226

- 5 HRIFA026764a
MRC OX-45 SURFACE ANTIGEN PRECURSOR (BCM1 SURFACE ANTIGEN) (BLAST-1) (CD48).
3.4e-05:162:25
RATTUS NORVEGICUS (RAT).
P10252
- 10 HRIFA026789a
PUTATIVE GENERAL NEGATIVE REGULATOR OF TRANSCRIPTION C16C9.04C.
8.1e-22:175:38
10 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q09818
- 15 HRIFA026813a
"PROTEIN KINASE C, MU TYPE (EC 2.7.1.-) (NPKC-MU)." 7.1e-89:256:67
HOMO SAPIENS (HUMAN).
Q15139
- 20 HRIFA026860a
MONOCARBOXYLATE TRANSPORTER 2 (MCT 2). 2.6e-19:103:43
MESOCRICETUS AURATUS (GOLDEN HAMSTER).
P53988
- 25 HRIFA026923a
CCAAT DISPLACEMENT PROTEIN (HOMEobox PROTEIN CLOX) (CLOX-1) (FRAGMENT). 0.18:119:36
CANIS FAMILIARIS (DOG).
P39881
- 30 HRIFA027012a
"MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE (EC 3.2.1.113) (MAN(9)-ALPHA-MANNOSIDASE) (ALPHA-MANNOSIDASE 1A)." 1.8e-44:234:41
35 MUS MUSCULUS (MOUSE).
P45700
- 35 HRIFA027045a
HYPOTHETICAL PROTEIN HI0519. 2.7e-27:181:38
40 HAEMOPHILUS INFLUENZAE.
P44742
- 45 HRIFA027125a
ZINC FINGER PROTEIN 133. 3.9e-33:70:61
HOMO SAPIENS (HUMAN).
P52736
- 50 HRIFA027173a
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (VMW118 PROTEIN). 0.15:137:27
55 HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HG52).
P28284
- 55 HRIFA027179a
EXCISION REPAIR PROTEIN ERCC-6 (COCKAYNE SYNDROME PROTEIN CSB). 3.6e-30:90:77

HOMO SAPIENS (HUMAN).
Q03468

5 HRIFA027187a
B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).
4.7e-11:44:61
HOMO SAPIENS (HUMAN).
P20931

10 HRIFA027327a
COLLAGEN ALPHA 1(X) CHAIN PRECURSOR.
3.8e-07:184:35
HOMO SAPIENS (HUMAN).
Q03692

15 HRIFA027329a
SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.
9.1e-08:195:29
DROSOPHILA ERECTA (FRUIT FLY).
P13730

20 HRIFA027355a
B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).
1.9e-06:33:72
HOMO SAPIENS (HUMAN).
P20931

25 HRIFA027485a
COLLAGEN ALPHA 1(XI) CHAIN PRECURSOR.
0.00099:174:36
HOMO SAPIENS (HUMAN).
P12107

30 HRIFA027536a
VITELLINE MEMBRANE PROTEIN VM26AB PRECURSOR (PROTEIN TU-4) (PROTEIN SV23).
0.0042:104:35
DROSOPHILA MELANOGASTER (FRUIT FLY).
P13238

35 HRIFA027549a
D(4) DOPAMINE RECEPTOR (D(2C) DOPAMINE RECEPTOR).
0.00023:101:44
HOMO SAPIENS (HUMAN).
P21917

40 HRIFA027622a
GUANOSINE-DIPHOSPHATASE (EC 3.6.1.42) (GDPASE).
2.2e-23:146:45
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P32621

45 HRIFA027625a
CALCIUM-TRANSPORTING ATPASE 1 (EC 3.6.1.38) (GOLGI CA2+-ATPASE).
1.1e-57:220:54
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P13586

HRIFA027644a

EP 1 130 094 A2

- COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).
7.5e-05:72:40
RATTUS NORVEGICUS (RAT).
P02454
- 5 HRIFA027656a
NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE 1).
1.6e-13:149:34
- 10 DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).
P18160
- HRIFA027673a
CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR.
6.4e-06:47:57
- 15 HOMO SAPIENS (HUMAN).
P29279
- HRIFA027681a
SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-).
1.1e-13:158:31
- 20 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P08458
- HRIFA027714a
HYPOTHETICAL 146.8 KD PROTEIN C34E10.5 IN CHROMOSOME III.
7.2e-06:146:30
- 25 CAENORHABDITIS ELEGANS.
P46580
- HRIFA027722a
SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).
2.7e-105:242:85
- 30 CANIS FAMILIARIS (DOG).
Q00004
- HRIFA027860a
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
8.3e-08:168:32
- 35 XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437
- HRIFA027867a
STANNIOCALCIN PRECURSOR (STC) (CORPUSCLES OF STANNIUS PROTEIN) (CS) (HYPOCALCIN) (TEL-EOCALCIN).
1.0:100:27
- 40 ANGUILLA AUSTRALIS (AUSTRALIAN EEL).
P18301
- HRIFA027940a
INHIBIN BETA C CHAIN PRECURSOR (ACTIVIN BETA-C CHAIN).
8.7e-15:149:38
- 45 HOMO SAPIENS (HUMAN).
P55103
- HRIFA028061a
PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).
9.7e-07:157:26
- 55 THERMOMONOSPORA CURVATA.

P49695

HRIFA028157a

5 HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 (CAT-1) (CAT1) (SYSTEM Y+ BASIC AMINO ACID
TRANSPORTER) (ECOTROPIC RETROVIRAL LEUKEMIA RECEPTOR HOMOLOG) (ERR) (ECOTROPIC RET-
ROVIRUS RECEPTOR HOMOLOG).

2.8e-71:201:68

HOMO SAPIENS (HUMAN).

P30825

10

HRIFA028187a

EBNA-1 NUCLEAR PROTEIN.

1.5e-09:131:38

EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).

15

P03211

10

HRIFA028262a

CELLULAR NUCLEIC ACID BINDING PROTEIN (CNBP).

7.2e-09:99:33

20

MUS MUSCULUS (MOUSE).

P53996

15

HRIFA028371a

PLASMINOGEN (EC 3.4.21.7) (FRAGMENT).

25

1.0e-08:103:33

RATTUS NORVEGICUS (RAT).

Q01177

20

HRIFA028402a

PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).

3.2e-33:204:39

THERMOMONOSPORA CURVATA.

P49695

25

HRIFA028440a

COLLAGEN ALPHA 4(IV) CHAIN PRECURSOR.

1.9e-07:192:36

HOMO SAPIENS (HUMAN).

P53420

30

HRIFA028468a

CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE IV CATALYTIC CHAIN (EC 2.7.1.123) (CAM
KINASE-GR) (CAMK IV) [CONTAINS: CALSPERMIN].

5.8e-32:178:44

35

RATTUS NORVEGICUS (RAT).

P13234

40

HRIFA028501a

VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.6 (RCK2) (KV2).

45

6.3e-05:161:31

RATTUS NORVEGICUS (RAT).

P17659

50

HRIFA028511a

ANKYRIN HOMOLOG PRECURSOR.

3.0e-19:176:34

CHROMATIUM VINOsum.

Q06527

- 5 HRIFA028576a
ACROSIN PRECURSOR (EC 3.4.21.10).
4.8e-08:78:46
ORYCTOLAGUS CUNICULUS (RABBIT).
P48038
- 10 HRIFA028614a
HISTIDINE-RICH GLYCOPROTEIN PRECURSOR.
1.0e-08:82:39
PLASMODIUM LOPHURAE.
P04929
- 15 HRIFA028651a
BAND 3 ANION TRANSPORT PROTEIN.
1.3e-18:156:32
GALLUS GALLUS (CHICKEN).
P15575
- 20 HRIFA028790a
PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38).
5.0e-18:212:29
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P39986
- 25 HRIFA028804a
CCAAT-BINDING FACTOR (CBF).
0.98:232:23
MUS MUSCULUS (MOUSE).
P53569
- 30 HRIFA028867a
REGULATORY PROTEIN E2.
0.0057:124:31
HUMAN PAPILLOMAVIRUS TYPE 25.
P36787
- 35 HRIFA028911a
HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR.
1.2e-09:206:33
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P47179
- 40 HRIFA028983a
HOMEOTIC GENE REGULATOR (BRAHMA PROTEIN).
0.0051:115:33
DROSOPHILA MELANOGASTER (FRUIT FLY).
P25439
- 45 HRIFA029002a
FIBRINOGEN BETA CHAIN.
3.2e-25:121:45
BOS TAURUS (BOVINE).
P02676
- 50 HRIFA029050a
RETINAL-CADHERIN PRECURSOR (R-CADHERIN) (R-CAD).
1.2e-10:134:32
GALLUS GALLUS (CHICKEN).

P24503

HRIFA029208a

RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17).

5 1.4e-14:64:59

RATTUS NORVEGICUS (RAT).

Q02975

HRIFA029209a

10 "ALPHA-MANNOSIDASE II (EC 3.2.1.114) (MANNOSYL-OLIGOSACCHARIDE 1,3-1,6-ALPHA-MANNOSIDASE) (MAN II) (GOLGI ALPHA-MANNOSIDASE II)."

2.3e-12:114:37

MUS MUSCULUS (MOUSE).

P27046

15

HRIFA029256a

GAP JUNCTION BETA-2 PROTEIN (CONNEXIN 26) (CX26).

1.8e-35:89:75

HOMO SAPIENS (HUMAN).

20

P29033

HRIFA029263a

SARCALUMENIN PRECURSOR.

2.1e-16:161:31

25

ORYCTOLAGUS CUNICULUS (RABBIT).

P13666

HRIFA029278a

30

"SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEP-TIDE IB-6" PEPTIDE P-H]."

3.5e-10:204:32

HOMO SAPIENS (HUMAN).

P04280

35

HRIFA029285a

GLYCOPROTEIN 25L PRECURSOR (GP25L).

4.9e-58:197:55

CANIS FAMILIARIS (DOG).

P27869

40

HRIFA029317a

HIGH AFFINITY SULPHATE TRANSPORTER 2.

2.3e-25:83:50

STYLOSANTHES HAMATA.

45

P53392

HRIFA029327a

MITOCHONDRIAL 2-OXOGLUTARATE/MALATE CARRIER PROTEIN (OGCP).

9.1e-34:227:37

50

BOS TAURUS (BOVINE).

P22292

HRIFA029349a

CUTICLE COLLAGEN 12 PRECURSOR.

55

5.1e-09:190:33

CAENORHABDITIS ELEGANS.

P20630

- 5 HRIFA029393a
PROBABLE G PROTEIN-COUPLED RECEPTOR APJ.
9.7e-69:165:84
HOMO SAPIENS (HUMAN).
P35414
- 10 HRIFA029398a
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (P135 PROTEIN) (IER 2.9/ER2.6).
0.011:170:34
BOVINE HERPESVIRUS TYPE 1 (STRAIN JURA).
P29128
- 15 HRIFA029425a
ALPHA CRYSTALLIN B CHAIN (ALPHA(B)-CRYSTALLIN).
2.0e-08:99:32
BOS TAURUS (BOVINE).
P02510
- 20 HRIFA029434a
"SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CPS) [CONTAINS: BASIC PEP-TIDE IB-6" PEPTIDE P-H].
2.6e-05:232:32
HOMO SAPIENS (HUMAN).
P04280
- 25 HRIFA029440a
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
0.00046:131:33
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437
- 30 HRIFA029460a
SYNAPTOTAGMIN III.
1.5e-08:102:35
RATTUS NORVEGICUS (RAT).
P40748
- 35 HRIFA029467a
GLYCOPROTEIN X PRECURSOR.
5.2e-07:182:31
EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).
P28968
- 40 HRIFA029508a
PROPERDIN PRECURSOR.
1.9e-06:218:32
HOMO SAPIENS (HUMAN).
P27918
- 45 HRIFA029511a
POTASSIUM CHANNEL PROTEIN EAG.
2.3e-66:139:61
DROSOPHILA MELANOGASTER (FRUIT FLY).
Q02280
- 50 HRIFA029602a
SEX-DETERMINING REGION Y PROTEIN (TESTIS-DETERMINING FACTOR).
1.0:37:37

SUS SCROFA (PIG).

P36393

HRIFA029649a

TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (VMW118 PROTEIN).

0.30:99:34

HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HG52).

P28284

HRIFA029715a

GROWTH ARREST AND DNA-DAMAGE-INDUCIBLE PROTEIN GADD153 (DNA-DAMAGE INDUCIBLE TRANSCRIPT 3) (DDIT3) (C/EBP-HOMOLOGOUS PROTEIN) (CHOP).

0.54:95:30

HOMO SAPIENS (HUMAN).

P35638

HRIFA029730a

HISTIDINE-RICH GLYCOPROTEIN PRECURSOR.

3.8e-05:131:29

PLASMODIUM LOPHURAE.

P04929

HRIFA029792a

PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).

9.0e-09:178:30

THERMOMONOSPORA CURVATA.

P49695

HRIFA029802a

TRAM PROTEIN (TRANSLOCATING CHAIN-ASSOCIATING MEMBRANE PROTEIN).

7.2e-73:204:69

CANIS FAMILIARIS (DOG).

Q01685

HRIFA029866a

PROTEIN KINASE BYR2 (EC 2.7.1.-) (PROTEIN KINASE STE8) (MAPK KINASE KINASE) (MAPKKK).

1.2e-27:144:45

SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).

P28829

HRIFA029932a

F-SPONDIN PRECURSOR.

9.1e-24:191:37

XENOPUS LAEVIS (AFRICAN CLAWED FROG).

P35447

HRIFA030025a

ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT).

1.0e-11:138:31

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P32802

HRIFA030045a

SARCALUMENIN PRECURSOR.

2.4e-20:151:32

ORYCTOLAGUS CUNICULUS (RABBIT).

P13666

- 5 HRIFA030103a
HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.
2.1e-05:215:29
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53214
- 10 HRIFA030106a
SCO-SPONDIN (FRAGMENT).
0.53:60:36
BOS TAURUS (BOVINE).
P98167
- 15 HRIFA030147a
PUTATIVE MITOCHONDRIAL CARRIER YGR096W.
1.8e-10:93:34
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53257
- 20 HRIFA030250a
ENAMELIN (TUFTELIN).
3.7e-108:250:86
BOS TAURUS (BOVINE).
P27628
- 25 HRIFA030264a
SODIUM/GLUCOSE COTRANSPORTER 1 (NA(+)/GLUCOSE COTRANSPORTER 1) (HIGH AFFINITY SODIUM-GLUCOSE COTRANSPORTER).
3.3e-09:119:27
ORYCTOLAGUS CUNICULUS (RABBIT).
P11170
- 30 HRIFA030342a
ESTRADIOL 17 BETA-DEHYDROGENASE 3 (EC 1.1.1.62) (17-BETA-HSD 3) (TESTICULAR 17-BETA-HYDROXYSTEROID DEHYDROGENASE).
1.5e-42:203:49
HOMO SAPIENS (HUMAN).
P37058
- 35 HRIFA030370a
HYPOTHETICAL 56.2 KD PROTEIN CY31.25C.
8.0e-12:88:48
MYCOBACTERIUM TUBERCULOSIS.
Q10555
- 40 HRIFA030371a
"PROTEIN KINASE C, MU TYPE (EC 2.7.1.-) (NPKC-MU)." 1.6e-68:228:59
HOMO SAPIENS (HUMAN).
Q15139
- 45 HRIFA030381a
COLLAGEN 1(X) CHAIN PRECURSOR.
3.0e-05:204:30
GALLUS GALLUS (CHICKEN).
P08125
- 50 HRIFA030385a
COLLAGEN ALPHA 1(X) CHAIN PRECURSOR.

- 0.029:162:31
HOMO SAPIENS (HUMAN).
Q03692
- 5 HRIFA030411a
SERINE PALMITOYLTRANSFERASE 2 (EC 2.3.1.50) (LONG CHAIN BASE BIOSYNTHESIS PROTEIN 2) (SPT 2).
1.2e-27:115:53
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
10 Q09925
- HRIFA030448a
PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-).
2.5e-92:225:77
- 15 HOMO SAPIENS (HUMAN).
P27448
- HRIFA030456a
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
20 9.3e-08:127:35
MUS MUSCULUS (MOUSE).
P05142
- HRIFA030461a
25 CUTICLE COLLAGEN 12 PRECURSOR.
0.046:140:31
CAENORHABDITIS ELEGANS.
P20630
- HRIFA030472a
30 NUC-1 NEGATIVE REGULATORY PROTEIN PREG.
0.0030:98:31
NEUROSPORA CRASSA.
Q06712
- 35 HRIFA030509a
"INTERFERON-INDUCED, DOUBLE-STRANDED RNA-ACTIVATED PROTEIN KINASE (EC 2.7.1.-) (INTERFERON-INDUCIBLE RNA-DEPENDENT PROTEIN KINASE) (P68 KINASE) (P1/EIF-2A PROTEIN KINASE)." 2.5e-09:65:43
- 40 HOMO SAPIENS (HUMAN).
P19525
- HRIFA030511a
45 T-LYMPHOCYTE MATURATION-ASSOCIATED PROTEIN.
0.00010:99:33
HOMO SAPIENS (HUMAN).
P21145
- HRIFA030545a
50 PROBABLE SERINE/THREONINE-PROTEIN KINASE YNL020C (EC 2.7.1.-).
7.6e-21:165:35
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53974
- 55 HRIFA030566a
"GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)." 2.7e-07:221:30

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P08640

5 HRIFA030599a
GLYCOPROTEIN X PRECURSOR.

2.8e-05:236:27
EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).
P28968

10 HRIFA030629a
PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1) (PROLYL 4-HYDROXYLASE BETA SUB-UNIT) (CELLULAR THYROID HORMONE BINDING PROTEIN) (P55).

3.5e-16:115:38
BOS TAURUS (BOVINE).
P05307

15 HRIFA030642a
SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185).

2.5e-12:93:47
20 VOLVOX CARTERI.
P21997

25 HRIFA030662a
NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 (EC 1.6.5.3).
9.1e-120:279:83

HOMO SAPIENS (HUMAN).
P03886

30 HRIFA030839a
HYPOTHETICAL GENE 51 MEMBRANE PROTEIN.
1.0:66:27
ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV).
Q00135

35 HRIFA031091a
PROTEIN Q300.
0.0042:27:62
MUS MUSCULUS (MOUSE).
Q02722

40 HRIFA031126a
P2Y PURINOCEPTOR 5 (P2Y5) (PURINERGIC RECEPTOR 5) (RB INTRON ENCODED G-PROTEIN COUPLED RECEPTOR).
1.3e-06:70:34
45 HOMO SAPIENS (HUMAN).
P43657

50 HRIFA031249a
ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP33).
5.9e-05:166:31
RATTUS NORVEGICUS (RAT).
P04474

55 HRIFA031336a
CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN SUBUNIT B).
6.6e-15:97:38
PETROMYZON MARINUS (SEA LAMPREY).

P25210

HRIFA031395a
 COLD SHOCK PROTEIN CSPB (FRAGMENT).

5 0.95:32:40

BACILLUS GLOBISPORUS.
 P41018

HRIFA031397a
 REGULATORY PROTEIN E2.
 0.0077:145:35
 HUMAN PAPILLOMAVIRUS TYPE 47.
 P22420

HRIFA031438a
 GLUCOSE REPRESSION MEDIATOR PROTEIN.
 1.3e-06:176:26
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 P14922

HRIFA031869a
 TRANSCRIPTION FACTOR HES-1 (HAIRY AND ENHANCER OF SPLIT 1) (HAIRY-LIKE) (RHL).
 1.7e-18:163:41
 RATTUS NORVEGICUS (RAT).

25 Q04666

HRIFA031935a
 EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).
 1.8e-06:192:32
 ZEA MAYS (MAIZE).
 P14918

HRIFA031986a
 SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA (EC 2.7.1.-) (P68-PAK) (P21-ACTIVATED KINASE) (ALPHA-PAK) (PROTEIN KINASE MUK2).
 2.4e-49:222:47
 RATTUS NORVEGICUS (RAT).
 P35465

HRIFA032009a
 PROBABLE G PROTEIN-COUPLED RECEPTOR FROM T-CELLS PRECURSOR (GLUCOCORTICOID-INDUCED RECEPTOR).
 1.0e-17:118:36
 MUS MUSCULUS (MOUSE).
 P30731

HRIFA032011a
 MUSCARINIC ACETYLCHOLINE RECEPTOR M4.
 7.8e-35:184:32
 HOMO SAPIENS (HUMAN).
 P08173

HRIFA032070a
 MITOCHONDRIAL RNA SPLICING PROTEIN MSR4.
 2.1e-18:107:44
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 P23500

- 5 HRIFA032073a
SECRETOGRANIN III PRECURSOR (SGIII).
9.7e-69:182:76
MUS MUSCULUS (MOUSE).
P47867
- 10 HRIFA032079a
HYPOTHETICAL 49.3 KD PROTEIN C30D11.06C IN CHROMOSOME I.
3.5e-12:96:39
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q09906
- 15 HRIFA032097a
GLYCOPROTEIN J.
0.023:61:32
HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).
P06480
- 20 HRIFA032161a
CCAAT/ENHANCER BINDING PROTEIN DELTA (C/EBP DELTA) (NUCLEAR FACTOR NF-IL6-BETA) (NF-IL6-BETA).
0.22:56:42
HOMO SAPIENS (HUMAN).
P49716
- 25 HRIFA032186a
D-BINDING PROTEIN (DBP) (ALBUMIN D BOX-BINDING PROTEIN) (TAXREB302).
0.86:50:38
HOMO SAPIENS (HUMAN).
Q10586
- 30 HRIFA032224a
HYPOTHETICAL 52.7 KD PROTEIN C38C10.2 IN CHROMOSOME III.
2.6e-43:196:45
CAENORHABDITIS ELEGANS.
Q03567
- 35 HRIFA032257a
GLUCOSE REPRESSION MEDIATOR PROTEIN.
4.7e-07:204:25
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P14922
- 40 HRIFA032274a
ZINC FINGER PROTEIN 38 (ZFP-38) (CTFIN51) (TRANSCRIPTION FACTOR RU49).
7.8e-60:163:74
MUS MUSCULUS (MOUSE).
Q07231
- 45 HRIFA032275a
CELL DIVISION CONTROL PROTEIN 28 (EC 2.7.1.-).
7.2e-41:179:38
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P00546
- 50 HRIFA032360a
HYPOTHETICAL 84.3 KD PROTEIN ZK945.10 IN CHROMOSOME II.
3.0e-05:198:28

CAENORHABDITIS ELEGANS.
Q09625

5 HRIFA032389a
EBNA-1 NUCLEAR PROTEIN.
1.3e-05:86:39
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4). P03211

10 HRIFA032433a
GONADOTROPIN-RELEASING HORMONE RECEPTOR (GNRH-R).
3.1e-14:54:53
RATTUS NORVEGICUS (RAT).
P30969

15 HRIFA032453a
BUTYROPHILIN PRECURSOR (BT).
5.9e-13:162:32
BOS TAURUS (BOVINE).
P18892

20 HRIFA032478a
GLYCOPROTEIN X PRECURSOR.
3.8e-06:253:28
EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).
P28968

25 HRIFA032506a
COLLAGEN ALPHA 3(VI) CHAIN PRECURSOR.
1.2e-06:226:34
HOMO SAPIENS (HUMAN).
P12111

30 HRIFA032511a
COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR.
8.7e-09:229:34
HOMO SAPIENS (HUMAN).
Q07092

35 HRIFA032530a
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
9.0e-05:159:33
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437

40 HRIFA032587a
SYNAPTOTAGMIN (P65).
3.2e-08:72:52
APLYSIA CALIFORNICA (CALIFORNIA SEA HARE).
P41823

45 HRIFA032605a
ANTIGEN PEPTIDE TRANSPORTER 1 (APT1) (PEPTIDE TRANSPORTER TAP1) (PEPTIDE TRANSPORTER PSF1) (PEPTIDE SUPPLY FACTOR 1) (PSF-1) (PEPTIDE TRANSPORTER INVOLVED IN ANTIGEN PROCESSING 1).
8.4e-37:192:41
HOMO SAPIENS (HUMAN).
Q03518

5 HRIFA032642a
 PROLINE-RICH PROTEIN MP-2 PRECURSOR.
 5.0e-05:127:33
 MUS MUSCULUS (MOUSE).
 P05142

10 HRIFA032696a
 COLLAGEN ALPHA 1(II) CHAIN (FRAGMENTS).
 1.4e-13:200:38
 BOS TAURUS (BOVINE).
 P02459

15 HRIFA032730a
 K-GLYPCAN PRECURSOR.
 4.8e-67:180:68
 MUS MUSCULUS (MOUSE).
 P51655

20 HRIFA032820a
 GLUTAMIC ACID-RICH PROTEIN PRECURSOR.
 7.5e-05:192:23
 PLASMODIUM FALCIPARUM (ISOLATE FC27 / PAPUA NEW GUINEA).
 P13816

25 Homology search result 2

[0290] Homology of representative sequences of the 5'-end cluster to the data in Swiss-Prot database
 [0291] Representative sequence of the 5'-end cluster exhibiting relatively high homology (304 cluster: "exhibiting relatively high homology" means that the P value is 10^{-10} or less)

30 HRIFA000327a, HRIFA000432a, HRIFA000553a, HRIFA000564a, HRIFA000631a, HRIFA000683a, HRIFA000776a, HRIFA000814a, HRIFA001132a, HRIFA001138a, HRIFA001337a, HRIFA001341a, HRIFA001489a, HRIFA001712a, HRIFA001720a, HRIFA001942a, HRIFA001975a, HRIFA001984a, HRIFA002384a, HRIFA002503a, HRIFA002743a, HRIFA002766a, HRIFA002805a, HRIFA002891a, HRIFA002919a, HRIFA002980a, HRIFA003063a, HRIFA003093a, HRIFA003635a, HRIFA004006a, HRIFA004034a, HRIFA004112a, HRIFA004426a, HRIFA004490a, HRIFA004523a, HRIFA004663a, HRIFA004696a, HRIFA004714a, HRIFA004745a, HRIFA004919a, HRIFA005184a, HRIFA005231a, HRIFA005240a, HRIFA005271a, HRIFA005372a, HRIFA005392a, HRIFA005409a, HRIFA005420a, HRIFA005438a, HRIFA005462a, HRIFA005644a, HRIFA005720a, HRIFA005732a, HRIFA005760a, HRIFA005781a, HRIFA006183a, HRIFA006494a, HRIFA006510a, HRIFA006566a, HRIFA006586a, HRIFA006596a, HRIFA006649a, HRIFA006667a, HRIFA006730a, HRIFA006926a, HRIFA007013a, HRIFA007219a, HRIFA007228a, HRIFA007243a, HRIFA007352a, HRIFA007424a, HRIFA007435a, HRIFA007463a, HRIFA007493a, HRIFA007571a, HRIFA007659a, HRIFA007722a, HRIFA007745a, HRIFA008000a, HRIFA008200a, HRIFA008284a, HRIFA008314a, HRIFA008362a, HRIFA008459a, HRIFA008483a, HRIFA008547a, HRIFA008611a, HRIFA008661a, HRIFA008717a, HRIFA008784a, HRIFA008981a, HRIFA009101a, HRIFA009171a, HRIFA009220a, HRIFA009451a, HRIFA009482a, HRIFA009783a, HRIFA009881a, HRIFA010085a, HRIFA010090a,

45 HRIFA010130a, HRIFA010319a, HRIFA010394a, HRIFA010460a, HRIFA010790a, HRIFA010975a, HRIFA011016a, HRIFA011179a, HRIFA011197a, HRIFA011449a, HRIFA011659a, HRIFA011947a, HRIFA012278a, HRIFA012584a, HRIFA012625a, HRIFA012692a, HRIFA012795a, HRIFA012885a, HRIFA012914a, HRIFA012969a, HRIFA012990a, HRIFA013254a, HRIFA013265a, HRIFA013276a, HRIFA013376a, HRIFA013477a, HRIFA013586a, HRIFA013726a, HRIFA013744a, HRIFA013911a, HRIFA014006a, HRIFA014185a, HRIFA014336a, HRIFA014465a, HRIFA014500a, HRIFA014561a, HRIFA014568a, HRIFA014621a, HRIFA014688a, HRIFA014819a, HRIFA014951a, HRIFA014967a, HRIFA015063a, HRIFA015070a, HRIFA015246a, HRIFA015423a, HRIFA015453a, HRIFA015486a, HRIFA015506a, HRIFA015536a, HRIFA015547a, HRIFA015568a, HRIFA015756a, HRIFA015811a, HRIFA016070a, HRIFA016290a, HRIFA016430a, HRIFA016654a, HRIFA016758a, HRIFA017031a, HRIFA017257a, HRIFA017295a, HRIFA017312a, HRIFA017703a, HRIFA017855a, HRIFA018092a, HRIFA018131a, HRIFA018134a, HRIFA018580a, HRIFA018827a,

55 HRIFA018904a, HRIFA018993a, HRIFA019105a, HRIFA019136a, HRIFA019175a, HRIFA019262a, HRIFA019466a, HRIFA019867a, HRIFA019869a, HRIFA020272a, HRIFA020335a, HRIFA020349a, HRIFA020862a, HRIFA021213a, HRIFA021398a, HRIFA021499a, HRIFA021637a, HRIFA021651a, HRIFA021754a, HRIFA021781a, HRIFA022065a, HRIFA022139a, HRIFA022166a, HRIFA022177a, HRIFA022182a, HRIFA022227a, HRIFA022249a, HRIFA022265a,

HRIFA022328a, HRIFA022423a, HRIFA022528a, HRIFA022546a, HRIFA022564a, HRIFA022616a, HRIFA022671a,
 5 HRIFA022691a, HRIFA022707a, HRIFA022729a, HRIFA022737a, HRIFA022776a, HRIFA022875a, HRAFA022895a,
 HRIFA023007a, HRIFA023227a, HRIFA023257a, HRIFA023304a, HRIFA023464a, HRIFA023767a, HRIFA023923a,
 HRIFA024132a, HRIFA024255a, HRIFA024392a, HRIFA024423a, HRIFA024504a, HRIFA024718a, HRIFA024767a,
 HRIFA024937a, HRIFA024994a, HRIFA025046a, HRIFA025250a, HRIFA025261a, HRIFA025353a, HRIFA025492a,
 HRIFA025636a, HRIFA025695a, HRIFA025706a, HRIFA025766a, HRIFA025800a, HRIFA025907a, HRIFA025913a,
 HRIFA026089a, HRIFA026364a, HRIFA026496a, HRIFA026789a, HRIFA026813a, HRIFA026860a, HRIFA027012a,
 HRIFA027045a, HRIFA027125a, HRIFA027179a, HRIFA027187a, HRIFA027622a, HRIFA027625a, HRIFA027656a,
 HRIFA027681a, HRIFA027722a, HRIFA027940a, HRIFA028157a, HRIFA028402a, HRIFA028468a, HRIFA028511a,
 10 HRIFA028651a, HRIFA028790a, HRIFA029002a, HRIFA029208a, HRIFA029209a, HRIFA029256a, HRIFA029263a,
 HRIFA029285a, HRIFA029317a, HRIFA029327a, HRIFA029393a, HRIFA029511a, HRIFA029802a, HRIFA029866a,
 HRIFA029932a, HRIFA030025a, HRIFA030045a, HRIFA030250a, HRIFA030342a, HRIFA030370a, HRIFA030371a,
 HRIFA030411a, HRIFA030448a, HRIFA030545a, HRIFA030629a, HRIFA030642a, HRIFA030662a, HRIFA031336a,
 15 HRIFA031869a, HRIFA031986a, HRIFA032009a, HRIFA032011a, HRIFA032070a, HRIFA032073a, HRIFA032079a,
 HRIFA032224a, HRIFA032274a, HRIFA032275a, HRIFA032433a,
 HRIFA032453a, HRIFA032605a, HRIFA032696a, HRIFA032730a,

Homology search result 3

20 [0292] Representative sequence of the 5'-end cluster exhibiting relatively low homology (221 cluster: "exhibiting relatively low homology" means that the P value is higher than 10^{-10} and 10^{-4} or less)
 HRIFA000016a, HRIFA000071a, HRIFA000116a, HRIFA000123a, HRIFA000264a, HRIFA000415a, HRIFA000446a,
 HRIFA000695a, HRIFA000845a, HRIFA001971a, HRIFA002063a, HRIFA002102a, HRIFA002284a, HRIFA002309a,
 25 HRIFA002694a, HRIFA002762a, HRIFA002787a, HRIFA003055a, HRIFA003340a, HRIFA003402a, HRIFA003504a,
 HRIFA003892a, HRIFA003946a, HRIFA004162a, HRIFA004401a, HRIFA004780a, HRIFA005072a, HRIFA005102a,
 HRIFA005214a, HRIFA005255a, HRIFA005300a, HRIFA005369a, HRIFA005702a, HRIFA005728a, HRIFA005944a,
 HRIFA006298a, HRIFA006448a, HRIFA006572a, HRIFA006633a, HRIFA006642a, HRIFA007068a, HRIFA007244a,
 HRIFA007262a, HRIFA007512a, HRIFA007532a, HRIFA007565a, HRIFA007728a, HRIFA007909a, HRIFA008174a,
 30 HRIFA008426a, HRIFA008596a, HRIFA008790a, HRIFA008989a, HRIFA009578a, HRIFA009825a, HRIFA009852a,
 HRIFA009983a, HRIFA010005a, HRIFA010078a, HRIFA010152a, HRIFA010301a, HRIFA010361a, HRIFA010425a,
 HRIFA010466a, HRIFA010799a, HRIFA011580a, HRIFA011820a, HRIFA012167a, HRIFA012354a, HRIFA012427a,
 HRIFA012436a, HRIFA012515a, HRIFA012702a, HRIFA012737a, HRIFA013135a, HRIFA013235a, HRIFA013279a,
 35 HRIFA013589a, HRIFA013620a, HRIFA013919a, HRIFA013932a, HRIFA014056a, HRIFA014111a, HRIFA014133a,
 HRIFA014396a, HRIFA014397a, HRIFA014598a, HRIFA014702a, HRIFA014868a, HRIFA015219a, HRIFA015995a,
 HRIFA016214a, HRIFA016240a, HRIFA016255a, HRIFA016639a, HRIFA016669a, HRIFA016963a, HRIFA017457a,
 HRIFA017643a, HRIFA017670a,
 HRIFA017801a, HRIFA017836a, HRIFA017921a, HRIFA018238a, HRIFA018262a, HRIFA018287a, HRIFA018666a,
 HRIFA018688a, HRIFA018754a, HRIFA018794a, HRIFA018870a, HRIFA018931a, HRIFA019412a, HRIFA019490a,
 HRIFA019498a, HRIFA019532a, HRIFA019651a, HRIFA0201440, HRIFA020184a, HRIFA020453a, HRIFA020693a,
 40 HRIFA020707a, HRIFA020748a, HRIFA021061a, HRIFA021224a, HRIFA021494a, HRIFA021794a, HRIFA021855a,
 HRIFA021906a, HRIFA022156a, HRIFA022203a, HRIFA022234a, HRIFA022702a, HRIFA022728a, HRIFA022782a,
 HRIFA022865a, HRIFA022890a, HRIFA022985a, HRIFA023048a, HRIFA023069a, HRIFA023129a, HRIFA023154a,
 HRIFA023212a, HRIFA023489a, HRIFA023634a, HRIFA023894a, HRIFA024088a, HRIFA024197a, HRIFA024218a,
 45 HRIFA024473a, HRIFA024482a, HRIFA024543a, HRIFA025327a, HRIFA025479a, HRIFA025488a, HRIFA025703a,
 HRIFA025771a, HRIFA025778a, HRIFA025904a, HRIFA025966a, HRIFA025978a, HRIFA026121a, HRIFA026242a,
 HRIFA026316a, HRIFA026382a, HRIFA026465a, HRIFA026519a, HRIFA026564a, HRIFA026576a, HRIFA026618a,
 HRIFA026659a, HRIFA026764a, HRIFA027327a, HRIFA027329a, HRIFA027355a, HRIFA027644a, HRIFA027673a,
 HRIFA027714a, HRIFA027860a, HRIFA028061a, HRIFA028187a, HRIFA028262a, HRIFA028371a, HRIFA028440a,
 50 HRIFA028501a, HRIFA028576a, HRIFA028614a, HRIFA028911a, HRIFA029050a, HRIFA029278a, HRIFA029349a,
 HRIFA029425a, HRIFA029434a, HRIFA029460a, HRIFA029467a, HRIFA029508a, HRIFA029730a, HRIFA029792a,
 HRIFA030103a, HRIFA03147a,
 HRIFA030264a, HRIFA030381a, HRIFA030456a, HRIFA030509a, HRIFA030511a, HRIFA030566a, HRIFA030599a,
 HRIFA031126a, HRIFA031249a, HRIFA031438a, HRIFA031935a, HRIFA032257a, HRIFA032360a, HRIFA032389a,
 HRIFA032478a, HRIFA032506a, HRIFA032511a, HRIFA032530a, HRIFA032587a, HRIFA032642a, HRIFA032820a,

55 Homology search result 4

[0293] Representative sequence of the 5'-end cluster exhibiting low homology (115 cluster: "exhibiting low homology"

means that the P value is higher than 10^{-4} and 1 or less)

HRIFA001099a, HRIFA001200a, HRIFA001413a, HRIFA001439a, HRIFA001558a, HRIFA001866a, HRIFA001972a,
 HRIFA002689a, HRIFA003357a, HRIFA003592a, HRIFA003640a, HRIFA003883a, HRIFA005296a, HRIFA005500a,
 HRIFA005540a, HRIFA006250a, HRIFA006609a, HRIFA006798a, HRIFA007032a, HRIFA007152a, HRIFA007547a,
 5 HRIFA007829a, HRIFA007985a, HRIFA008212a, HRIFA008252a, HRIFA008976a, HRIFA009071a, HRIFA009123a,
 HRIFA009136a, HRIFA009339a, HRIFA009762a, HRIFA010176a, HRIFA010490a, HRIFA010736a, HRIFA010859a,
 HRIFA010891a, HRIFA010988a, HRIFA011105a, HRIFA011128a, HRIFA011484a, HRIFA011512a, HRIFA011926a,
 HRIFA012069a, HRIFA012151a, HRIFA013092a, HRIFA013103a, HRIFA013980a, HRIFA014024a, HRIFA014590a,
 10 HRIFA014620a, HRIFA015122a, HRIFA015351a, HRIFA015802a, HRIFA015902a, HRIFA015947a, HRIFA016599a,
 HRIFA017146a, HRIFA017190a, HRIFA017456a, HRIFA017791a, HRIFA017818a, HRIFA018447a, HRIFA019437a,
 HRIFA019958a, HRIFA020883a, HRIFA021007a, HRIFA021040a, HRIFA021445a, HRIFA021543a, HRIFA021620a,
 HRIFA021787a, HRIFA022055a, HRIFA022335a, HRIFA022348a, HRIFA022411a, HRIFA022462a, HRIFA022493a,
 15 HRIFA022714a, HRIFA023434a, HRIFA024185a, HRIFA024305a, HRIFA024884a, HRIFA024893a, HRIFA024978a,
 HRIFA025033a, HRIFA025290a, HRIFA026265a, HRIFA026303a, HRIFA026351a, HRIFA026615a, HRIFA026923a,
 HRIFA027173a, HRIFA027485a, HRIFA027536a, HRIFA027549a, HRIFA027867a, HRIFA028804a, HRIFA028867a,
 20 HRIFA028983a, HRIFA029398a,
 HRIFA029440a, HRIFA029602a, HRIFA029649a, HRIFA029715a, HRIFA030106a, HRIFA030385a, HRIFA030461a,
 HRIFA030472a, HRIFA030839a, HRIFA031091a, HRIFA031395a, HRIFA031397a, HRIFA032097a, HRIFA032161a,
 HRIFA032186a,

Homology search result 5

[0294] The result of the homology search in the SwissProt using the clone sequences of the 5'-ends.

25 Indicated are from the top,
 the name of the clone sequence,
 definition of the top hit data,
 the P-value: the length of the sequence used for comparison (nucleotide):similarity (%),
 the organism of which the top hit data is obtained,
 30 the Accession No. of the top hit data.

[0295] Data were not shown for the clones in which the P-value was higher than 1.

35 F-BNGH41000020
 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 (EC 1.6.5.3).
 1.2e-119:279:83
 HOMO SAPIENS (HUMAN).
 P03886

40 F-BNGH41000087
 PROPERDIN PRECURSOR.
 2.5e-06:218:32
 HOMO SAPIENS (HUMAN).
 P27918

45 F-BNGH41000091
 POTASSIUM CHANNEL PROTEIN EAG.
 3.1e-66:139:61
 DROSOPHILA MELANOGASTER (FRUIT FLY).
 Q02280

50 F-HEMBA1000006
 S-ANTIGEN PROTEIN PRECURSOR.
 3.0e-05:164:31
 PLASMODIUM FALCIPARUM (ISOLATE V1).
 P09593

F-HEMBA1000121

EP 1 130 094 A2

HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III.

8.2e-06:83:27

CAENORHABDITIS ELEGANS.

P34679

5

F-HEMBA1000128

PATHOGENESIS-RELATED PROTEIN 1 PRECURSOR (PR-1).

8.2e-08:89:34

ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).

10

P33154

F-HEMBA1000275

PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.

1.9e-06:231:34

15

GALLUS GALLUS (CHICKEN).

P02457

F-HEMBA1000300

!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!

20

1.4e-13:73:56

HOMO SAPIENS (HUMAN).

P39195

F-HEMBA1000349

25

ATP-BINDING CASSETTE TRANSPORTER 1.

2.6e-16:238:31

MUS MUSCULUS (MOUSE).

P41233

30

F-HEMBA1000443

PROLINE-RICH PROTEIN MP-2 PRECURSOR.

4.8e-06:120:35

MUS MUSCULUS (MOUSE).

P05142

35

F-HEMBA1000462

PUTATIVE GENERAL NEGATIVE REGULATOR OF TRANSCRIPTION C16C9.04C.

2.9e-21:86:52

40

SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).

Q09818

F-HEMBA1000477

HYPOTHETICAL 64.8 KD PROTEIN IN GDI1-COX15 INTERGENIC REGION.

3.3e-09:138:34

45

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P40085

50

F-HEMBA1000590

CARTILAGE MATRIX PROTEIN PRECURSOR (MATRILIN-1).

2.2e-27:117:48

GALLUS GALLUS (CHICKEN).

P05099

55

F-HEMBA1000634

TRAMS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (ALPHA-0 PROTEIN).

0.00027:85:43

HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).

P08393

- 5 F-HEMBA1000671
ZINC FINGER PROTEIN 140.
1.1e-44:155:47
HOMO SAPIENS (HUMAN).
P52738
- 10 F-HEMBA1000713
BLADDER CANCER 10 KD PROTEIN.
1.5e-42:81:97
HOMO SAPIENS (HUMAN).
060629
- 15 F-HEMBA1000732
FIBRILLIN 1 PRECURSOR.
6.3e-18:77:46
HOMO SAPIENS (HUMAN).
P35555
- 20 F-HEMBA1000745
SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEP-TIDE IB-6; PEPTIDE P-H].
5.2e-06:105:33
- 25 HOMO SAPIENS (HUMAN).
P04280
- 30 F-HEMBA1000835
FIBRILLIN 2 PRECURSOR.
2.1e-42:214:44
HOMO SAPIENS (HUMAN).
P35556
- 35 F-HEMBA1000875
ZINC FINGER PROTEIN 133.
5.8e-16:49:87
HOMO SAPIENS (HUMAN).
P52736
- 40 F-HEMBA1000907
PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.
2.2e-05:172:34
MUS MUSCULUS (MOUSE).
P11087
- 45 F-HEMBA1000940
GAP JUNCTION CX43.4 PROTEIN (CONNEXIN 43.4) (CX43.4).
1.4e-20:90:42
- 50 BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO).
Q92052
- F-HEMBA1000962
WATER-STRESS INDUCIBLE PROTEIN RAB21.
0.089:122:25
- 55 ORYZA SATIVA (RICE).
P12253
- F-HEMBA1001184

EP 1 130 094 A2

SH3BGR PROTEIN (21-GLUTAMIC ACID-RICH PROTEIN) (21-GARP).

4.9e-33:100:60

HOMO SAPIENS (HUMAN).

P55822

5

F-HEMBA1001221

AGRIN PRECURSOR.

1.7e-26:239:32

GALLUS GALLUS (CHICKEN).

10

P31696

F-HEMBA1001228

CARTILAGE OLIGOMERIC MATRIX PROTEIN PRECURSOR (COMP).

7.7e-114:147:83

15

HOMO SAPIENS (HUMAN).

P49747

F-HEMBA1001272

SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53).

20

5.8e-06:129:33

HOMO SAPIENS (HUMAN).

Q15427

25

F-HEMBA1001296

TRANSCRIPTION FACTOR BF-2 (BRAIN FACTOR 2) (BF2) (CBF-2) (T-14-6).

0.0019:115:36

GALLUS GALLUS (CHICKEN).

Q98937

30

F-HEMBA1001297

50S RIBOSOMAL PROTEIN L37E (L35E).

0.65:40:40

HALOARCULA MARISMORTUI (HALOBACTERIUM MARISMORTUI).

P32410

35

F-HEMBA1001390

SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).

0.00050:89:33

NEPHILA CLAVIPES (ORB SPIDER).

40

P46804

F-HEMBA1001563

B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).

0.00041:34:61

45

HOMO SAPIENS (HUMAN).

P20931

50

F-HEMBA1001621

PROBABLE G PROTEIN-COUPLED RECEPTOR APJ.

1.1e-64:105:72

HOMO SAPIENS (HUMAN).

P35414

55

F-HEMBA1001878

VEGETABLE INCOMPATIBILITY PROTEIN HET-E-1.

1.3e-24:170:35

PODOSPORA ANSERINA.

Q00808

- 5 F-HEMBA1001886
 ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).
 1.8e-94:273:64
 HOMO SAPIENS (HUMAN).
 Q03923
- 10 F-HEMBA1002048
 EARLY ANTIGEN PROTEIN D (EA-D).
 0.13:93:34
 EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
 P03191
- 15 F-HEMBA1002131
 PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE 1 PRECURSOR (EC 1.14.11.4) (LYSYL HYDROXYLASE 1) (LH1).
 6.3e-12:140:30
 GALLUS GALLUS (CHICKEN).
 P24802
- 20 F-HEMBA1002163
 HYPOTHETICAL 40.7 KD PROTEIN IN DAK1-ORC1 INTERGENIC REGION.
 2.1e-10:204:27
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 Q04651
- 25 F-HEMBA1002164
 BIOTIN CARBOXYL CARRIER PROTEIN OF ACETYL-COA CARBOXYLASE PRECURSOR (EC 6.4.1.2) (BC-CP).
 0.022:62:32
 30 GLYCINE MAX (SOYBEAN).
 Q42783
- 35 F-HEMBA1002167
 ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7).
 5.2e-31:247:31
 BUNGARUS FASCIATUS (BANDED KRAIT).
 Q92035
- 40 F-HEMBA1002178
 PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE 1 PRECURSOR (EC 1.14.11.4) (LYSYL HYDROXYLASE 1) (LH1).
 1.5e-11:140:30
 GALLUS GALLUS (CHICKEN).
 P24802
- 45 F-HEMBA1002195
 VEGETABLE INCOMPATIBILITY PROTEIN HET-E-1.
 5.0e-07:52:36
 50 PODOSPORA ANSERINA.
 Q00808
- 55 F-HEMBA1002227
 MYRISTOYLATED ALANINE-RICH C-KINASE SUBSTRATE (MARCKS) (ACAMP-81).
 0.00063:21:100
 BOS TAURUS (BOVINE).
 P12624
- F-HEMBA1002239

EP 1 130 094 A2

!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!

1.5e-33:101:70

HOMO SAPIENS (HUMAN).

P39192

5

F-HEMBA1002316

EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).

4.6e-08:186:32

SORGHUM VULGARE (SORGHUM).

10 P24152

10

F-HEMBA1002420

WISKOTT-ALDRICH SYNDROME PROTEIN HOMOLOG (WASP).

0.0078:19:68

15 MUS MUSCULUS (MOUSE).

P70315

15

F-HEMBA1002421

SYNDECAN-2 PRECURSOR (FIBROGLYCAN) (HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN)
(HSPG) (SYND2).

1.1e-52:107:97

HOMO SAPIENS (HUMAN).

P34741

20

F-HEMBA1002524

ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP33).

5.0e-05:104:34

RATTUS NORVEGICUS (RAT).

P04474

25

F-HEMBA1002551

HYPOTHETICAL WD-REPEAT PROTEIN SLR0143.

9.9e-09:128:29

SYNECHOCYSTIS SP. (STRAIN PCC 6803).

30 P74442

30

F-HEMBA1002767

N-ACETYLGLUCOSAMINE SYNTHASE (EC 2.4.1.90) (N-ACETYLGLUCOSAMINE (BETA 1→4)GALACTOSYL-TRANSFERASE) (EC 2.4.1.38) (LACTOSE SYNTHASE A PROTEIN (EC 2.4.1.22)) (GALACTOSYLTRANSFERASE) (GT).

8.0e-92:246:67

MUS MUSCULUS (MOUSE).

P15535

35

F-HEMBA1002985

TRANSCRIPTION FACTOR GATA-6 (GATA BINDING FACTOR-6).

0.060:49:34

MUS MUSCULUS (MOUSE).

Q61169

40

F-HEMBA1002992

HOLOTRICIN 3 PRECURSOR.

0.0035:64:37

HOLOTRICHIA DIOMPHALIA.

45 Q25055

50

F-HEMBA1003047

BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (EC 3.4.24.-) (BMP-1).

1.5e-23:216:31
HOMO SAPIENS (HUMAN).
P13497

5 F-HEMBA1003072
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
6.8e-09:129:41
MUS MUSCULUS (MOUSE).
P05142

10 F-HEMBA1003101
PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR.
2.2e-10:124:37
HOMO SAPIENS (HUMAN).
P08123

15 F-HEMBA1003120
ZINC FINGER PROTEIN 140.
4.8e-23:43:74
HOMO SAPIENS (HUMAN).
P52738

20 F-HEMBA1003230
FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90).
2.7e-41:239:39
MUS MUSCULUS (MOUSE).
Q08878

25 F-HEMBA1003294
!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!
7.0e-34:84:69
HOMO SAPIENS (HUMAN).
P39194

30 F-HEMBA1003315
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1.8 PRECURSOR (GRP 1.8).
0.00012:178:32
PHASEOLUS VULGARIS (KIDNEY BEAN) (FRENCH BEAN).
P10496

35 F-HEMBA1003392
LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR (LRP) (ALPHA-2-MAC-ROGLOBULIN RECEPTOR) (A2MR).
1.1e-31:202:37

40 GALLUS GALLUS (CHICKEN).
P98157

45 F-HEMBA1003399
MVP1 PROTEIN.
5.6e-12:67:38
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P40959

50 F-HEMBA1003487
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
4.5e-08:175:29
MUS MUSCULUS (MOUSE).
P05142

EP 1 130 094 A2

- 5 F-HEMBA1003497
ZINC FINGER PROTEIN 151 (POLYOMAVIRUS LATE INITIATOR PROMOTER BINDING PROTEIN) (LP-1)
(ZINC FINGER PROTEIN Z13).
9.3e-18:171:33
MUS MUSCULUS (MOUSE).
Q60821
- 10 F-HEMBA1003530
SALIVARY PROLINE-RICH PROTEIN II-1 (FRAGMENT).
9.9e-12:122:35
HOMO SAPIENS (HUMAN).
P81489
- 15 F-HEMBA1003602
PROLINE-RICH PROTEIN MP-3 (FRAGMENT).
0.98:114:33
MUS MUSCULUS (MOUSE).
P05143
- 20 F-HEMBA1003732
TRANSCRIPTIONAL REGULATORY PROTEIN ALGP (ALGINATE REGULATORY PROTEIN ALGR3).
0.35:225:28
PSEUDOMONAS AERUGINOSA.
P15276
- 25 F-HEMBA1003945
HYPOTHETICAL 43.7 KD PROTEIN C24B11.08C IN CHROMOSOME I.
2.9e-48:268:41
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q09895
- 30 F-HEMBA1004007
THYROID TRANSCRIPTION FACTOR 1 (THYROID NUCLEAR FACTOR 1) (TTF-1) (FRAGMENT).
0.90:60:30
CAVIA PORCELLUS (GUINEA PIG).
P97273
- 35 F-HEMBA1004067
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (AL-
PHA-0 PROTEIN).
3.0e-05:200:31
HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).
P08393
- 40 F-HEMBA1004085
GLUCOSE REPRESSION MEDIATOR PROTEIN.
0.0030:190:26
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P14922
- 45 F-HEMBA1004110
EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15).
1.2e-14:102:36
MUS MUSCULUS (MOUSE).
P42567
- 50 F-HEMBA1004250
CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).

1.8e-08:150:33
 DROSOPHILA MELANOGASTER (FRUIT FLY).
 P33450

5 F-HEMBA1004391
 TUMOR SUPPRESSOR PROTEIN DCC PRECURSOR.
 4.5e-09:96:35
 MUS MUSCULUS (MOUSE).
 P70211

10 F-HEMBA1004444
 GLYCOPROTEIN 25L PRECURSOR (GP25L).
 4.6e-41:148:52
 CANIS FAMILIARIS (DOG).
 P27869

15 F-HEMBA1004454
 CD9 ANTIGEN.
 0.0070:24:70
 20 BOS TAURUS (BOVINE).
 P30932

F-HEMBA1004505
 25 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ISOFORM 1 (EC 3.2.1.113) (MAN(9)-ALPHA-MANNOSIDASE).
 7.0e-45:239:43
 DROSOPHILA MELANOGASTER (FRUIT FLY).
 P53624

30 F-HEMBA1004785
 MODIFIER 3 PROTEIN (M33).
 7.4e-26:76:61
 MUS MUSCULUS (MOUSE).
 P30658

35 F-HEMBA1004797
 PROTEIN Q300.
 0.00071:21:66
 MUS MUSCULUS (MOUSE).
 Q02722

40 F-HEMBA1004952
 EBNA-1 NUCLEAR PROTEIN.
 2.4e-05:67:49
 45 EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
 P03211

F-HEMBA1004971

50 F-HEMBA1004982
 MULTIDRUG RESISTANCE PROTEIN 2 (MULTIDRUG-EFFLUX TRANSPORTER 2).
 8.6e-08:144:25
 BACILLUS SUBTILIS.
 P39843

55 F-HEMBA1005070
 HYPOTHETICAL PROTEIN KIAA0310.
 1.0e-38:140:68

HOMO SAPIENS (HUMAN).
O15027

F-HEMBA1005084

NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE 1).

2.5e-10:102:37

DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).

P18160

10 F-HEMBA1005145

PROLINE-RICH PROTEIN MP-2 PRECURSOR.

1.8e-06:85:37

MUS MUSCULUS (MOUSE).

P05142

15 F-HEMBA1005230

ZINC FINGER PROTEIN 140.

8.2e-20:83:66

HOMO SAPIENS (HUMAN).

20 P52738

F-HEMBA1005246

TRANSCRIPTION REGULATORY PROTEIN SNF5 (SWI/SNF COMPLEX COMPONENT SNF5) (TRANSCRIPTION FACTOR TYE4).

25 1.5e-09:132:34

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P18480

30 F-HEMBA1005267

B-CELL LYMPHOMA 3-ENCODED PROTEIN (BCL-3 PROTEIN).

1.9e-15:192:32

HOMO SAPIENS (HUMAN).

P20749

35 F-HEMBA1005337

ACIDIC PHOSPHOPROTEIN PRECURSOR (50 KD ANTIGEN).

8.0e-05:31:64

PLASMODIUM CHABAUDI.

Q02752

40 F-HEMBA1005430

MALE SPECIFIC SPERM PROTEIN MST84DB.

0.34:42:42

DROSOPHILA MELANOGASTER (FRUIT FLY).

45 Q01643

F-HEMBA1005449

PROCYCLIC FORM SPECIFIC POLYPEPTIDE B-ALPHA PRECURSOR (PROCYCLIN) (PARP B-ALPHA) (PSA-1).

50 4.5e-09:95:33

TRYPANOSOMA BRUCEI BRUCEI.

Q06084

F-HEMBA1005489

CHANNEL ASSOCIATED PROTEIN OF SYNAPSE-110 (CHAPSYN-110).

7.2e-05:90:36

HOMO SAPIENS (HUMAN).

Q15700

- 5 F-HEMBA1005522
COAGULATION FACTOR VII PRECURSOR (EC 3.4.21.21).
3.3e-17:78:51
ORYCTOLAGUS CUNICULUS (RABBIT).
P98139
- 10 F-HEMBA1005545
MUSCARINIC ACETYLCHOLINE RECEPTOR M3.
7.2e-91:211:85
HOMO SAPIENS (HUMAN).
P20309
- 15 F-HEMBA1005698
PROTEIN TRANSPORT PROTEIN SEC22 (PROTEIN SLY2).
3.3e-08:132:28
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P22214
- 20 F-HEMBA1005913
HYPOTHETICAL 5.8 KD PROTEIN.
0.97:43:30
CLOVER YELLOW MOSAIC VIRUS (CYMV).
P16485
- 25 F-HEMBA1005929
PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-).
6.6e-104:275:72
HOMO SAPIENS (HUMAN).
P27448
- 30 F-HEMBA1005945
BRITTLE-1 PROTEIN PRECURSOR.
7.8e-30:214:35
ZEA MAYS (MAIZE).
P29518
- 35 F-HEMBA1006016
!!!! ALU SUBFAMILY J WARNING ENTRY !!!!
1.9e-07:34:76
HOMO SAPIENS (HUMAN).
P39188
- 40 F-HEMBA1006171
PROBABLE E5 PROTEIN.
0.98:66:31
HUMAN PAPILLOMAVIRUS TYPE 33.
P06426
- 45 F-HEMBA1006276
ZINC FINGER PROTEIN 90 (ZFP-90) (ZINC FINGER PROTEIN NK10).
4.1e-07:56:57
MUS MUSCULUS (MOUSE).
Q61967
- 50 F-HEMBA1006299
BASIC PROLINE-RICH PEPTIDE P-E (IB-9).
0.11:38:28
HOMO SAPIENS (HUMAN).

P02811

F-HEMBA1006311

ZINC FINGER PROTEIN 23 (ZINC FINGER PROTEIN KOX16) (FRAGMENT).

5 0.91:22:45

HOMO SAPIENS (HUMAN).

P17027

F-HEMBA1006335

10 PERIPHERAL MYELIN PROTEIN 22 (PMP-22) (GROWTH-ARREST-SPECIFIC PROTEIN 3) (GAS3).

0.017:125:27

MUS MUSCULUS (MOUSE).

P16646

F-HEMBA1006357

SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2.

5.2e-40:136:52

HOMO SAPIENS (HUMAN).

O15127

F-HEMBA1006430

OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG.

2.7e-38:96:72

CAENORHABDITIS ELEGANS.

25 P46975

F-HEMBA1006482

SCO1 PROTEIN PRECURSOR.

7.1e-25:84:45

30 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P23833

F-HEMBA1006517

HYPOTHETICAL 93.4 KD PROTEIN IN STE3-GIN10 INTERGENIC REGION.

35 0.48:145:30

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P34239

F-HEMBA1006544

40 TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).

7.0e-11:210:37

HOMO SAPIENS (HUMAN).

000268

45 F-HEMBA1006572

ANTITHROMBIN-III PRECURSOR (ATIII) (FRAGMENT).

0.011:50:40

GALLUS GALLUS (CHICKEN).

Q03352

50 F-HEMBA1006658

SERINE/THREONINE-PROTEIN KINASE MIG-15 (EC 2.7.1.-).

4.6e-44:234:45

CAENORHABDITIS ELEGANS.

55 Q23356

F-HEMBA1006707

CARTILAGE MATRIX PROTEIN PRECURSOR (MATRILIN-1).

- 9.3e-34:159:50
GALLUS GALLUS (CHICKEN).
P05099
- 5 F-HEMBA1006724
PLATELET FACTOR 4 (PF-4).
0.025:65:27
SUS SCROFA (PIG).
P30034
- 10 F-HEMBA1006749
CARTILAGE MATRIX PROTEIN PRECURSOR (MATRILIN-1).
7.9e-37:147:53
GALLUS GALLUS (CHICKEN).
P05099
- 15 F-HEMBA1006770
FLOWERING TIME CONTROL PROTEIN FCA.
3.4e-27:139:39
- 20 ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
004425
- 25 F-HEMBA1006902
CARTILAGE MATRIX PROTEIN PRECURSOR (MATRILIN-1).
1.5e-37:137:51
GALLUS GALLUS (CHICKEN).
P05099
- 30 F-HEMBA1006912
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (AL-PHA-0 PROTEIN).
0.27:121:29
HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).
P08393
- 35 F-HEMBA1006916
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
1.1e-05:163:30
- 40 XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437
- 45 F-HEMBA1006960
SMALL PROLINE-RICH PROTEIN 2-1.
1.0:34:35
- 50 HOMO SAPIENS (HUMAN).
P35326
- 55 F-HEMBA1007013
S-ANTIGEN PROTEIN PRECURSOR.
2.8e-09:226:28
PLASMODIUM FALCIPARUM (ISOLATE V1).
P09593
- F-HEMBA1007057
PROCYCLIC FORM SPECIFIC POLYPEPTIDE B-ALPHA PRECURSOR (PROCYCLIN) (PARP B-ALPHA) (PS-SA-1).
4.0e-10:33:72
TRYPANOSOMA BRUCEI BRUCEI.

Q06084

5 F-HEMBA1007063
 AGAMOUS PROTEIN.

1.0:40:42
 ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
 P17839

10 F-HEMBA1007226
 PUTATIVE CUTICLE COLLAGEN C09G5.5.
 0.10:105:38

CAENORHABDITIS ELEGANS.
 Q09456

15 F-HEMBA1007241
 HYPOTHETICAL 24.5 KD PROTEIN IN SAP185-BCK1 INTERGENIC REGION.
 3.3e-15:106:42
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 P40857

20 F-HEMBA1007291
 RETINOIC ACID RECEPTOR RXR-BETA.
 0.0013:124:33
 HOMO SAPIENS (HUMAN).

25 P28702

F-HEMBA1007332
 ALPHA-2A ADRENERGIC RECEPTOR (ALPHA-2A ADRENOCEPTOR) (ALPHA-2AAR).
 0.0024:130:34
 30 MUS MUSCULUS (MOUSE).
 Q01338

35 F-HEMBB1000106
 CELLULAR NUCLEIC ACID BINDING PROTEIN (CNBP).
 9.5e-09:99:33
 MUS MUSCULUS (MOUSE).
 P53996

40 F-HEMBB1000276

F-HEMBB1000309

45 F-HEMBB1000407
 TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (VMW118 PROTEIN).
 0.38:99:34
 HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HG52).
 P28284

50 F-HEMBB1000447
 HISTIDINE-RICH GLYCOPROTEIN PRECURSOR.
 0.0076:80:31
 PLASMODIUM LOPHURAE.
 P04929

55 F-HEMBB1000542
 BETA-2 BUNGAROTOXIN B CHAIN PRECURSOR (BUNGAROTOXIN, B2 CHAIN).
 0.017:53:33
 BUNGARUS MULTICINCTUS (MANY-BANDED KRAIT).

P00989

- 5 F-HEMBB1000567
HISTIDINE-RICH GLYCOPROTEIN PRECURSOR.
5.0e-05:131:29
PLASMODIUM LOPHURAE.
P04929
- 10 F-HEMBB1000642
BASIC PROLINE-RICH PEPTIDE IB-1.
0.0074:66:31
HOMO SAPIENS (HUMAN).
P04281
- 15 F-HEMBB1000668
VEGETABLE INCOMPATIBILITY PROTEIN HET-E-1.
7.3e-10:184:32
PODOSPORA ANSERINA.
Q00808
- 20 F-HEMBB1000679
TRAM PROTEIN (TRANSLOCATING CHAIN-ASSOCIATING MEMBRANE PROTEIN).
9.5e-73:204:69
CANIS FAMILIARIS (DOG).
Q01685
- 25 F-HEMBB1000881
F-SPONDIN PRECURSOR.
1.2e-23:191:37
30 XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P35447
- 35 F-HEMBB1000905
TRANSCRIPTIONAL REPRESSOR RCO-1.
0.068:105:34
NEUROSPORA CRASSA.
P78706
- 40 F-HEMBB1001026
ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-
FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT).
1.3e-11:138:31
45 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P32802
- 50 F-HEMBB1001048
SARCALUMENIN PRECURSOR.
3.1e-20:151:32
ORYCTOLAGUS CUNICULUS (RABBIT).
P13666
- 55 F-HEMBB1001200
HYPOTHETICAL GENE 51 MEMBRANE PROTEIN.
1.0:66:27
ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV).
Q00135
- F-HEMBB1001407

EP 1 130 094 A2

!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!

2.0e-24:58:60

HOMO SAPIENS (HUMAN).

P39194

5

F-HEMBB1001530

SLS1 PROTEIN PRECURSOR.

0.0012:37:51

YARROWIA LIPOLYTICA (CANDIDA LIPOLYTICA).

10

Q99158

F-HEMBB1001547

HYPOTHETICAL 71.7 KD PROTEIN F52H3.2 IN CHROMOSOME II.

4.1e-49:200:55

15

CAENORHABDITIS ELEGANS.

Q20680

F-HEMBB1001573

PROTEIN Q300.

20

0.0055:27:62

MUS MUSCULUS (MOUSE).

Q02722

F-HEMBB1001847

25

ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP33).

7.8e-05:166:31

RATTUS NORVEGICUS (RAT).

P04474

30

F-HEMBB1001959

CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN SUBUNIT B).

8.8e-15:97:38

PETROMYZON MARINUS (SEA LAMPREY).

35

P25210

F-HEMBB1001978

MICROCIN B17 PROCESSING PROTEIN MCBC.

0.049:100:31

40

ESCHERICHIA COLI.

P23185

F-HEMBB1002039

COLD SHOCK PROTEIN CSPB (FRAGMENT).

45

0.98:32:40

BACILLUS GLOBISPORUS.

P41018

F-HEMBB1002041

50

REGULATORY PROTEIN E2.

0.010:145:35

HUMAN PAPILLOMAVIRUS TYPE 47.

P22420

55

F-HEMBB1002051

FLI-1 ONCOGENE (ERGB TRANSCRIPTION FACTOR).

0.0056:89:31

HOMO SAPIENS (HUMAN).

Q01543

F-HEMBB1002120

5 UDP-N-ACETYLGLUCOSAMINE--PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE 110 KD SUBUNIT
(EC 2.4.1.-) (O-GLCNAC TRANSFERASE P110 SUBUNIT).

1.4e-08:154:30

RATTUS NORVEGICUS (RAT).

P56558

10 F-HEMBB1002162

IMMEDIATE-EARLY PROTEIN IE180.

0.86:130:31

PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).

P11675

15 F-HEMBB1002228

PTB-ASSOCIATED SPLICING FACTOR (PSF).

0.00092:97:34

HOMO SAPIENS (HUMAN).

20 P23246

F-HEMBB1002245

25 PROSTAGLANDIN F2-ALPHA RECEPTOR REGULATORY PROTEIN PRECURSOR (PROSTAGLANDIN F2-AL-
PHA RECEPTOR ASSOCIATED PROTEIN).

2.5e-55:128:88

RATTUS NORVEGICUS (RAT).

Q62786

30 F-HEMBB1002302

REGULATORY PROTEIN E2.

0.042:100:37

HUMAN PAPILLOMAVIRUS TYPE 25.

P36787

35 F-HEMBB1002427

FUCOSYLGlycoprotein ALPHA-N-ACETYLGLACTOSAMINYLTRANSFERASE (EC 2.4.1.40) (HISTO-BLOOD GROUP A TRANSFERASE) (A TRANSFERASE) / FUCOSYLGlycoprotein 3-ALPHA-GALACTOSYLTRANSFERASE (EC 2.4.1.37) (HISTO-BLOOD GROUP B TRANSFERASE) (B TRANSFERASE) (NAGAT).

5.0e-15:53:54

40 HOMO SAPIENS (HUMAN).

P16442

F-HEMBB1002465

45 ACYL-COA DEHYDROGENASE (EC 1.3.99.-).

8.2e-35:162:50

BACILLUS SUBTILIS.

P45857

50 F-HEMBB1002661

TRANSCRIPTION FACTOR HES-1 (C-HAIRY1).

2.2e-18:159:40

GALLUS GALLUS (CHICKEN).

057337

55 F-HEMBB1002663

F-HEMBB1002693

GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12; CORE SHELL PROTEIN

P30; NUCLEOPROTEIN P10].

0.83:74:28

DUPLAN MURINE LEUKEMIA VIRUS.

P23090

5

F-MAMMA1000046

!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!

2.3e-24:98:67

HOMO SAPIENS (HUMAN).

10

P39191

F-MAMMA1000102

APOLIPOPROTEIN L PRECURSOR (APO-L).

4.3e-22:213:34

15

HOMO SAPIENS (HUMAN).

O14791

F-MAMMA1000106

PISTIL-SPECIFIC EXTENSIN-LIKE PROTEIN PRECURSOR (PELP).

20

1.6e-07:99:31

NICOTIANA TABACUM (COMMON TOBACCO).

Q03211

F-MAMMA1000118

25

HYPOTHETICAL 29.3 KD PROTEIN (ORF92).

0.00059:155:30

ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV). O10341

30

F-MAMMA1000141

!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!

0.00011:39:66

HOMO SAPIENS (HUMAN).

P39195

35

F-MAMMA1000204

SYNAPTOTAGMIN III (SYTIII).

5.9e-05:93:33

MUS MUSCULUS (MOUSE).

035681

40

F-MAMMA1000226

GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT DX5 PRECURSOR.

4.6e-06:224:28

TRITICUM AESTIVUM (WHEAT).

45

P10388

F-MAMMA1000403

COLLAGEN ALPHA 1(IX) CHAIN PRECURSOR (FRAGMENTS).

1.1e-06:158:35

50

GALLUS GALLUS (CHICKEN).

P12106

55

F-MAMMA1000449

SYNAPSINS IA AND IB (BRAIN PROTEIN 4.1).

6.3e-05:137:32

HOMO SAPIENS (HUMAN).

P17600

- 5 F-MAMMA1000457
NADH-CYTOCHROME B5 REDUCTASE (EC 1.6.2.2).
7.6e-48:151:62
BOS TAURUS (BOVINE).
P07514
- 10 F-MAMMA1000473
SPERM PROTAMINE P1.
0.024:29:44
DROMICIOPS AUSTRALIS (MONITO DEL MONTE) (DROMICIOPS GLIROIDES). P42132
- 15 F-MAMMA1000496
HYPOTHETICAL 73.0 KD PROTEIN IN CLA4-MID1 INTERGENIC REGION.
9.8e-09:188:26
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P48566
- 20 F-MAMMA1000528
DNA BINDING PROTEIN S1FA.
0.77:43:37
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
P42551
- 25 F-MAMMA1000591
SALIVARY PROLINE-RICH PROTEIN PO PRECURSOR (ALLELLE S).
0.018:88:32
HOMO SAPIENS (HUMAN).
P10163
- 30 F-MAMMA1000614
HYPOTHETICAL 29.3 KD PROTEIN (ORF92).
7.5e-08:148:36
ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV). O10341
- 35 F-MAMMA1000652
!!!! ALU SUBFAMILY SB WARNING ENTRY !!!
5.3e-36:56:85
HOMO SAPIENS (HUMAN).
P39189
- 40 F-MAMMA1000681
PROBABLE G PROTEIN-COUPLED RECEPTOR EDG-1.
7.5e-41:167:51
MUS MUSCULUS (MOUSE).
008530
- 45 F-MAMMA1000706
T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11).
8.1e-10:135:38
ORYCTOLAGUS CUNICULUS (RABBIT).
P06333
- 50 F-MAMMA1000788
HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.
2.0e-06:214:32
SACCHAROMYCES CEREVISIAE (BAKERS YEAST).
P53214

- 5 F-MAMMA1000810
REGULATORY PROTEIN E2.
0.0031:132:31
HUMAN PAPILLOMAVIRUS TYPE 9.
P36780
- 10 F-MAMMA1000814
PROTEIN Q300.
1.6e-05:27:66
MUS MUSCULUS (MOUSE).
Q02722
- 15 F-MAMMA1000881
SERINE/THREONINE-PROTEIN KINASE SGK (EC 2.7.1.-) (SERUM/GLUCOCORTICOID-REGULATED KI-
NASE).
2.7e-10:81:45
RATTUS NORVEGICUS (RAT).
Q06226
- 20 F-MAMMA1000986
INVOLUCRIN.
0.95:125:24
SUS SCROFA (PIG).
P18175
- 25 F-MAMMA1000994
CUTICLE COLLAGEN 2C (FRAGMENT).
0.00062:97:34
HAEMONCHUS CONTORTUS.
P16252
- 30 F-MAMMA1001043
MRC OX-45 SURFACE ANTIGEN PRECURSOR (BCM1 SURFACE ANTIGEN) (BLAST-1) (CD48).
4.5e-05:162:25
RATTUS NORVEGICUS (RAT).
P10252
- 35 F-MAMMA1001066
B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).
2.6e-06:33:72
HOMO SAPIENS (HUMAN).
P20931
- 40 F-MAMMA1001094
PUTATIVE GENERAL NEGATIVE REGULATOR OF TRANSCRIPTION C16C9.04C.
1.1e-21:175:38
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q09818
- 45 F-MAMMA1001141
PTB-ASSOCIATED SPLICING FACTOR (PSF).
0.13:196:27
HOMO SAPIENS (HUMAN).
P23246
- 50 F-MAMMA1001150
PROTEIN KINASE C, MU TYPE (EC 2.7.1.-) (NPKC-MU).
9.4e-89:256:67

HOMO SAPIENS (HUMAN).
Q15139

5 F-MAMMA1001237
MONOCARBOXYLATE TRANSPORTER 2 (MCT 2).
3.5e-19:103:43
MESOCRICETUS AURATUS (GOLDEN HAMSTER).
P53988

10 F-MAMMA1001284
AUTOIMMUNE REGULATOR (APECED PROTEIN).
0.027:178:30
HOMO SAPIENS (HUMAN).
043918

15 F-MAMMA1001310
HYPOTHETICAL 57.3 KD TRP-ASP REPEATS CONTAINING PROTEIN IN POM152-REC114 INTERGENIC REGION.
1.9e-14:151:31
20 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
Q04225

25 F-MAMMA1001344
MALE SPECIFIC SPERM PROTEIN MST84DC.
0.16:35:42
DROSOPHILA MELANOGASTER (FRUIT FLY).
Q01644

30 F-MAMMA1001418
HYPOTHETICAL PROTEIN HI0519.
3.5e-27:181:38
HAEMOPHILUS INFLUENZAE.
P44742

35 F-MAMMA1001532
ZINC FINGER PROTEIN 90 (ZFP-90) (ZINC FINGER PROTEIN NK10).
1.1e-34:78:58
MUS MUSCULUS (MOUSE).
Q61967

40 F-MAMMA1001609
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (VMW118 PROTEIN).
0.20:137:27
45 HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HG52).
P28284

F-MAMMA1001615
5E5 ANTIGEN.
2.3e-07:205:34
50 RATTUS NORVEGICUS (RAT).
Q63003

55 F-MAMMA1001623
EXCISION REPAIR PROTEIN ERCC-6 (COCKAYNE SYNDROME PROTEIN CSB).
4.8e-30:90:77
HOMO SAPIENS (HUMAN).
Q03468

- 5 F-MAMMA1001634
 B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).
 6.1e-11:44:61
 HOMO SAPIENS (HUMAN).
 P20931
- 10 F-MAMMA1001893
 COLLAGEN ALPHA 1(XI) CHAIN PRECURSOR.
 0.0013:174:36
 HOMO SAPIENS (HUMAN).
 P12107
- 15 F-MAMMA1001901
 !!!! ALU SUBFAMILY SX WARNING ENTRY !!!!
 1.3e-21:65:66
 HOMO SAPIENS (HUMAN).
 P39195
- 20 F-MAMMA1001957
 VITELLINE MEMBRANE PROTEIN VM26AB PRECURSOR (PROTEIN TU-4) (PROTEIN SV23).
 0.0055:104:35
 DROSOPHILA MELANOGASTER (FRUIT FLY).
 P13238
- 25 F-MAMMA1001978
 D(4) DOPAMINE RECEPTOR (D(2C) DOPAMINE RECEPTOR).
 0.00030:101:44
 HOMO SAPIENS (HUMAN).
 P21917
- 30 F-MAMMA1002070
 PLASMINOGEN (EC 3.4.21.7) (FRAGMENT).
 1.4e-08:103:33
 RATTUS NORVEGICUS (RAT).
 Q01177
- 35 F-MAMMA1002080
 FMRFAMIDE-RELATED NEUROPEPTIDES PRECURSOR.
 8.2e-08:131:32
 LYMNAEA STAGNALIS (GREAT POND SNAIL).
 P42565
- 40 F-MAMMA1002087
 MALE SPECIFIC SPERM PROTEIN MST84DD.
 0.65:24:45
 DROSOPHILA MELANOGASTER (FRUIT FLY).
 Q01645
- 45 F-MAMMA1002091
 APYrase PRECURSOR (EC 3.6.1.5) (ATP-DIPHOSPHATASE) (ADENOSINE DIPHOSPHATASE) (ADPASE)
 (ATP-DIPHOSPHOHYDROLASE).
 2.6e-24:155:43
 SOLANUM TUBEROSUM (POTATO).
 P80595
- 50 F-MAMMA1002095
 CALCIUM-TRANSPORTING ATPASE 1 (EC 3.6.1.38) (P-TYPE CALCIUM ATPASE).
 2.3e-58:213:56

YARROWIA LIPOLYTICA (CANDIDA LIPOLYTICA).
043108

- 5 F-MAMMA1002128
 COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).
 9.9e-05:72:40
 RATTUS NORVEGICUS (RAT).
 P02454
- 10 F-MAMMA1002142
 NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE 1).
 2.1e-13:149:34
 DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).
 P18160
- 15 F-MAMMA1002165
 CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR.
 8.4e-06:47:57
 HOMO SAPIENS (HUMAN).
 P29279
- 20 F-MAMMA1002205
 !!!! ALU SUBFAMILY J WARNING ENTRY !!!!
 5.9e-26:56:78
 HOMO SAPIENS (HUMAN).
 P39188
- 25 F-MAMMA1002224
 !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!
 3.7e-16:62:67
 HOMO SAPIENS (HUMAN).
 P39194
- 30 F-MAMMA1002234
 SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).
 3.5e-105:242:85
 CANIS FAMILIARIS (DOG).
 Q00004
- 35 F-MAMMA1002586
 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE (EC 3.2.1.113) (MAN(9)-ALPHA-MANNOSIDASE) (ALPHA-MANNOSIDASE 1A).
 4.7e-24:203:35
 MUS MUSCULUS (MOUSE).
 P45700
- 40 F-MAMMA1002633
 !!!! ALU SUBFAMILY J WARNING ENTRY !!!!
 7.3e-27:49:73
 HOMO SAPIENS (HUMAN).
 P39188
- 45 F-MAMMA1003126
 SARCALUMENIN PRECURSOR.
 7.9e-30:156:35
 ORYCTOLAGUS CUNICULUS (RABBIT).
 P13666

- 5 F-NT2RM1000407
 LACTOSE OPERON REPRESSOR.
 1.4e-07:36:86
 ESCHERICHIA COLI.
 P03023
- 10 F-NT2RM1000462
 ATRIAL GLAND-SPECIFIC ANTIGEN PRECURSOR (AGSA).
 6.7e-11:85:41
 APLYSIA CALIFORNICA (CALIFORNIA SEA HARE).
 P15287
- 15 F-NT2RM1000542
 BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE) (ACID BETA-GALACTOSIDASE).
 3.5e-19:104:48
 FELIS SILVESTRIS CATUS (CAT).
 O19015
- 20 F-NT2RM1000580
 GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).
 3.4e-36:180:43
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 P43636
- 25 F-NT2RM1000789
 T-CELL-SPECIFIC TRANSCRIPTION FACTOR 1 (TCF-1) (T-CELL FACTOR 1) (TRANSCRIPTION FACTOR-7).
 1.5e-40:112:75
 MUS MUSCULUS (MOUSE).
 Q00417
- 30 F-NT2RM1000855
 PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.
 2.5e-81:152:94
 CANIS FAMILIARIS (DOG).
 P38377
- 35 F-NT2RM1000858
 HYPOTHETICAL 36.7 KD PROTEIN AH6.2 IN CHROMOSOME II.
 3.1e-50:127:54
 CAENORHABDITIS ELEGANS.
 Q09201
- 40 F-NT2RM1000899
 MITOCHONDRIAL RNA SPLICING PROTEIN MSR4.
 6.6e-17:107:43
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 P23500
- 45 F-NT2RM2000241
 DOUBLESEX PROTEIN, MALE-SPECIFIC.
 0.0021:64:32
 DROSOPHILA MELANOGASTER (FRUIT FLY).
 P23023
- 50 F-NT2RM2000306
 PUTATIVE GTP-BINDING PROTEIN W08E3.3.
 1.1e-69:198:69
 CAENORHABDITIS ELEGANS.

P91917

F-NT2RM2000410

BETA-LYTIC METALLOENDOPEPTIDASE PRECURSOR (EC 3.4.24.32) (BETA-LYTIC PROTEASE).

5 0.73:118:31

ACHROMOBACTER LYTICUS.

P27458

F-NT2RM2000423

10 BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR.

1.3e-23:235:34

HOMO SAPIENS (HUMAN).

P16279

15 F-NT2RM2000497

DNA-REPAIR PROTEIN COMPLEMENTING XP-D CELLS (XERODERMA PIGMENTOSUM GROUP D COMPLEMENTING PROTEIN) (DNA EXCISION REPAIR PROTEIN ERCC-2).

9.4e-19:199:31

CRICETULUS GRISEUS (CHINESE HAMSTER).

20 Q60452

F-NT2RM2000514

HYPOTHETICAL PROTEIN HI1558.

7.7e-06:82:34

25 HAEMOPHILUS INFLUENZAE.

P45252

F-NT2RM2000565

HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I.

30 2.8e-57:232:52

SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).

Q09782

F-NT2RM2000582

35 PROTEIN Q300.

0.066:13:84

MUS MUSCULUS (MOUSE).

Q02722

40 F-NT2RM2000589

RAC-FAMILY SERINE/THREONINE KINASE HOMOLOG (EC 2.7.1.-).

2.1e-07:90:32

DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).

P54644

45

F-NT2RM2000622

GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT PW212 PRECURSOR.

1.9e-07:133:35

TRITICUM AESTIVUM (WHEAT).

50 P08489

F-NT2RM2000632

EXCISION REPAIR PROTEIN ERCC-6 (COCKAYNE SYNDROME PROTEIN CSB).

4.6e-28:194:35

55 HOMO SAPIENS (HUMAN).

Q03468

F-NT2RM2000773

EP 1 130 094 A2

MYC-ASSOCIATED ZINC FINGER PROTEIN (MAZI) (PUR-1) (ZF87).
3.4e-24:156:47
HOMO SAPIENS (HUMAN).
P56270

5 F-NT2RM2001126
NEURON-SPECIFIC X11 PROTEIN (FRAGMENT).
1.5e-05:118:32
MUS MUSCULUS (MOUSE).
P98084

10 F-NT2RM2001558
MAJOR FIBROUS SHEATH PROTEIN PRECURSOR (FSC1) (P82).
1.9e-24:164:40
15 MUS MUSCULUS (MOUSE).
Q60662

15 F-NT2RM2001626
HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR.
20 1.6e-09:206:33
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P47179

25 F-NT2RM2001643
HYPOTHETICAL PROTEIN MJ1025.
0.21:203:22
METHANOCOCCUS JANNASCHII.
Q58431

30 F-NT2RM2001738
REGULATORY PROTEIN E2.
0.0076:124:31
HUMAN PAPILLOMAVIRUS TYPE 25.
P36787

35 F-NT2RM2001767
HOMEOTIC GENE REGULATOR (BRAhma PROTEIN).
0.0068:115:33
40 DROSOPHILA MELANOGASTER (FRUIT FLY).
P25439

45 F-NT2RM2001792
FIBRINOGEN BETA CHAIN.
4.3e-25:121:45
45 BOS TAURUS (BOVINE).
P02676

50 F-NT2RM2001818
EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).
2.4e-06:192:32
ZEA MAYS (MAIZE).
P14918

55 F-NT2RM2001902
SERINE/THREONINE-PROTEIN KINASE PAK-BETA (EC 2.7.1.-) (BETA-PAK) (P21-ACTIVATED KINASE 3)
(P65-PAK).
2.3e-52:250:45
RATTUS NORVEGICUS (RAT).

Q62829

F-NT2RM2001939

PROBABLE G PROTEIN-COUPLEID RECEPTOR GPR19 (GPR-NGA).

4.0e-97:204:92

HOMO SAPIENS (HUMAN).

Q15760

F-NT2RM2001941

MUSCARINIC ACETYLCHOLINE RECEPTOR M4.

1.0e-34:184:32

HOMO SAPIENS (HUMAN).

P08173

F-NT2RM4000100

EBNA-1 NUCLEAR PROTEIN.

1.7e-05:86:39

EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).

P03211

F-NT2RM4000115

DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RNA POLYMERASE II SUBUNIT 1).

9.5e-05:116:35

SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).

P36594

F-NT2RM4000198

BUTYROPHILIN PRECURSOR (BT).

8.6e-14:162:33

MUS MUSCULUS (MOUSE).

Q62556

F-NT2RM4000284

COLLAGEN ALPHA 2(VI) CHAIN (FRAGMENT).

0.86:95:37

HOMO SAPIENS (HUMAN).

P12110

F-NT2RM4000295

COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR.

1.1e-08:229:34

HOMO SAPIENS (HUMAN).

Q07092

F-NT2RM4000326

SH3 DOMAIN-BINDING PROTEIN 3BP-2.

6.1e-05:187:31

HOMO SAPIENS (HUMAN).

P78314

F-NT2RM4000417

SYNAPTOTAGMIN (P65).

4.2e-08:72:52

APLYSIA CALIFORNICA (CALIFORNIA SEA HARE).

P41823

F-NT2RM4000444

ANTIGEN PEPTIDE TRANSPORTER 1 (APT1) (PEPTIDE TRANSPORTER TAP1) (PEPTIDE TRANSPORTER

PSF1) (PEPTIDE SUPPLY FACTOR 1) (PSF-1) (PEPTIDE TRANSPORTER INVOLVED IN ANTIGEN PROCESSING 1).
1.1e-36:192:41
HOMO SAPIENS (HUMAN).
Q03518

F-NT2RM4000587
COLLAGEN ALPHA 1(II) CHAIN (FRAGMENTS).
1.8e-13:200:38
BOS TAURUS (BOVINE).
P02459

F-NT2RM4000593

F-NT2RM4000648
K-GLYPLICAN PRECURSOR.
6.4e-67:180:68
MUS MUSCULUS (MOUSE).
P51655

F-NT2RM4000761
CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1).
2.3e-53:107:81
RATTUS NORVEGICUS (RAT).
P05503

F-NT2RM4000965
PUTATIVE IMPORTIN BETA-4 SUBUNIT (KARYOPHERIN BETA-4 SUBUNIT).
4.9e-14:188:34
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
060100

F-NT2RM4000997
HISTONE H1C (CLONE XLHW2).
0.88:73:26
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P15866

F-NT2RM4001321
HOMEobox PROTEIN HOX-A2.
0.27:77:37
GALLUS GALLUS (CHICKEN).
Q08727

F-NT2RM4001325
CHONDROITIN 6-SULFOTRANSFERASE (EC 2.8.2.17) (C6ST).
3.8e-30:184:39
GALLUS GALLUS (CHICKEN).
Q92179

F-NT2RM4001377
HYPOTHETICAL BLHF1 PROTEIN.
5.9e-06:216:33
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03181

F-NT2RM4001735
GNS 1 PROTEIN.

0.0028:114:29
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P25358

5 F-NT2RM4001768
PROBABLE OXIDOREDUCTASE (EC 1.-.-.-).
8.6e-24:205:36
STREPTOMYCES ANTIBIOTICUS.
Q03326

10 F-NT2RM4001843
BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE).
4.6e-33:258:37
XANTHOMONAS MANIHOTIS.
P48982

15 F-NT2RM4002352
BASEMENT MEMBRANE PROTEOGLYCAN PRECURSOR (PERLECAN HOMOLOG).
1.0e-15:85:45

20 CAENORHABDITIS ELEGANS.
Q06561

25 F-NT2RP1000002
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN (CLONE W10-1) (FRAGMENT).
0.00011:24:62
LYCOPERSICON ESCULENTUM (TOMATO).
Q01157

30 F-NT2RP1000050
A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.
2.5e-07:198:33
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P32323

35 F-NT2RP1000181
CYTOCHROME B5.
4.4e-11:117:29
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P40312

40 F-NT2RP1000239
TARNS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (VMW118 PROTEIN).
7.8e-05:141:33

45 HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HG52).
P28284

50 F-NT2RP1000261
ORM1 PROTEIN.
2.2e-18:137:35
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53224

55 F-NT2RP1000271
ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).
8.3e-81:194:70
HOMO SAPIENS (HUMAN).
Q03923

EP 1 130 094 A2

5 F-NT2RP1000300
HYPOTHETICAL 57.1 KD PROTEIN IN MAP2-TEL1 INTERGENIC REGION.
2.0e-07:202:24
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P38176

10 F-NT2RP1000325
MITOCHONDRIAL PHOSPHATE CARRIER PROTEIN PRECURSOR.
1.6e-55:86:81
10 HOMO SAPIENS (HUMAN).
Q00325

15 F-NT2RP1000448
PROLINE-RICH PEPTIDE P-B.
0.094:32:43
15 HOMO SAPIENS (HUMAN).
P02814

20 F-NT2RP1000465
EBNA-1 NUCLEAR PROTEIN.
3.1e-07:101:39
20 EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211

25 F-NT2RP1000468
CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN B) (NF-YB) (CAAT-
BOX DIVA BINDING PROTEIN SUBUNIT B).
1.4e-14:97:38
25 PETROMYZON MARINUS (SEA LAMPREY).
P25210

30 F-NT2RP1000551
INTERFERON-RELATED PROTEIN PC4 (TPA INDUCED SEQUENCE 7) (TIS7 PROTEIN).
1.9e-33:221:41
30 MUS MUSCULUS (MOUSE).
P19182

35 F-NT2RP1000579
SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR (EC 1.3.5.1) (FP)
40 (FLAVOPROTEIN SUBUNIT OF COMPLEX II).
3.4e-68:247:62
35 HOMO SAPIENS (HUMAN).
P31040

45 F-NT2RP1000613
CARBONIC ANHYDRASE VI (EC 4.2.1.1) (SALIVARY) (CARBONATE DEHYDRATASE VI).
1.9e-19:137:37
45 OVIS ARIES (SHEEP).
P08060

50 F-NT2RP1000679
EBNA-1 NUCLEAR PROTEIN.
0.00055:54:50
50 EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211

55 F-NT2RP1000740
TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).

0.071:71:45
HOMO SAPIENS (HUMAN).
000268

5 F-NT2RP1000903
SPORE COAT PROTEIN SP96.
0.016:124:26
DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).
P14328

10 F-NT2RP1000981
CELL SURFACE A33 ANTIGEN PRECURSOR.
1.1e-08:196:28
HOMO SAPIENS (HUMAN).
Q99795

15 F-NT2RP1001004
F-SPONDIN PRECURSOR.
1.2e-11:155:31
20 XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P35447

25 F-NT2RP1001020
SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-).
2.2e-05:126:29
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P08458

30 F-NT2RP1001031
PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).
5.8e-26:159:38
THERMOMONOSPORA CURVATA.
P49695

35 F-NT2RP1001563
METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF).
0.00036:42:40
BOS TAURUS (BOVINE).
P37359

40 F-NT2RP2000092
ZINC FINGER PROTEIN 136.
2.9e-44:129:62
45 HOMO SAPIENS (HUMAN).
P52737

45 F-NT2RP2000178
HOMEOTIC GENE REGULATOR (BRAHMA PROTEIN).
0.0050:75:37
50 DROSOPHILA MELANOGASTER (FRUIT FLY).
P25439

55 F-NT2RP2000240
PUTATIVE CUTICLE COLLAGEN C09G5.5.
9.2e-08:137:34
CAENORHABDITIS ELEGANS.
Q09456

- 5 F-NT2RP2000394
 PROCYCCLIC FORM SPECIFIC POLYPEPTIDE A-BETA PRECURSOR (PROCYCLIN) (PARP A-BETA).
 0.00019:28:64
 TRYpanosoma brucei brucei.
 P09791
- 10 F-NT2RP2000447
 GOLGIN-95.
 6.4e-25:55:67
 HOMO SAPIENS (HUMAN).
 Q08379
- 15 F-NT2RP2000479
 PROBABLE E5B PROTEIN.
 1.0:32:37
 HUMAN PAPILLOMAVIRUS TYPE 6B.
 P06461
- 20 F-NT2RP2000514
 AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1) (TRANSIENT AXONAL GLYCOPROTEIN 1).
 1.5e-18:201:33
 HOMO SAPIENS (HUMAN).
 Q02246
- 25 F-NT2RP2000533
 CORNICHON PROTEIN.
 5.6e-52:144:65
 DROSOPHILA MELANOGASTER (FRUIT FLY).
 P49858
- 30 F-NT2RP2000610
 CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN SUBUNIT B).
 8.7e-15:97:38
 PETROMYZON MARINUS (SEA LAMPREY).
 P25210
- 35 F-NT2RP2000616
 PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.
 0.028:163:30
 MUS MUSCULUS (MOUSE).
 P11087
- 40 F-NT2RP2000649
 POTENTIAL CAAX PRENYL PROTEASE 1 (EC 3.4.24.-) (PRENYL PROTEIN- SPECIFIC ENDOPROTEASE 1) (PPSEP 1).
 9.5e-22:241:32
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
 Q10071
- 45 F-NT2RP2000663
 PANCREATIC HORMONE PRECURSOR (PANCREATIC POLYPEPTIDE) (PP).
 0.71:28:46
 GALLUS GALLUS (CHICKEN), AND MELEAGRIS GALLOPAVO (COMMON TURKEY).
 P01306
- 50 F-NT2RP2000694
 WISKOTT-ALDRICH SYNDROME PROTEIN HOMOLOG (WASP).

8.8e-10:90:42
MUS MUSCULUS (MOUSE).
P70315

5 F-NT2RP2000712
ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).
2.3e-50:166:50
HOMO SAPIENS (HUMAN).
Q03923

10 F-NT2RP2000739
ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).
8.9e-45:180:43
HOMO SAPIENS (HUMAN).
Q03923

15 F-NT2RP2000818
SYG1 PROTEIN.
2.4e-14:164:35
20 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P40528

25 F-NT2RP2000903
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
0.28:149:34
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437

30 F-NT2RP2001200
MIC1 PROTEIN.
1.8e-13:115:38
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53258

35 F-NT2RP2001223
CCAAT DISPLACEMENT PROTEIN (HOMEobox PROTEIN CLOX) (CLOX-1) (FRAGMENT).
0.00017:92:35
CANIS FAMILIARIS (DOG).
P39881

40 F-NT2RP2001276
NPDC-1 PROTEIN PRECURSOR.
4.9e-35:96:71
45 MUS MUSCULUS (MOUSE).
Q64322

F-NT2RP2001388
CECROPIN B PRECURSOR.
0.98:31:51
50 DROSOPHILA MELANOGASTER (FRUIT FLY).
P14956

F-NT2RP2001469
VEGETABLE INCOMPATIBILITY PROTEIN HET-E-1.
55 6.0e-07:146:22
PODOSPORA ANSERINA.
Q00808

- 5 F-NT2RP2001480
THROMBOSPONDIN 3 PRECURSOR.
2.1e-100:209:88
HOMO SAPIENS (HUMAN).
P49746
- 10 F-NT2RP2001495
HYPOTHETICAL 53.3 KD PROTEIN IN HXT8-CAN1 INTERGENIC REGION.
3.1e-11:174:24
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P39981
- 15 F-NT2RP2001514
PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38).
4.0e-18:163:36
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P39986
- 20 F-NT2RP2001529
DEATH-ASSOCIATED PROTEIN KINASE 1 (EC 2.7.1.-) (DAP KINASE 1).
4.4e-83:186:78
HOMO SAPIENS (HUMAN).
P53355
- 25 F-NT2RP2001538
PAIRED AMPHIPATHIC HELIX PROTEIN.
1.7e-06:152:26
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P22579
- 30 F-NT2RP2001562
CLATHRIN LIGHT CHAIN B (BRAIN AND LYMPHOCYTE LCB).
0.0093:124:27
HOMO SAPIENS (HUMAN).
P09497
- 35 F-NT2RP2001662
5'-TG-3'INTERACTING FACTOR (HOMEobox PROTEIN TGIF).
5.6e-36:146:57
HOMO SAPIENS (HUMAN).
Q15583
- 40 F-NT2RP2001755
F-SPONDIN PRECURSOR.
1.2e-33:84:89
RATTUS NORVEGICUS (RAT).
P35446
- 45 F-NT2RP2001769
PROTEIN KINASE CEK1 (EC 2.7.1.-).
1.3e-37:159:53
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
P38938
- 50 F-NT2RP2001817
HST1 PROTEIN (HOMOLOGOUS TO SIR2 PROTEIN 1).
6.4e-32:85:48
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P53685

F-NT2RP2001878

EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).

5 1.1e-06:173:28

NICOTIANA TABACUM (COMMON TOBACCO).

P13983

F-NT2RP2001903

10 CALPAIN P94, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM- ACTIVATED NEUTRAL PROTEIN-
ASE) (CANP) (P94 PROTEIN) (MUSCLE-SPECIFIC CALCIUM-ACTIVATED NEUTRAL PROTEASE 3 LARGE
SUBUNIT).

2.4e-10:110:37

HOMO SAPIENS (HUMAN).

15 P20807

F-NT2RP2001915

TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (VMW118 PROTEIN).

0.0069:74:39

20 HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HG52).

P28284

F-NT2RP2001921

TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (P135 PROTEIN) (IER 2.9/ER2.6).

25 0.016:51:45

BOVINE HERPESVIRUS TYPE 1 (STRAIN K22).

P29836

F-NT2RP2001948

30 COLLAGEN ALPHA 1(X) CHAIN PRECURSOR.

6.7e-08:121:37

HOMO SAPIENS (HUMAN).

Q03692

35 F-NT2RP2001956

ORM1 PROTEIN.

7.6e-17:106:36

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P53224

40

F-NT2RP2002015

HOMEobox PROTEIN HOX-A2.

0.12:77:37

GALLUS GALLUS (CHICKEN).

45 Q08727

F-NT2RP2002063

HYPOTHETICAL 51.5 KD PROTEIN D2024.3 IN CHROMOSOME IV.

3.2e-47:213:41

50 CAENORHABDITIS ELEGANS.

P49191

F-NT2RP2002188

ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7) (ACHE).

55 9.2e-15:109:36

TORPEDO CALIFORNICA (PACIFIC ELECTRIC RAY).

P04058

EP 1 130 094 A2

- 5 F-NT2RP2002232
HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I.
2.0e-12:92:50
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q09782
- 10 F-NT2RP2002304
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN (CLONE W10-1) (FRAGMENT).
0.00059:16:68
LYCOPERSICON ESCULENTUM (TOMATO).
Q01157
- 15 F-NT2RP2002409
COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).
0.00039:184:33
BOS TAURUS (BOVINE).
P02453
- 20 F-NT2RP2002510
T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11).
0.0010:97:37
ORYCTOLAGUS CUNICULUS (RABBIT).
P06333
- 25 F-NT2RP2002527
CYTOCHROME B5.
1.3e-11:77:38
SACCHAROMYCES CEREVISIAE (BAKERS YEAST).
P40312
- 30 F-NT2RP2002533
DIHYDROPYRIDINE-SENSITIVE L-TYPE, CALCIUM CHANNEL ALPHA-2/DELTA SUBUNITS PRECURSOR.
2.0e-37:165:42
ORYCTOLAGUS CUNICULUS (RABBIT).
P13806
- 35 F-NT2RP2002564
EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).
4.7e-06:81:35
NICOTIANA TABACUM (COMMON TOBACCO).
P13983
- 40 F-NT2RP2002674
SOLUBLE EPOXIDE HYDROLASE (SEH) (EC 3.3.2.3) (EPOXIDE HYDRATASE) (CYTOSOLIC EPOXIDE HYDROLASE) (CEH).
2.4e-25:147:41
HOMO SAPIENS (HUMAN).
P34913
- 45 F-NT2RP2002721
GLUCOSE 6-PHOSPHATE TRANSLOCASE.
0.0073:88:26
HOMO SAPIENS (HUMAN).
043826
- 50 F-NT2RP2002824
ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT).

1.0e-16:139:36
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 P32802

5 F-NT2RP2002942
 NEURAL CELL ADHESION MOLECULE L1 PRECURSOR (N-CAM L1).
 5.1e-18:153:30
 HOMO SAPIENS (HUMAN).
 P32004

10 F-NT2RP2002974
 HOMEobox PROTEIN SIX5 (DM LOCUS-ASSOCIATED HOMEODOMAIN PROTEIN HOMOLOG) (FRAGMENT).
 3.6e-80:187:84
 MUS MUSCULUS (MOUSE).
 P70178

15 F-NT2RP2002976
 HYPOTHETICAL 149.7 KD PROTEIN IN IRE1-KSP1 INTERGENIC REGION.
 2.8e-18:99:47
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 P38800

20 F-NT2RP2003042
 PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR (EC 2.3.1.43) (LECITHIN-CHOLESTEROL ACYLTRANSFERASE) (PHOSPHOLIPID-CHOLESTEROL ACYLTRANSFERASE) (FRAGMENT).
 1.2e-41:135:57
 GALLUS GALLUS (CHICKEN).
 P53760

25 F-NT2RP2003138
 5'-TG-3'INTERACTING FACTOR (HOMEobox PROTEIN TGIF).
 3.3e-09:104:45
 MUS MUSCULUS (MOUSE).
 P70284

30 F-NT2RP2003179
 CARBON CATABOLITE DEREPRESSING PROTEIN KINASE (EC 2.7.1.-).
 7.2e-15:96:40
 40. SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 P06782

35 F-NT2RP2003210
 LONG-CHAIN FATTY ACID TRANSPORT PROTEIN (FATP).
 6.2e-69:235:57
 MUS MUSCULUS (MOUSE).
 Q60714

45 F-NT2RP2003302
 ZINC FINGER PROTEIN 136.
 9.7e-52:140:52
 HOMO SAPIENS (HUMAN).
 P52737

50 F-NT2RP2003369
 SALIVARY PROLINE-RICH PROTEIN PO (ALLELE M) [CONTAINS: PEPTIDE P-D] (FRAGMENT).
 0.00020:87:32
 HOMO SAPIENS (HUMAN).

P10161

F-NT2RP2003383

LONG NEUROTOXIN 2 (TOXINS I AND V).

5 0.86:38:39

DENDROASPIS VIRIDIS (WESTERN GREEN MAMBA).

P01395

F-NT2RP2003390

10 NPL1 PROTEIN (SEC63 PROTEIN).

1.1e-14:113:38

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P14906

F-NT2RP2003469

MYO-INOSITOL TRANSPORTER 2.

1.7e-09:148:28

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P30606

20

F-NT2RP2003545

SERINE/THREONINE-PROTEIN KINASE NRK1 (EC 2.7.1.-) (N-RICH KINASE 1).

9.2e-32:198:41

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

25 P38692

F-NT2RP2003593

PROLINE-RICH PROTEIN MP-2 PRECURSOR.

0.00019:128:32

30

MUS MUSCULUS (MOUSE).

P05142

F-NT2RP2003599

ATP-DEPENDENT BILE ACID PERMEASE.

35

0.88:69:34

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P32386

F-NT2RP2003655

40 HYPOTHETICAL 26.3 KD PROTEIN IN OYE2-GND1 INTERGENIC REGION.

2.9e-16:93:47

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P38869

F-NT2RP2003664

HYPOTHETICAL 15.7 KD PROTEIN IN NUP85-SSC1 INTERGENIC REGION.

5.6e-08:121:32

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P47111

50

F-NT2RP2003931

ACROSIN PRECURSOR (EC 3.4.21.10).

0.38:20:70

HOMO SAPIENS (HUMAN).

55

P10323

F-NT2RP2003940

ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).

- 1.3e-84:126:74
HOMO SAPIENS (HUMAN).
Q03923
- 5 F-NT2RP2003950
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (AL-PHA-0 PROTEIN).
1.5e-05:134:33
- 10 HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).
P08393
- F-NT2RP2004069
HYPOTHETICAL 26.4 KD PROTEIN EED8.8 IN CHROMOSOME II.
- 15 4.3e-13:68:54
CAENORHABDITIS ELEGANS.
Q09297
- F-NT2RP2004108
ZINC FINGER PROTEIN 136.
- 20 8.6e-47:126:67
HOMO SAPIENS (HUMAN).
P52737
- F-NT2RP2004141
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
- 25 0.013:127:35
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437
- F-NT2RP2004179
GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE (EC 3.1.4.46) (GLYCEROPHOSPHODIESTER PHOSPHODIESTERASE).
- 30 5.9e-10:110:36
ESCHERICHIA COLI.
P10908
- F-NT2RP2004205
MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR.
- 35 4.6e-10:99:34
HOMO SAPIENS (HUMAN).
Q16653
- F-NT2RP2004447
PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR.
- 40 0.86:48:37
MUS MUSCULUS (MOUSE).
Q01149
- F-NT2RP2004495
HYPOTHETICAL 53.3 KD PROTEIN IN HXT8-CAN1 INTERGENIC REGION.
- 45 0.031:135:31
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P39981
- F-NT2RP2004524
HYPOTHETICAL 18.7 KD PROTEIN IN HMS1-ABF2 INTERGENIC REGION.
- 50 0.042:96:23
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

Q04767

F-NT2RP2004556

SALIVARY PROLINE-RICH PROTEIN II-1 (FRAGMENT).

5 0.0082:87:35

HOMO SAPIENS (HUMAN).

P81489

F-NT2RP2004606

10 METALLOPROTEINASE INHIBITOR 1 PRECURSOR (TIMP-1) (ERYTHROID POTENTIATING ACTIVITY) (EPA) (TISSUE INHIBITOR OF METALLOPROTEINASES) (FIBROBLAST COLLAGENASE INHIBITOR) (COLLAGENASE INHIBITOR).

2.2e-57:163:73

HOMO SAPIENS (HUMAN).

15 P01033

F-NT2RP2004648

BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE) (ACID BETA-GALACTOSIDASE).

3.2e-25:90:62

20 FELIS SILVESTRIS CATUS (CAT).

O19015

F-NT2RP2004670

CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123) (CAM KINASE I).

25 6.6e-14:108:34

RATTUS NORVEGICUS (RAT).

Q63450

F-NT2RP2004794

30 HYPOTHETICAL 24.5 KD PROTEIN IN SAP185-BCK1 INTERGENIC REGION.

5.7e-11:140:31

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P40857

35 F-NT2RP2004837

F-NT2RP2004847

ADULT ENHANCER FACTOR 1 (AEF-1).

7.9e-09:81:37

40 DROSOPHILA MELANOGASTER (FRUIT FLY).

P39413

F-NT2RP2005027

GLUCOSE TRANSPORTER TYPE 3, BRAIN.

45 3.6e-64:130:96

HOMO SAPIENS (HUMAN).

P11169

F-NT2RP2005069

50 CCAAT DISPLACEMENT PROTEIN (CDP) (CDP2) (FRAGMENT).

0.22:116:32

RATTUS NORVEGICUS (RAT).

P53565

55 F-NT2RP2005163

ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR.

5.3e-06:70:38

ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).

P40602

F-NT2RP2005181

HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 (CAT-1) (CAT1) (SYSTEM Y+ BASIC AMINO ACID TRANSPORTER) (ECOTROPIC RETROVIRAL LEUKEMIA RECEPTOR HOMOLOG) (ERR) (ECOTROPIC RETROVIRUS RECEPTOR HOMOLOG).

4.2e-54:153:69

HOMO SAPIENS (HUMAN).

P30825

10

F-NT2RP2005247

EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).

2.0e-11:106:35

SORGHUM VULGARE (SORGHUM).

15

P24152

F-NT2RP2005378

A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.

0.11:97:32

20

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P32323

F-NT2RP2005391

G-BOX BINDING FACTOR (GBF).

25

5.1e-10:156:30

DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).

P36417

30

F-NT2RP2005425

M PROTEIN, SEROTYPE 49 PRECURSOR.

2.1e-05:183:27

STREPTOCOCCUS PYOGENES.

P16947

35

F-NT2RP2005463

OVOMUCOID (FRAGMENT).

1.0:21:52

BAMBUSICOLA THORACICA (CHINESE BAMBOO-PARTRIDGE).

P52259

40

F-NT2RP2005514

MOBC PROTEIN.

1.0:26:53

THIOBACILLUS FERROOXIDANS.

P22899

45

F-NT2RP2005535

ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).

3.8e-92:243:69

50

HOMO SAPIENS (HUMAN).

Q03923

F-NT2RP2005541

N-ACETYLGLUCOSAMINE-6-SULFATASE PRECURSOR (EC 3.1.6.14) (G6S) (GLUCOSAMINE-6-SULFATASE).

8.8e-16:78:51

HOMO SAPIENS (HUMAN).

P15586

- 5 F-NT2RP2005597
DOLICHYL-PHOSPHATE-MANNOSE--PROTEIN MANNOSYLTRANSFERASE 4 (EC
2.4.1.109).
7.4e-13:99:34
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P46971
- 10 F-NT2RP2005632
ADENYLATE CYCLASE, TYPE V (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (CA(2+)-INHIBITABLE ADENY-
LYL CYCLASE).
3.0e-05:73:43
CANIS FAMILIARIS (DOG).
P30803
- 15 F-NT2RP2005666
HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B).
0.086:105:31
MUS MUSCULUS (MOUSE).
P35583
- 20 F-NT2RP2005774
ZINC FINGER PROTEIN 136.
7.8e-33:128:57
HOMO SAPIENS (HUMAN).
P52737
- 25 F-NT2RP2005878
PUTATIVE STEROID DEHYDROGENASE KIK-I (EC 1.1.1.-).
6.8e-23:96:48
MUS MUSCULUS (MOUSE).
070503
- 30 F-NT2RP2005883
DOPAMINE-BETA-MONOXYGENASE PRECURSOR (EC 1.14.17.1) (DOPAMINE BETA- HYDROXYLASE)
(DBH).
6.4e-23:185:32
RATTUS NORVEGICUS (RAT).
Q05754
- 35 F-NT2RP2005887
DNA-DIRECTED RNA POLYMERASE SUBUNIT K (EC 2.7.7.6).
1.0:40:30
METHANOCOCCUS JANNASCHII.
Q57650
- 40 F-NT2RP2005941
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
3.5e-08:136:32
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437
- 45 F-NT2RP2005994
HYPOTHETICAL 51.5 KD PROTEIN D2024.3 IN CHROMOSOME IV.
4.4e-36:144:47
CAENORHABDITIS ELEGANS.
P49191
- 50 F-NT2RP2006004

EP 1 130 094 A2

- 5 BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN) (PG40) (DERMATAN SULFATE PROTEOGLYCAN-II) (DSPG).
0.030:28:50
RATTUS NORVEGICUS (RAT).
Q01129
- 10 F-NT2RP2006042
HYPOTHETICAL PROTEIN KIAA0144.
1.2e-22:228:39
HOMO SAPIENS (HUMAN).
Q14157
- 15 F-NT2RP2006092
TRANSCRIPTIONAL ACTIVATOR FE65.
3.1e-27:101:54
RATTUS NORVEGICUS (RAT).
P46933
- 20 F-NT2RP2006099
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
7.0e-07:123:34
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437
- 25 F-NT2RP2006134
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (EARLY PROTEIN 0) (EP0).
0.0041:118:30
PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).
P29129
- 30 F-NT2RP2006269
DOLICHYL-PHOSPHATE-MANNOSE--PROTEIN MANNOSYLTRANSFERASE 4 (EC 2.4.1.109).
6.3e-17:119:36
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P46971
- 35 F-NT2RP2006512
GNS1 PROTEIN.
8.6e-14:186:30
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P25358
- 40 F-NT2RP3000011
PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).
2.9e-12:137:32
THERMOMONOSPORA CURVATA.
P49695
- 45 F-NT2RP3000022
SERINE/THREONINE-PROTEIN KINASE MAK (EC 2.7.1.-) (MALE GERM CELL-ASSOCIATED KINASE).
1.6e-47:121:79
RATTUS NORVEGICUS (RAT).
P20793
- 50 F-NT2RP3000059
COLLAGEN ALPHA 1(III) CHAIN.
1.5e-05:211:33
BOS TAURUS (BOVINE).

P04258

F-NT2RP3000063
 EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).

5 4.2e-23:230:28

ZEA MAYS (MAIZE).
 P14918

10 F-NT2RP3000125

CARBOXYPEPTIDASE KEX1 PRECURSOR (EC 3.4.16.6) (CARBOXYPEPTIDASE D).
 2.3e-08:110:30
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 P09620

15 F-NT2RP3000148

ZINC FINGER PROTEIN 133.
 1.4e-34:84:48
 HOMO SAPIENS (HUMAN).
 P52736

20 F-NT2RP3000169

SMALL PROLINE-RICH PROTEIN 2-1.
 0.00092:14:57
 HOMO SAPIENS (HUMAN).
 P35326

25 F-NT2RP3000171

24.1 KD PROTEIN IN VMA12-APN1 INTERGENIC REGION.
 4.6e-10:134:32
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 P28707

30 F-NT2RP3000172

CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123) (CAM KINASE I).
 1.8e-33:161:42
 RATTUS NORVEGICUS (RAT).
 Q63450

35 F-NT2RP3000201

SERINE/THREONINE-PROTEIN KINASE MIG-15 (EC 2.7.1.-).
 4.1e-79:254:64
 CAENORHABDITIS ELEGANS.
 Q23356

40 F-NT2RP3000232

ZINC FINGER PROTEIN 184 (FRAGMENT).
 8.5e-23:119:45
 HOMO SAPIENS (HUMAN).
 Q99676

45 F-NT2RP3000304

LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR (LRP) (ALPHA-2-MAC-ROGLOBULIN RECEPTOR) (A2MR) (APOLIPOPROTEIN E RECEPTOR) (APOER) (CD91).
 9.8e-36:172:43
 HOMO SAPIENS (HUMAN).
 Q07954

50 F-NT2RP3000378

5 PAIRED AMPHIPATHIC HELIX PROTEIN.
2.7e-26:186:36
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P22579

10 F-NT2RP3000427
5E5 ANTIGEN.
0.086:204:31
RATTUS NORVEGICUS (RAT).
Q63003

15 F-NT2RP3000436
PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).
1.3e-23:106:33
CAENORHABDITIS ELEGANS.
Q11067

20 F-NT2RP3000444
TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).
0.00052:166:36
HOMO SAPIENS (HUMAN).
000268

25 F-NT2RP3000460
PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.
1.0e-98:194:100
RATTUS NORVEGICUS (RAT).
P38378

30 F-NT2RP3000481
NONSENSE-MEDIATED MRNA DECAY PROTEIN 5.
7.4e-19:217:29
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P46970

35 F-NT2RP3000616
BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN).
1.2e-13:115:33
BOS TAURUS (BOVINE).
P21793

40 F-NT2RP3000645
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
2.3e-10:237:30
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437

45 F-NT2RP3000652
ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).
3.1e-106:283:67
HOMO SAPIENS (HUMAN).
Q03923

50 F-NT2RP3000676
ADP,ATP CARRIER PROTEIN, HEART/SKELETAL MUSCLE ISOFORM T1 (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1).
7.4e-07:102:32
HOMO SAPIENS (HUMAN).

P12235

F-NT2RP3000677

MHC CLASS II REGULATORY FACTOR RFX1 (RFX) (ENHANCER FACTOR C) (EF-C).

5 1.5e-27:66:54

HOMO SAPIENS (HUMAN).

P22670

F-NT2RP3000721

HYPOTHETICAL 62.5 KD PROTEIN IN SEC53-ACT1 INTERGENIC REGION.

10 1.6e-22:208:32

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P43560

F-NT2RP3000789

ONCONEURAL VENTRAL ANTIGEN-1 (NOVA-1) (PARANEOPLASTIC RI ANTIGEN) (VENTRAL NEURON-SPECIFIC PROTEIN 1).

15 1.0e-07:190:26

HOMO SAPIENS (HUMAN).

20 P51513

F-NT2RP3000818

HYPOTHETICAL 67.5 KD PROTEIN IN APE1/LAP4-CWP1 INTERGENIC REGION.

25 5.9e-05:100:32

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P34248

F-NT2RP3000820

BIOTIN SYNTHASE (EC 2.8.1.6) (BIOTIN SYNTHETASE).

30 0.92:97:26

SYNECHOCYSTIS SP. (STRAIN PCC 6803).

P73538

F-NT2RP3000838

SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).

35 6.4e-07:231:31

XENOPUS LAEVIS (AFRICAN CLAWED FROG).

P17437

F-NT2RP3000871

COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).

40 2.8e-07:221:33

RATTUS NORVEGICUS (RAT).

P02454

45 F-NT2RP3000907

PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38).

2.2e-41:104:48

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

50 P39986

F-NT2RP3000921

BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC).

55 4.5e-08:149:31

HOMO SAPIENS (HUMAN).

P98160

- 5 F-NT2RP3001012
HISTIDINE-RICH GLYCOPROTEIN PRECURSOR.
5.5e-06:37:51
PLASMODIUM LOPHURAE.
P04929
- 10 F-NT2RP3001044
RNA POLYMERASE PRINCIPAL SIGMA FACTOR HRDA.
0.10:61:31
STREPTOMYCES COELICOLOR.
P18182
- 15 F-NT2RP3001061
GLYCOPROTEIN X PRECURSOR.
0.00011:140:27
EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).
P28968
- 20 F-NT2RP3001159
A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.
1.1e-09:249:32
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P32323
- 25 F-NT2RP3001170
POU DOMAIN PROTEIN 1 (DJPOU1).
0.020:173:29
DUGESIA JAPONICA (PLANARIAN).
P31370
- 30 F-NT2RP3001195
GALACTOSE-PROTON SYMPORT (GALACTOSE TRANSPORTER).
1.2e-14:180:30
ESCHERICHIA COLI.
P37021 |
- 35 F-NT2RP3001240
PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.
3.1e-118:229:88
RATTUS NORVEGICUS (RAT).
P38378
- 40 F-NT2RP3001271
EBNA-1 NUCLEAR PROTEIN.
2.3e-08:113:45
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211
- 45 F-NT2RP3001322
PROBABLE CALCIUM-TRANSPORTING ATPASE 3 (EC 3.6.1.38) (ENDOPLASMIC RETICULUM CA2+-ATPASE).
1.7e-23:222:29
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P39524
- 50 F-NT2RP3001388
SYNAPTOTAGMIN IV.
4.8e-19:168:38

RATTUS NORVEGICUS (RAT).
P50232

F-NT2RP3001542

5 TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN).

2.7e-12:132:37

HOMO SAPIENS (HUMAN).

Q13829

10 F-NT2RP3001560

SYNAPSINS IA AND IB.

0.59:104:35

BOS TAURUS (BOVINE).

P17599

15 F-NT2RP3001592

GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 2 PRECURSOR.

1.3e-11:75:46

ORYZA SATIVA (RICE).

20 P29834

F-NT2RP3001650

CCAAT DISPLACEMENT PROTEIN (HOMEobox PROTEIN CLOX) (CLOX-1) (FRAGMENT).

0.23:119:36

25 CANIS FAMILIARIS (DOG).

P39881

F-NT2RP3001685

HYPOTHETICAL PROTEIN IN MMSB 3'REGION (ORF1) (FRAGMENT).

30 2.2e-48:207:48

PSEUDOMONAS AERUGINOSA.

P28812

35 F-NT2RP3001738

CYTOCHROME B5.

9.5e-13:133:33

ORYCTOLAGUS CUNICULUS (RABBIT).

P00169

40 F-NT2RP3001754

SYNAPSINS IA AND IB (BRAIN PROTEIN 4.1).

7.9e-05:117:29

HOMO SAPIENS (HUMAN).

P17600

45 F-NT2RP3001858

CUTICLE COLLAGEN 2.

0.030:118:35

CAENORHABDITIS ELEGANS.

50 P17656

F-NT2RP3001976

ZINC FINGER PROTEIN 140.

7.8e-24:122:52

55 HOMO SAPIENS (HUMAN).

P52738

F-NT2RP3002015

EP 1 130 094 A2

PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.
0.018:224:30
GALLUS GALLUS (CHICKEN).
P02457

5 F-NT2RP3002160
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
0.0058:206:29

10 XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437

F-NT2RP3002281
HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN F (HNRNP F).
1.3e-14:86:40

15 HOMO SAPIENS (HUMAN).
P52597

F-NT2RP3002286
ETS-DOMAIN TRANSCRIPTION FACTOR ERF.
0.65:128:29

20 HOMO SAPIENS (HUMAN).
P50548

F-NT2RP3002311
BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE) (ACID BETA-GALACTOSIDASE).
6.1e-46:172:54

25 FELIS SILVESTRIS CATUS (CAT).
O19015

30 F-NT2RP3002324
HYPOTHETICAL 13.6 KD PROTEIN IN SPT4-ROM1 INTERGENIC REGION.
0.012:23:65

35 SACCHAROMYCES CEREVIAE (BAKER'S YEAST).
P53245

35 F-NT2RP3002342
HYPOTHETICAL 53.3 KD PROTEIN IN HXT8-CAN1 INTERGENIC REGION.
1.8e-13:219:26

40 SACCHAROMYCES CEREVIAE (BAKER'S YEAST).
P39981

F-NT2RP3002353
REGULATORY PROTEIN E2.
0.0027:167:31

45 HUMAN PAPILLOMAVIRUS TYPE 8.
P06422

F-NT2RP3002409
MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (72 KD MITOCHONDRIAL OUTER MEM-
BRANE PROTEIN) (MITOCHONDRIAL IMPORT RECEPTOR FOR THE ADP/ATP CARRIER) (TRANSLOCASE
OF OUTER MEMBRANE TOM70).
9.9e-09:93:34

50 NEUROSPORA CRASSA.
P23231

55 F-NT2RP3002411
PUTATIVE STEROID DEHYDROGENASE KIK-I (EC 1.1.1.-).
5.6e-107:254:80

MUS MUSCULUS (MOUSE).
070503

5 F-NT2RP3002448
TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).

1.5e-05:163:33

HOMO SAPIENS (HUMAN).
000268

10 F-NT2RP3002571
HYPOTHETICAL 116.3 KD PROTEIN C26F1.09 IN CHROMOSOME I.
6.4e-23:172:33
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q10496

15 F-NT2RP3002664
CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-6 (FRAGMENT).
0.062:47:29
HOMO SAPIENS (HUMAN).
P18850

F-NT2RP3002721
CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7).
6.2e-140:283:92
25 SUS SCROFA (PIG).
P00889

30 F-NT2RP3002737
VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.9.
4.1e-40:136:61
MUS MUSCULUS (MOUSE).
P97414

35 F-NT2RP3002738
SALIVARY PROLINE-RICH PROTEIN PO PRECURSOR (ALLELLE S).
0.029:195:28
HOMO SAPIENS (HUMAN).
P10163

40 F-NT2RP3002790
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
1.7e-08:130:36
MUS MUSCULUS (MOUSE).
P05142

45 F-NT2RP3002836
TRANSMEMBRANE PROTEIN SEX PRECURSOR.
8.9e-24:119:43
HOMO SAPIENS (HUMAN).
P51805

50 F-NT2RP3002887
SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONE CP7) [CONTAINS: BASIC PEPTIDE P-F] (FRAGMENT).
2.9e-11:198:34
HOMO SAPIENS (HUMAN).
P02812

- 5 F-NT2RP3002900
 COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).
 2.8e-18:109:41
 CRICETULUS GRISEUS (CHINESE HAMSTER).
 P49020
- 10 F-NT2RP3002958
 TRANS-GOLGI NETWORK INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR.
 6.4e-06:172:27
 RATTUS NORVEGICUS (RAT).
 P19814
- 15 F-NT2RP3002983
 COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).
 4.4e-05:106:41
 BOS TAURUS (BOVINE).
 P02453
- 20 F-NT2RP3003000
 SODIUM CHANNEL PROTEIN (NA+ CHANNEL).
 9.7e-30:221:31
 ELECTROPHORUS ELECTRICUS (ELECTRIC EEL).
 P02719
- 25 F-NT2RP3003076
 ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (MA) [CONTAINS: GLYCOPROTEIN GP220].
 0.00033:173:30
 EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
 P03200
- 30 F-NT2RP3003354
 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 3.
 2.0e-54:204:51
 MUS MUSCULUS (MOUSE).
 035609
- 35 F-NT2RP3003448
 PROTEASE DEGS PRECURSOR (EC 3.4.21.-).
 4.0e-05:112:33
 40 ESCHERICHIA COLI.
 P31137
- 45 F-NT2RP3003469
 !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!
 1.2e-17:70:64
 HOMO SAPIENS (HUMAN).
 P39194
- 50 F-NT2RP3003473
 BACTENECIN 7 PRECURSOR (BAC7) (PR-59).
 0.0037:33:63
 BOS TAURUS (BOVINE).
 P19661
- 55 F-NT2RP3003527
 SERINE/THREONINE-SPECIFIC PROTEIN KINASE MINIBRAIN HOMOLOG (EC 2.7.1.-) (HP86) (DYRK).
 1.8e-53:159:69
 HOMO SAPIENS (HUMAN).

Q13627

F-NT2RP3003532

OX-2 MEMBRANE GLYCOPROTEIN PRECURSOR (FRAGMENT).

5 2.3e-114:219:97

HOMO SAPIENS (HUMAN).

P41217

F-NT2RP3003535

10 HYPOTHETICAL 7.2 KD PROTEIN IN RPS2 3 REGION (ORF57).

0.98:36:30

ASTASIA LONGA (EUGLENOPHYCEAN ALGA).

P34774

F-NT2RP3003559

MALE SPECIFIC SPERM PROTEIN MST84DB.

0.047:29:48

DROSOPHILA MELANOGASTER (FRUIT FLY).

Q01643

F-NT2RP3003614

TRYPSIN INHIBITOR II (BDTI-II).

0.98:23:39

BRYONIA DIOICA (RED BRYONY).

25 P11968

F-NT2RP3003729

HYPOTHETICAL 42.1 KD PROTEIN IN SNZ1-YPK2 INTERGENIC REGION.

4.1e-11:204:30

30 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

Q03151

F-NT2RP3003849

PROTEIN KINASE C, BRAIN ISOZYME (EC 2.7.1.-) (PKC) (DPKC53E(BR)).

35 9.7e-17:126:34

DROSOPHILA MELANOGASTER (FRUIT FLY).

P05130

F-NT2RP3003874

40 MYOSIN I ALPHA (MMI-ALPHA).

3.1e-64:141:84

MUS MUSCULUS (MOUSE).

P46735

F-NT2RP3003939

CELL DIVISION PROTEIN FTSH HOMOLOG 4 (EC 3.4.24.-).

7.1e-34:76:61

SYNECHOCYSTIS SP. (STRAIN PCC 6803).

P72991

50

F-NT2RP3003963

HISTIDINE-RICH, METAL BINDING POLYPEPTIDE.

0.95:31:38

HELOCOBACTER PYLORI (CAMPYLOBACTER PYLORI).

55 Q48251

F-NT2RP3004000

DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT).

7.1e-07:187:29
CRICETULUS GRISEUS (CHINESE HAMSTER).
P11414

5 F-NT2RP3004025
EBNA-1 NUCLEAR PROTEIN.
0.022:79:40
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211

10 F-NT2RP3004067
COLLAGEN ALPHA 1(X) CHAIN PRECURSOR.
5.0e-07:184:35
HOMO SAPIENS (HUMAN).
Q03692

15 F-NT2RP3004075
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN PRECURSOR.
2.9e-07:92:40
20 HORDEUM VULGARE (BARLEY).
P17816

25 F-NT2RP3004083
ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).
0.013:24:45
COTURNIX COTURNIX JAPONICA (JAPANESE QUAIL).
P50682

30 F-NT2RP3004090
SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.
1.2e-07:195:29
DROSOPHILA ERECTA (FRUIT FLY).
P13730

35 F-NT2RP3004119
PEREGRIN (BR140 PROTEIN).
4.1e-40:227:43
HOMO SAPIENS (HUMAN).
P55201

40 F-NT2RP3004130
CELL SURFACE ANTIGEN 114/A10 PRECURSOR.
2.4e-08:71:42
45 MUS MUSCULUS (MOUSE).
P19467

50 F-NT2RP3004133
GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).
1.5e-28:111:44
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P43636

55 F-NT2RP3004202
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
3.0e-06:104:37
MUS MUSCULUS (MOUSE).
P05142

EP 1 130 094 A2

- 5 F-NT2RP3004294
HYPOTHETICAL 22.2 KD PROTEIN IN NSR1-TIF4631 INTERGENIC REGION.
8.8e-10:129:31
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53288
- 10 F-NT2RP3004309
A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.
1.9e-05:212:30
10 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P32323
- 15 F-NT2RP3004321
REGULATORY PROTEIN SIR2 HOMOLOG (LMSIR2RP).
2.8e-09:81:40
LEISHMANIA MAJOR.
Q25337
- 20 F-NT2RP3004345
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 2 PRECURSOR.
1.3e-11:75:46
ORYZA SATIVA (RICE).
P29834
- 25 F-NT2RP3004355
HYDROGENASE EXPRESSION/FORMATION PROTEIN HUPV.
0.81:154:26
AZOTOBACTER CHROOCOCCUM MCD 1.
Q43959
- 30 F-NT2RP3004374
HOMEobox PROTEIN HOX-A2.
0.28:77:37
30 GALLUS GALLUS (CHICKEN).
Q08727
- 35 F-NT2RP3004406
HYPOTHETICAL 37.4 KD PROTEIN IN IRR1-TIM44 INTERGENIC REGION.
4.9e-18:165:33
40 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P40544
- 45 F-NT2RP3004481
BUTYROPHILIN PRECURSOR (BT).
4.0e-13:152:31
HOMO SAPIENS (HUMAN).
Q13410
- 50 F-NT2RP3004552
COMPLEMENT RECEPTOR TYPE 1 PRECURSOR (C3B/C4B RECEPTOR) (CD35 ANTIGEN).
3.4e-05:211:28
HOMO SAPIENS (HUMAN).
P17927
- 55 F-NT2RP3004557
INTERFERON GAMMA UP-REGULATED I-5111 PROTEIN PRECURSOR (IGUP I-5111).
1.6e-23:129:35
HOMO SAPIENS (HUMAN).

Q06323

F-NT2RP3004625

GLYCOPROTEIN X PRECURSOR.

5 2.4e-10:225:25

EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).

P28968

F-NT2RP3004640

10 ENAMELIN (TUFTELIN).

2.6e-70:167:85

BOS TAURUS (BOVINE).

P27628

F-NT2RP3004647

ADP,ATP CARRIER PROTEIN, HEART/SKELETAL MUSCLE ISOFORM T1 (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1).

4.6e-10:116:34

HOMO SAPIENS (HUMAN).

20 P12235

F-NT2RP4000108

NEUROFILAMENT TRIPLET L PROTEIN (68 KD NEUROFILAMENT PROTEIN) (NF-L) (NF68).

3.4e-107:255:87

25 RATTUS NORVEGICUS (RAT).

P19527

F-NT2RP4000634

MAPK/ERK KINASE KINASE 2 (EC 2.7.1.-) (MEK KINASE 2) (MEKK 2).

30 7.9e-142:267:88

MUS MUSCULUS (MOUSE).

Q61083

F-NT2RP4000962

35 SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-).

1.5e-13:158:31

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P08458

40 F-NT2RP4001001

F-NT2RP4001009

POTENTIAL CAAX PRENYL PROTEASE 1 (EC 3.4.24.-) (PRENYL PROTEIN- SPECIFIC ENDOPROTEASE 1) (PPSEP 1).

45 7.7e-24:235:31

SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).

Q10071

F-NT2RP4001467

50 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) (ECTO-NUCLEOTIDASE) (5'-NT) (CD73 ANTIGEN).

1.2e-120:237:97

HOMO SAPIENS (HUMAN).

P21589

55 F-NT2RP4001877

GLYCINE-RICH RNA-BINDING PROTEIN.

1.4e-08:89:34

DAUCUS CAROTA (CARROT).

Q03878

F-NT2RP4001879

VERY HYPOTHETICAL 8.9 KD PROTEIN CY441.05 PRECURSOR.

5 0.98:49:34

MYCOBACTERIUM TUBERCULOSIS.

P71934

F-NT2RP4002187

10 PUTATIVE STEROID DEHYDROGENASE KIK-I (EC 1.1.1.-).

4.5e-98:246:78

MUS MUSCULUS (MOUSE).

070503

F-NT2RP4002451

15 CUTICLE COLLAGEN 2.

0.85:92:35

CAENORHABDITIS ELEGANS.

P17656

F-NT2RP4002715

20 HYPOTHETICAL 13.6 KD PROTEIN IN SPT4-ROM1 INTERGENIC REGION.

0.47:31:48

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

25 P53245

F-NT2RP4002750

30 HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 (CAT-1) (CAT1) (SYSTEM Y+ BASIC AMINO ACID TRANSPORTER) (ECOTROPIC RETROVIRAL LEUKEMIA RECEPTOR HOMOLOG) (ERR) (ECOTROPIC RETROVIRUS RECEPTOR HOMOLOG).

3.3e-63:185:67

HOMO SAPIENS (HUMAN).

P30825

F-OVARC1000003

35 RENAL SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN 2 (SODIUM/PHOSPHATE COTRANSPORTER 2) (NA(+)/PI COTRANSPORTER 2) (RENAL SODIUM-PHOSPHATE TRANSPORT PROTEIN 2) (RENAL NA+-DEPENDENT PHOSPHATE COTRANSPORTER 2).

2.2e-82:197:72

40 HOMO SAPIENS (HUMAN).

Q06495

F-OVARC1000090

45 HOMEobox PROTEIN HOX-B1 (GHOX-LAB).

0.049:120:32

GALLUS GALLUS (CHICKEN).

P31259

F-OVARC1000105

50 UBIQUITIN-CONJUGATING ENZYME E2-28.4 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN).

8.6e-47:159:58

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P33296

55

F-OVARC1000137

HYPOTHETICAL 22.7 KD PROTEIN IN PAS1-MST1 INTERGENIC REGION.

0.058:28:64

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P36015

5 F-OVARC1000208
!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!
2.2e-12:51:74
HOMO SAPIENS (HUMAN).
P39195

10 F-OVARC1000255
TYROSINE-PROTEIN KINASE SYK (EC 2.7.1.112) (SPLEEN TYROSINE KINASE).
1.1e-112:144:86
HOMO SAPIENS (HUMAN).
P43405

15 F-OVARC1000275
GASTRIN PRECURSOR.
0.11:59:37
HOMO SAPIENS (HUMAN).

20 P01350

F-OVARC1000298
PROLINE-RICH PROTEIN MP-3 (FRAGMENT).
0.014:74:39
MUS MUSCULUS (MOUSE).

25 P05143

F-OVARC1000307
EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).
1.0:33:54
NICOTIANA TABACUM (COMMON TOBACCO).
P13983

30 F-OVARC1000313
PROTEIN DISULFIDE ISOMERASE-RELATED PROTEIN PRECURSOR (ERP72) (CALCIUM-BINDING PROTEIN 2) (CABP2).
4.0e-15:127:37
RATTUS NORVEGICUS (RAT).
P38659

35 F-OVARC1000331
GMP REDUCTASE (EC 1.6.6.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCTASE).
2.0e-24:64:84
HOMO SAPIENS (HUMAN).

40 P36959

F-OVARC1000410
FIBRINOGEN-LIKE PROTEIN A PRECURSOR (FREP-A).
1.9e-44:229:41
PARASTICHOPUS PARVIMENSIS (SEA CUCUMBER).

50 P19477

F-OVARC1000439
SALIVARY GLUE PROTEIN SGS-7 PRECURSOR.
0.99:41:43
DROSOPHILA MELANOGASTER (FRUIT FLY).
P02841

EP 1 130 094 A2

- 5 F-OVARC1000467
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN (CLONE W10-1) (FRAGMENT).
0.0061:30:63
LYCOPERSICON ESCULENTUM (TOMATO).
Q01157
- 10 F-OVARC1000529
PROBABLE SERINE/THREONINE-PROTEIN KINASE YKL 101 W (EC 2.7.1.-).
1.5e-20:127:42
10 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P34244
- 15 F-OVARC1000553
DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (THYMOCYTE-ACTIVATING MOLECULE) (THAM).
7.6e-26:169:40
15 MUS MUSCULUS (MOUSE).
P28843
- 20 F-OVARC1000775
METALLOTHIONEIN (MT).
0.91:31:38
CARASSIUS AURATUS (GOLDFISH).
P52723
- 25 F-OVARC1000811
COAGULATION FACTOR XII PRECURSOR (EC 3.4.21.38) (HAGEMAN FACTOR) (HAF).
2.8e-11:69:43
25 HOMO SAPIENS (HUMAN).
P00748
- 30 F-OVARC1000853
CUTICLE COLLAGEN 40.
0.00013:130:33
30 CAENORHABDITIS ELEGANS.
P34804
- 35 F-OVARC1000873
MALE SPECIFIC SPERM PROTEIN MST84DB.
0.00015:53:33
35 DROSOPHILA MELANOGASTER (FRUIT FLY).
Q01643
- 40 F-OVARC1000916
GALACTOSYLTRANSFERASE ASSOCIATED PROTEIN KINASE P58/GTA (EC 2.7.1.-).
2.5e-26:109:53
40 MUS MUSCULUS (MOUSE).
P24788
- 45 F-OVARC1000956
D(4) DOPAMINE RECEPTOR (D(2C) DOPAMINE RECEPTOR).
0.00073:115:33
45 HOMO SAPIENS (HUMAN).
P21917
- 50 F-OVARC1000995
POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L2 (SNF2-ALPHA).
0.00031:139:25
50 HOMO SAPIENS (HUMAN).

P51531

- 5 F-OVARC1001030
5E5 ANTIGEN.
1.9e-09:89:41
RATTUS NORVEGICUS (RAT).
Q63003
- 10 F-OVARC1001049
PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.
1.5e-08:146:38
GALLUS GALLUS (CHICKEN).
P02457
- 15 F-OVARC1001086
VITELLOGENIN II PRECURSOR (MAJOR VITELLOGENIN) [CONTAINS: LIPOVITELLIN I (LVI); PHOSVITIN (PV); LIPOVITELLIN II (LVII); YGP40].
5.3e-08:182:32
GALLUS GALLUS (CHICKEN).
P02845
- 20 F-OVARC1001132
GC-RICH SEQUENCE DNA-BINDING FACTOR (GCF) (TRANSCRIPTION FACTOR 9) (TCF-9).
9.2e-40:229:37
HOMO SAPIENS (HUMAN).
P16383
- 25 F-OVARC1001163
HYPOTHETICAL 49.3 KD PROTEIN C30D 11.06C IN CHROMOSOME I.
8.8e-05:38:44
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q09906
- 30 F-OVARC1001222
AMELOGENIN, CLASS I PRECURSOR.
0.72:96:31
BOS TAURUS (BOVINE).
P02817
- 35 F-OVARC1001260
- 40 F-OVARC1001336
RENAL SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN 2 (SODIUM/PHOSPHATE COTRANSPORTER 2) (NA(+)/Pi COTRANSPORTER 2) (RENAL SODIUM-PHOSPHATE TRANSPORT PROTEIN 2) (RENAL NA+-DEPENDENT PHOSPHATE COTRANSPORTER 2).
1.1e-33:103:71
RATTUS NORVEGICUS (RAT).
Q06496
- 45 F-OVARC1001338
SERINE/THREONINE-PROTEIN KINASE UNC-51 (EC 2.7.1.-).
3.8e-30:89:46
CAENORHABDITIS ELEGANS.
Q23023
- 50 F-OVARC1001569
ACROSIN PRECURSOR (EC 3.4.21.10) (53 KD FUCOSE-BINDING PROTEIN).
2.2e-06:28:64

SUS SCROFA (PIG).
P08001

5 F-OVARC1001570
CATHEPSIN E PRECURSOR (EC 3.4.23.34).
1.8e-09:121:33
CAVIA PORCELLUS (GUINEA PIG).
P25796

10 F-OVARC1001596
REGULATORY PROTEIN E2.
0.33:77:37
HUMAN PAPILLOMAVIRUS TYPE 14.
P36783

15 F-OVARC1001607
ALPHA-1,6-MANNOSYL-GLYCOPROTEIN BETA-1,2-N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.143) (N-GLYCOSYL-OLIGOSACCHARIDE-GLYCOPROTEIN N-ACETYLGLUCOSAMINYLTRANSFERASE II) (BETA-1,2-N-ACETYLGLUCOSAMINYLTRANSFERASE II) (GNT-II) (GLCNAC-T II).
20 1.0e-28:69:84
HOMO SAPIENS (HUMAN).
Q10469

25 F-OVARC1001725
F-OVARC1001727

30 F-OVARC1001807
EARLY RESPONSE PROTEIN NAK1 (TR3 ORPHAN RECEPTOR).
2.4e-51:153:75
HOMO SAPIENS (HUMAN).
P22736

35 F-OVARC1001833
CIS-GOLGI MATRIX PROTEIN GM130.
1.2e-55:169:75
RATTUS NORVEGICUS (RAT).
Q62839

40 F-OVARC1001952
EBNA-1 NUCLEAR PROTEIN.
3.5e-19:130:43
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211

45 F-OVARC1001991
HYPOTHETICAL PROTEIN KIAA0176 (FRAGMENT).
3.7e-16:141:43
HOMO SAPIENS (HUMAN).
Q14681

50 F-OVARC1002058
LAMININ ALPHA-5 CHAIN (FRAGMENT).
2.8e-22:163:33
MUS MUSCULUS (MOUSE).
Q61001

F-OVARC1002178

EP 1 130 094 A2

TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (AL-PHA-0 PROTEIN).
0.12:73:36
HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).
5 P08393

F-PLACE1000033
VON WILLEBRAND FACTOR PRECURSOR.
10 1.7e-19:190:28
CANIS FAMILIARIS (DOG).
Q28295

F-PLACE1000231
DNA-BINDING PROTEIN MNB1A.
15 0.24:60:33
ZEA MAYS (MAIZE).
P38564

F-PLACE1000258
ZINC FINGER PROTEIN 177.
20 3.6e-19:55:61
HOMO SAPIENS (HUMAN).
Q13360

F-PLACE1000442
ZINC FINGER PROTEIN 136.
25 1.7e-80:180:72
HOMO SAPIENS (HUMAN).
P52737

30 F-PLACE1000560
COLICIN E9 (EC 3.1.21.1).
0.015:47:44
ESCHERICHIA COLI.
35 P09883

F-PLACE1000740
NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3).
1.6e-05:75:36

40 MUS MUSCULUS (MOUSE).
P31695

F-PLACE1000907
ZINC FINGER PROTEIN 141.
45 2.8e-15:43:88
HOMO SAPIENS (HUMAN).
Q15928

F-PLACE1000912
PROBABLE E4 PROTEIN (E1^E4).
50 0.19:46:36
HUMAN PAPILLOMAVIRUS TYPE 6B.
P06459

55 F-PLACE1000914
MALE SPECIFIC SPERM PROTEIN MST87F.
0.054:27:44
DROSOPHILA MELANOGASTER (FRUIT FLY).

P08175

F-PLACE1000927
 HYPOTHETICAL PROTEIN HI0044.
 5 3.9e-07:139:30
 HAEMOPHILUS INFLUENZAE.
 P44477

F-PLACE1000986

10 F-PLACE1001016
 SODIUM CHANNEL PROTEIN, BRAIN II ALPHA SUBUNIT.
 2.7e-05:120:32
 RATTUS NORVEGICUS (RAT).
 15 P04775

F-PLACE1001100

20 F-PLACE1001114
 PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.
 2.5e-07:250:28
 MUS MUSCULUS (MOUSE).
 P11087

25 F-PLACE1001123
 INTESTINAL MEMBRANE A4 PROTEIN (DIFFERENTIATION-DEPENDENT PROTEIN A4).
 6.2e-09:95:31
 HOMO SAPIENS (HUMAN).
 Q04941

30 F-PLACE1001183
 NONHISTONE CHROMOSOMAL PROTEIN HMG-17.
 0.31:52:34
 GALLUS GALLUS (CHICKEN).
 35 P02314

F-PLACE1001229
 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT).
 1.0:38:47
 40 ARTEMIA SAUNA (BRINE SHRIMP).
 P19047

F-PLACE1001231
 45 SODIUM/GLUCOSE COTRANSPORTER 1 (NA(+)/GLUCOSE COTRANSPORTER 1) (HIGH AFFINITY SODIUM-GLUCOSE COTRANSPORTER).
 4.7e-06:181:27
 ORYCTOLAGUS CUNICULUS (RABBIT).
 P11170

50 F-PLACE1001340
 MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (72 KD MITOCHONDRIAL OUTER MEMBRANE PROTEIN) (MITOCHONDRIAL IMPORT RECEPTOR FOR THE ADP/ATP CARRIER) (TRANSLOCASE OF OUTER MEMBRANE TOM70).
 6.5e-14:136:29
 55 NEUROSPORA CRASSA.
 P23231

F-PLACE1001401

EP 1 130 094 A2

- 5 HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT (FCERI) (IGE FC RECEPTOR, BETA-SUBUNIT).
1.3e-11:103:40
RATTUS NORVEGICUS (RAT).
P13386
- 10 F-PLACE1001407
INTEGUMENTARY MUCIN C.1 (FIM-C.1) (FRAGMENT).
0.013:121:32
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
Q05049
- 15 F-PLACE1001464
5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) (ECTO-NUCLEOTIDASE) (5'-NT) (CD73 ANTIGEN).
1.4e-119:246:89
HOMO SAPIENS (HUMAN).
P21589
- 20 F-PLACE1001500
BLOOM'S SYNDROME PROTEIN.
8.3e-26:203:34
HOMO SAPIENS (HUMAN).
P54132
- 25 F-PLACE1001516
GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).
7.4e-07:204:30
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P08640
- 30 F-PLACE1001536
- 35 F-PLACE1001564
LEUCOCYTE ANTIGEN CD97 PRECURSOR.
2.1e-09:170:24
HOMO SAPIENS (HUMAN).
P48960
- 40 F-PLACE1001655
VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV2.1 (DRK1).
4.0e-34:189:39
RATTUS NORVEGICUS (RAT).
P15387
- 45 F-PLACE1001788
HYPOTHETICAL 36.7 KD PROTEIN C2F7.02C IN CHROMOSOME I.
6.2e-21:75:58
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q09695
- 50 F-PLACE1001795
HYPOTHETICAL 30.6 KD PROTEIN IN SCP160-SMC3 INTERGENIC REGION PRECURSOR.
3.8e-21:159:40
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P47032
- F-PLACE1001836

EP 1 130 094 A2

ENV POLYPROTEIN PRECURSOR (COAT POLYPROTEIN) [CONTAINS: OUTER MEMBRANE PROTEIN GP70; TRANSMEMBRANE PROTEIN P20E].

4.5e-29:134:47

BABOON ENDOGENOUS VIRUS (STRAIN M7).

5 P10269

F-PLACE1001918

ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT).

10 1.5e-30:228:32

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P32802

F-PLACE1001949

15 PROBABLE CALCIUM-TRANSPORTING ATPASE 9 (EC 3.6.1.38).

5. 1e-36:210:46

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

Q12697

F-PLACE1002080

20 HYPOTHETICAL PROTEIN KIAA0288 (HA6116).

3.5e-26:207:45

HOMO SAPIENS (HUMAN).

P56524

25

F-PLACE1002095

N-ACETYLGLUCOSAMINE SYNTHASE (EC 2.4.1.90) (N-ACETYLGLUCOSAMINE (BETA 1→4)GALACTOSYL-TRANSFERASE) (EC 2.4.1.38) (LACTOSE SYNTHASE A PROTEIN (EC 2.4.1.22)) (GALACTOSYLTRANSFERASE) (GT).

30 0.32:50:34

MUS MUSCULUS (MOUSE).

P15535

F-PLACE1002153

35 CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (SLAYER PROTEIN 1).

0.00021:214:26

CLOSTRIDIUM THERMOCELLUM.

Q06852

40

F-PLACE1002329

EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8.

1.1e-35:179:44

MUS MUSCULUS (MOUSE).

Q08509

45

F-PLACE1002355

COMPLEMENT C4 PRECURSOR [CONTAINS: C4A ANAPHYLATOXIN] (FRAGMENTS).

1.0e-14:183:32

BOS TAURUS (BOVINE).

50 P01030

F-PLACE1002374

CATHEPSIN L PRECURSOR (EC 3.4.22.15) (MAJOR EXCRETED PROTEIN) (MEP).

9.2e-107:225:86

55

HOMO SAPIENS (HUMAN).

P07711

F-PLACE1002518

EP 1 130 094 A2

HYPOTHETICAL 13.2 KD PROTEIN IN ORC2-TIP1 INTERGENIC REGION.

6.1e-05:59:44

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P38239

5

F-PLACE1002547

MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (72 KD MITOCHONDRIAL OUTER MEMBRANE PROTEIN) (MITOCHONDRIAL IMPORT RECEPTOR FOR THE ADP/ATP CARRIER) (TRANSLOCASE OF OUTER MEMBRANE TOM70).

10

1.0e-22:230:31

NEUROSPORA CRASSA.

P23231

15

F-PLACE1002726

COLLAGEN ALPHA 1(I) CHAIN (FRAGMENT).

0.61:25:48

ORYCTOLAGUS CUNICULUS (RABBIT).

P02456

20

F-PLACE1002905

ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DIAZEPAM BINDING INHIBITOR) (MA-DBI).

5.0e-31:93:64

BOS TAURUS (BOVINE).

25

P07106

30

F-PLACE1002911

T-CELL SURFACE PROTEIN TACTILE PRECURSOR (CD96 ANTIGEN).

6.6e-06:95:35

HOMO SAPIENS (HUMAN).

P40200

35

F-PLACE1002967

HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT (FCER1) (IGE FC RECEPTOR, BETA-SUBUNIT).

9.4e-08:95:37

MUS MUSCULUS (MOUSE).

P20490

40

F-PLACE1003135

SERINE/THREONINE-PROTEIN KINASE STE20 (EC 2.7.1.-).

1.9e-33:99:50

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

Q03497

45

F-PLACE1003163

ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DIAZEPAM BINDING INHIBITOR) (MA-DBI).

9.8e-15:105:38

50

BOS TAURUS (BOVINE).

P07106

55

F-PLACE1003407

CLN5 PROTEIN.

4.2e-109:217:89

HOMO SAPIENS (HUMAN).

075503

- 5 F-PLACE1003428
BIOTINIDASE PRECURSOR (EC 3.5.1.12).
1.0e-36:104:46
HOMO SAPIENS (HUMAN).
P43251
- 10 F-PLACE1003438
HYPOTHETICAL 104.4 KD PROTEIN C17A5.16 IN CHROMOSOME I.
1.1e-10:148:33
10 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
013776
- 15 F-PLACE1003460
2-HYDROXY-6-KETONONA-2,4-DIENEDIOIC ACID HYDROLASE (EC 3.7.1.-).
0.00028:134:27
ESCHERICHIA COLI.
P77044
- 20 F-PLACE1003529
TRANSCRIPTION REGULATORY PROTEIN SNF5 (SWI/SNF COMPLEX COMPONENT SNF5) (TRANSCRIPTION FACTOR TYE4).
0.00047:157:27
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P18480
- 25 F-PLACE1003573
T-CELL SURFACE GLYCOPROTEIN YE1/48 (T LYMPHOCYTE ANTIGEN A1) (LY49-A ANTIGEN).
0.022:129:25
30 MUS MUSCULUS (MOUSE).
P20937
- 35 F-PLACE1003598
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (P135 PROTEIN) (IER 2.9/ER2.6).
0.0017:102:44
BOVINE HERPESVIRUS TYPE 1 (STRAIN JURA).
P29128
- 40 F-PLACE1003644
PROTEIN Q300.
6.7e-05:24:70
MUS MUSCULUS (MOUSE).
Q02722
- 45 F-PLACE1003737
TOLL PROTEIN PRECURSOR.
7.3e-08:203:27
DROSOPHILA MELANOGASTER (FRUIT FLY).
P08953
- 50 F-PLACE1003772
SALIVARY PROLINE-RICH PROTEIN II-1 (FRAGMENT).
3.7e-07:141:32
HOMO SAPIENS (HUMAN).
P81489
- 55 F-PLACE1003839
PROLINE-RICH PROTEIN MP-3 (FRAGMENT).
1.3e-09:201:31

MUS MUSCULUS (MOUSE).
P05143

F-PLACE1003845

PUTATIVE UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP-GALACTOSE 4-EPI-MERASE).

5.0e-13:103:33

METHANOCOCCUS JANNASCHII.

Q57664

10

F-PLACE1003852

CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR (EMR1 HORMONE RECEPTOR).

2.0e-18:189:29

HOMO SAPIENS (HUMAN).

15

Q14246

F-PLACE1004028

HYPOTHETICAL 9.7 KD PROTEIN IN PURC-PURL INTERGENIC REGION.

0.97:47:31

20

BACILLUS SUBTILIS.

P12049

F-PLACE1004078

ADSEVERIN (SCINDERIN) (SC).

25

5.3e-98:176:90

BOS TAURUS (BOVINE).

Q28046

30

F-PLACE1004166

CREB-BINDING PROTEIN.

9.6e-08:107:34

HOMO SAPIENS (HUMAN).

Q92793

35

F-PLACE1004168

GENERAL NEGATIVE REGULATOR OF TRANSCRIPTION SUBUNIT 1.

6.8e-05:147:30

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P25655

40

F-PLACE1004199

!!!! ALU SUBFAMILY J WARNING ENTRY !!!!

4.2e-05:65:52

HOMO SAPIENS (HUMAN).

45

P39188

F-PLACE1004279

HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME III.

3.6e-11:166:30

50

CAENORHABDITIS ELEGANS.

P30638

F-PLACE1004282

HISTONE H1C (CLONE XLHW2).

0.74:73:26

55

XENOPUS LAEVIS (AFRICAN CLAWED FROG).

P15866

- 5 F-PLACE1004305
RAS-RELATED PROTEIN RAC1.
2.3e-23:161:39
DROSOPHILA MELANOGASTER (FRUIT FLY).
P40792
- 10 F-PLACE1004441
PROBABLE G PROTEIN-COUPLED RECEPTOR GPR1.
5.4e-70:156:89
HOMO SAPIENS (HUMAN).
P46091
- 15 F-PLACE1004450
AMINOPEPTIDASE N (EC 3.4.11.2) (MICROSOMAL AMINOPEPTIDASE).
3.1e-40:196:44
RATTUS NORVEGICUS (RAT).
P15684
- 20 F-PLACE1004482
ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).
0.23:26:30
GALLUS GALLUS (CHICKEN).
P14093
- 25 F-PLACE1004492
COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).
1.2e-05:150:34
BOS TAURUS (BOVINE).
P02453
- 30 F-PLACE1004519
ENL PROTEIN.
0.68:170:30
HOMO SAPIENS (HUMAN).
Q03111
- 35 F-PLACE1004520
PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN PRECURSOR.
3.5e-50:150:74
HOMO SAPIENS (HUMAN).
P11462
- 40 F-PLACE1004630
INTEGRIN BETA-6 SUBUNIT PRECURSOR.
9.1e-31:189:39
HOMO SAPIENS (HUMAN).
P18564
- 45 F-PLACE1004637
MALE SPECIFIC SPERM PROTEIN MST84DA.
0.47:29:44
DROSOPHILA MELANOGASTER (FRUIT FLY).
Q01642
- 50 F-PLACE1004648
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
8.4e-05:89:40
MUS MUSCULUS (MOUSE).

P05142

F-PLACE1004816

MICROFIBRIL-ASSOCIATED GLYCOPROTEIN 4.

5 1.0e-25:117:46

HOMO SAPIENS (HUMAN).

P55083

F-PLACE1004887

10 SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.

8.4e-09:195:30

DROSOPHILA ERECTA (FRUIT FLY).

P13730

F-PLACE1005003

PROSTASIN PRECURSOR (EC 3.4.21.-).

15 1.2e-24:139:40

HOMO SAPIENS (HUMAN).

Q16651

20

F-PLACE1005005

UBIQUITIN-CONJUGATING ENZYME E2 G2 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN).

25 2.5e-28:51:84

HOMO SAPIENS (HUMAN).

P56554

F-PLACE1005031

CHLORINE CHANNEL PROTEIN P64.

30

2.7e-52:142:76

BOS TAURUS (BOVINE).

P35526

F-PLACE1005239

35 SPLICING FACTOR, ARGinine/SERINE-RICH 6 (PRE-MRNA SPLICING FACTOR SRP55) (FRAGMENT).

0.27:78:26

ORYCTOLAGUS CUNICULUS (RABBIT).

018776

40

F-PLACE1005250

HYPOTHETICAL 9.0 KD PROTEIN IN ADH4 5'REGION.

0.22:35:48

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P53056

45

F-PLACE1005383

FIBRILLIN 1 PRECURSOR.

6.7e-09:134:32

50

MUS MUSCULUS (MOUSE).

Q61554

F-PLACE1005410

PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.

55

9.5e-105:204:100

RATTUS NORVEGICUS (RAT).

P38378

F-PLACE1005426

EP 1 130 094 A2

PREGNANCY-SPECIFIC BETA-1-GLYCOPROTEIN 4 PRECURSOR (PSBG-4).

3.2e-33:184:46

HOMO SAPIENS (HUMAN).

Q00888

5

F-PLACE1005519

SERINE/THREONINE-PROTEIN KINASE NRK1 (EC 2.7.1.-) (N-RICH KINASE 1).

1.2e-23:143:41

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

10

P38692

F-PLACE1005539

ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX) (FRAGMENT).

5.5e-05:94:37

15

BRASSICA NAPUS (RAPE).

P40603

20

F-PLACE1005544

CELL SURFACE A33 ANTIGEN PRECURSOR.

0.00015:132:31

HOMO SAPIENS (HUMAN).

Q99795

25

F-PLACE1005569

PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP).

0.00092:122:31

EQUUS CABALLUS (HORSE).

Q28381

30

F-PLACE1005601

TOXIN S4C8.

0.34:32:37

DENDROASPIS JAMESONI KAIMOSAE (EASTERN JAMESON'S MAMBA).

P25683

35

F-PLACE1005660

SALIVARY GLUE PROTEIN SGS-7 PRECURSOR.

0.99:41:43

40

DROSOPHILA MELANOGASTER (FRUIT FLY).

P02841

F-PLACE1005669

COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN).

0.0078:105:37

45

HOMO SAPIENS (HUMAN).

Q02388

50

F-PLACE1005682

THYROID RECEPTOR INTERACTING PROTEIN 9 (TRIP9).

2.7e-12:81:41

HOMO SAPIENS (HUMAN).

Q15653

55

F-PLACE1005725

HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.

7.5e-08:142:31

CAENORHABDITIS ELEGANS.

Q11073

5 F-PLACE1005736
 RAC-FAMILY SERINE/THREONINE KINASE HOMOLOG (EC 2.7.1.-).
 9.0e-11:91:37
 DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).
 P54644

10 F-PLACE1005745
 ORM1 PROTEIN.
 2.2e-18:137:35
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 P53224

15 F-PLACE1005768
 NEUROTOXINS I AND I' PRECURSOR (AAH I AND AAH I').
 0.63:13:69
 ANDROCTONUS AUSTRALIS HECTOR (SAHARA SCORPION). P01479

20 F-PLACE1005815
 COLORECTAL MUTANT CANCER PROTEIN (MCC PROTEIN).
 1.8e-12:73:50
 HOMO SAPIENS (HUMAN).
 P23508

25 F-PLACE1005878
 CHLORINE CHANNEL PROTEIN P64.
 1.6e-49:115:79
 BOS TAURUS (BOVINE).
 P35526

30 F-PLACE1005927
 HYPOTHETICAL 35.8 KD PROTEIN C12G12.12 IN CHROMOSOME I.
 3.2e-16:152:34
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
 Q09875

35 F-PLACE1006071
 LAMININ BETA-1 CHAIN PRECURSOR (LAMININ B1 CHAIN).
 4.1e-08:215:26
 MUS MUSCULUS (MOUSE).
 P02469

40 F-PLACE1006073
 SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).
 2.1e-05:137:34
 NEPHILA CLAVIPES (ORB SPIDER).
 P46804

45 F-PLACE1006079
 HOMEobox PROTEIN DLX-3.
 1.5e-58:144:83
 HOMO SAPIENS (HUMAN).
 060479

50 F-PLACE1006093
 SYNAPSINS IA AND IB (BRAIN PROTEIN 4.1).
 3.8e-05:72:40
 HOMO SAPIENS (HUMAN).
 P17600

EP 1 130 094 A2

- 5 F-PLACE1006208
EBNA-2 NUCLEAR PROTEIN.
3.8e-15:28:75
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4). P12978
- 10 F-PLACE1006219
UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP-GALACTOSE 4-EPIMERASE)
(FRAGMENT)
2.0e-09:38:42
KLEBSIELLA PNEUMONIAE.
P45602
- 15 F-PLACE1006277
CELL SURFACE A33 ANTIGEN PRECURSOR.
1.2e-07:183:29
HOMO SAPIENS (HUMAN).
Q99795
- 20 F-PLACE1006290
GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).
8.2e-39:171:43
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P43636
- 25 F-PLACE1006443
HYPOTHETICAL 60.0 KD PROTEIN IN IMP1-HLJ1 INTERGENIC REGION.
0.0010:155:27
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
Q03795
- 30 F-PLACE1006515
ZINC FINGER Y-CHROMOSOMAL PROTEIN 1.
0.046:98:28
MUS MUSCULUS (MOUSE).
P10925
- 35 F-PLACE1006716
30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN PRECURSOR (ACRP30) (ADIPOCYTE SPECIFIC
PROTEIN ADIPOQ).
3.6e-25:177:35
MUS MUSCULUS (MOUSE).
Q60994
- 40 F-PLACE1006786
PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN (LTP) (BASIC PROTEIN) (WBP) (FRAGMENT).
1.0:19:42
TRITICUM AESTIVUM (WHEAT).
P26913
- 45 F-PLACE1006809
SLS1 PROTEIN PRECURSOR.
0.0011:37:51
YARROWIA LIPOLYTICA (CANDIDA LIPOLYTICA).
Q99158
- 50 F-PLACE1006959
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
5.3e-05:96:41

MUS MUSCULUS (MOUSE).
P05142

5 F-PLACE1007028
EBNA-1 NUCLEAR PROTEIN.
5.9e-09:219:33
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211

10 F-PLACE1007040
SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONE CP7) [CONTAINS: BASIC PEPTIDE P-F] (FRAGMENT).
0.68:138:24
HOMO SAPIENS (HUMAN).
P02812

F-PLACE1007077
SERINE/THREONINE-PROTEIN KINASE CLA4 (EC 2.7.1.-).
0.73:177:25
20 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P48562

F-PLACE1007081
COAGULATION FACTOR V PRECURSOR (ACTIVATED PROTEIN C COFACTOR).
3.0e-20:182:39
BOS TAURUS (BOVINE).
Q28107

F-PLACE1007096
HYPOTHETICAL SYMPORTER SLL1374.
2.8e-14:162:30
SYNECHOCYSTIS SP. (STRAIN PCC 6803).
P74168

35 F-PLACE1007296
ER LUMEN PROTEIN RETAINING RECEPTOR 1 (KDEL RECEPTOR 1).
9.4e-50:120:86
HOMO SAPIENS (HUMAN).
P24390

40 F-PLACE1007591
MEIOTIC RECOMBINATION PROTEIN REC104.
0.68:73:31
45 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P33323

F-PLACE1007626
PTB-ASSOCIATED SPLICING FACTOR (PSF).
0.00083:97:34
50 HOMO SAPIENS (HUMAN).
P23246

F-PLACE1007702
ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR.
1.9e-08:87:36
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
P40602

- 5 F-PLACE1007845
 GLYCOSYLYTRANSFERASE ALG2 (EC 2.4.1.-).
 1.3e-16:158:40
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 P43636
- 10 F-PLACE1007881
 HYPOTHETICAL 69.4 KD PROTEIN F13H10.3 IN CHROMOSOME IV.
 1.2e-11:113:37
 CAENORHABDITIS ELEGANS.
 Q19425
- 15 F-PLACE1007971
 METALLOTHIONEIN 20-III ISOFORMS A AND B (MT-20-IIIA AND MT-20-IIIB).
 1.0:32:43
 MYTILUS EDULIS (BLUE MUSSEL).
 P80253
- 20 F-PLACE1008282
 HEME-REGULATED EUKARYOTIC INITIATION FACTOR EIF-2-ALPHA KINASE (EC 2.7.1.-) (HRI).
 8.1e-87:178:87
 ORYCTOLAGUS CUNICULUS (RABBIT).
 P33279
- 25 F-PLACE1008297
 MYOSIN HEAVY CHAIN KINASE B (EC 2.7.1.129) (MHCK B).
 3.6e-17:187:33
 DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).
 P90648
- 30 F-PLACE1008359
 BEM46 PROTEIN (FRAGMENT).
 4.9e-07:103:33
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
 P54069
- 35 F-PLACE1008469
 D(4) DOPAMINE RECEPTOR (D(2C) DOPAMINE RECEPTOR).
 0.0018:78:37
 HOMO SAPIENS (HUMAN).
 P21917
- 40 F-PLACE1008549
 FLI-1 ONCOGENE (ERGB TRANSCRIPTION FACTOR).
 0.0034:89:30
 HOMO SAPIENS (HUMAN).
 Q01543
- 45 F-PLACE1008657
 ADSEVERIN (SCINDERIN) (SC).
 6.7e-127:257:91
 BOS TAURUS (BOVINE).
 Q28046
- 50 F-PLACE1008716
 ALPHA-1,6-MANNOSYL-GLYCOPROTEIN BETA-1,2-N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.143) (N-GLYCOSYL-OLIGOSACCHARIDE-GLYCOPROTEIN N-ACETYLGLUCOSAMINYLTRANSFERASE II) (BETA-1,2-N-ACETYLGLUCOSAMINYLTRANSFERASE II) (GNT-II) (GLCNAC-T II).

4.5e-20:66:78
HOMO SAPIENS (HUMAN).
Q10469

5 F-PLACE1008744
C4B-BINDING PROTEIN ALPHA CHAIN PRECURSOR (PROLINE-RICH PROTEIN) (PRP).
3.6e-19:221:33
HOMO SAPIENS (HUMAN).
P04003

10 F-PLACE1008984
BIOTIN CARBOXYL CARRIER PROTEIN OF ACETYL-COA CARBOXYLASE PRECURSOR (EC 6.4.1.2) (BC-CP).
0.089:61:31

15 GLYCINE MAX (SOYBEAN).
Q42783

20 F-PLACE1008985
SYNAPTOTAGMIN V.
8.6e-09:123:35
HOMO SAPIENS (HUMAN).
000445

25 F-PLACE1009067
HYPOTHETICAL 33.4 KD PROTEIN.
4.3e-09:60:50
HOMO SAPIENS (HUMAN).
Q04323

30 F-PLACE1009196
SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE).
0.050:23:34
GORILLA GORILLA GORILLA (LOWLAND GORILLA).
P35303

35 F-PLACE1009279
8.6 KD TRANSGLUTAMINASE SUBSTRATE.
1.4e-07:62:35

40 TACHYPLEUS TRIDENTATUS (JAPANESE HORSESHOE CRAB).
P81281

45 F-PLACE1009527
MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).
0.037:71:38
HOMO SAPIENS (HUMAN).
Q02817

50 F-PLACE1009546
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
5.9e-07:86:39
MUS MUSCULUS (MOUSE).
P05142

55 F-PLACE1009600
TETRACYCLINE RESISTANCE PROTEIN, CLASS H (TETA(H)).
1.7e-08:113:31
PASTEURELLA MULTOCIDA.
P51564

EP 1 130 094 A2

- 5 F-PLACE1009735
TARNS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE1 10) (VMW110) (AL-
PHA-0 PROTEIN).
2.6e-09:182:35
- 5 HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).
P08393
- 10 F-PLACE1009982
REGULATORY PROTEIN E2.
0.99:94:28
- 10 HUMAN PAPILLOMAVIRUS TYPE 8.
P06422
- 15 F-PLACE1010011
DIACYLGLYCEROL CHOLINEPHOSPHOTRANSFERASE (EC 2.7.8.2) (SN-1,2-DIACYLGLYCEROL
CHOLINEPHOSPHOTRANSFERASE) (CHOPT).
2.8e-20:119:42
- 15 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P17898
- 20 F-PLACE1010078
ORM1 PROTEIN.
3.4e-20:137:37
- 20 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53224
- 25 F-PLACE1010081
SERINE/THREONINE-PROTEIN KINASE CTR1 (EC 2.7.1.37).
1.5e-11:147:32
- 25 ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
Q05609
- 30 F-PLACE1010251
NEL-LIKE PROTEIN (FRAGMENT).
1.8e-10:73:42
- 30 HOMO SAPIENS (HUMAN).
Q92832
- 35 F-PLACE1010445
HYPOTHETICAL BHLF1 PROTEIN.
0.0042:227:33
- 35 EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03181
- 40 F-PLACE1010713
PUTATIVE STEROID DEHYDROGENASE KIK-I (EC 1.1.1.-).
1.5e-77:177:80
- 40 MUS MUSCULUS (MOUSE).
070503
- 45 F-PLACE1010784
P2Y PURINOCEPTOR 5 (P2Y5) (PURINERGIC RECEPTOR 5) (6H1).
1.7e-18:102:40
- 45 GALLUS GALLUS (CHICKEN).
P32250
- 50 F-PLACE1010827
COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).

2.8e-18:109:41
CRICETULUS GRISEUS (CHINESE HAMSTER).
P49020

5 F-PLACE1010968
PROTEIN-TYROSINE PHOSPHATASE DLAR PRECURSOR (EC 3.1.3.48) (PROTEIN-TYROSINE-PHOSPHATE
PHOSPHOHYDROLASE).
2.3e-06:191:28

10 DROSOPHILA MELANOGASTER (FRUIT FLY).
P16621

F-PLACE1011045
HYPOTHETICAL 71.4 KD PROTEIN IN NMD3-ENO2 INTERGENIC REGION.
6.0e-14:153:34

15 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P38862

F-PLACE1011116
GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-
GLUCAN GLUCOHYDROLASE).
2.3e-06:195:27

20 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P08640

F-PLACE1011181
MSP1 PROTEIN HOMOLOG.
4.3e-06:93:25

25 CAENORHABDITIS ELEGANS.
P54815

30 F-PLACE1011236
HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME III.
4.1e-17:180:28

35 CAENORHABDITIS ELEGANS.
P30638

F-PLACE1011364
HYPOTHETICAL 141.2 KD PROTEIN EEE8.9 IN CHROMOSOME II.
2.1e-24:158:41

40 CAENORHABDITIS ELEGANS.
Q09298

F-PLACE1011407
ZINC FINGER PROTEIN 140.
3.8e-10:47:74

45 HOMO SAPIENS (HUMAN).
P52738

F-PLACE1011516
HYPOTHETICAL 21.5 KD PROTEIN IN SEC15-SAP4 INTERGENIC REGION.
1.6e-13:117:34

50 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53073

55 F-PLACE1011708
DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR (EC 3.4.24.-).
9.9e-22:203:32

DROSOPHILA MELANOGASTER (FRUIT FLY).

P25723

- 5 F-PLACE1011824
 SERINE/THREONINE-PROTEIN KINASE PAK-BETA (EC 2.7.1.-) (BETA-PAK) (P21-ACTIVATED KINASE 3)
 (CDC42/RAC EFFECTOR KINASE PAK-B).
 1.6e-15:103:36
 MUS MUSCULUS (MOUSE).
 Q61036
- 10 F-PLACE1011978
 ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).
 3.3e-55:188:50
 HOMO SAPIENS (HUMAN).
 Q03923
- 15 F-PLACE2000118
 EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).
 2.8e-23:169:43
 NICOTIANA TABACUM (COMMON TOBACCO).
 P13983
- 20 F-PLACE2000219
 MALE SPECIFIC SPERM PROTEIN MST84DA.
 0.11:29:41
 25 DROSOPHILA MELANOGASTER (FRUIT FLY).
 Q01642
- 30 F-PLACE3000181
 CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).
 9.5e-26:193:37
 DROSOPHILA MELANOGASTER (FRUIT FLY).
 P33450
- 35 F-PLACE3000213
 COMPLEMENT RECEPTOR TYPE 1 PRECURSOR (C3B/C4B RECEPTOR) (CD35 ANTIGEN).
 2.3e-23:191:34
 HOMO SAPIENS (HUMAN).
 P17927
- 40 F-PLACE4000354
 E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1) (LEUKOCYTE-
 ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E).
 3.2e-25:150:30
 45 ORYCTOLAGUS CUNICULUS (RABBIT).
 P27113
- 50 F-PLACE4000455
 IG KAPPA CHAIN PRECURSOR V-III REGION (VG) (FRAGMENT).
 0.66:52:36
 HOMO SAPIENS (HUMAN).
 P04433
- 55 F-SKNMC1000004
 OPTOMOTOR-BLIND PROTEIN (LETHAL(1)OPTOMOTOR-BLIND) (L(1)OMB) (BIFID PROTEIN).
 0.079:88:30
 DROSOPHILA MELANOGASTER (FRUIT FLY).
 Q24432

- 5 F-SKNMC1000014
 SCO-SPONDIN (FRAGMENT).
 0.63:60:36
 BOS TAURUS (BOVINE).
 P98167
- 10 F-SKNMC1000082
 PUTATIVE MITOCHONDRIAL CARRIER YGR096W.
 2.4e-10:93:34
 10 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 P53257
- 15 F-THYRO1000036
 PROLINE-RICH PROTEIN MP-3 (FRAGMENT).
 0.72:69:36
 MUS MUSCULUS (MOUSE).
 P05143
- 20 F-THYRO1000061
 COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).
 0.0068:70:38
 BOS TAURUS (BOVINE).
 P25508
- 25 F-THYRO1000099
 SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).
 0.0063:207:28
 NEPHILA CLAVIPES (ORB SPIDER).
 P46804
- 30 F-THYRO1000196
 RETINAL-CADHERIN PRECURSOR (R-CADHERIN) (R-CAD).
 1.6e-10:134:32
 35 GALLUS GALLUS (CHICKEN).
 P24503
- 40 F-THYRO1000400
 ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN (STOMATIN) (PROTEIN 7.2B).
 3.9e-28:163:38
 MUS MUSCULUS (MOUSE).
 P54116
- 45 F-THYRO1000580
 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17).
 3.3e-15:64:62
 MUS MUSCULUS (MOUSE).
 Q61751
- 50 F-THYRO1000584
 EPIDIDYMIS-SPECIFIC ALPHA-MANNOSIDASE (EC 3.2.1.24) (ALPHA-D-MANNOSIDE MANNOHYDROLASE)
 (135 KD PROTEIN).
 1.5e-89:197:72
 SUS SCROFA (PIG).
 Q28949
- 55 F-THYRO1000678
 GAP JUNCTION BETA-6 PROTEIN (CONNEXIN 30) (CX30).
 7.7e-39:89:87

MUS MUSCULUS (MOUSE).
P70689

5 F-THYRO1000776
HIGH AFFINITY SULPHATE TRANSPORTER 2.
3.0e-25:83:50
STYLOSANTHES HAMATA.
P53392

10 F-THYRO1000795
MITOCHONDRIAL 2-OXOGLUTARATE/MALATE CARRIER PROTEIN (OGCP).
1.2e-33:227:37
BOS TAURUS (BOVINE).
P22292

15 F-THYRO1000846
CUTICLE COLLAGEN 12 PRECURSOR.
6.7e-09:190:33
CAENORHABDITIS ELEGANS.
P20630

20 F-THYRO1000866
HYPOTHETICAL 146.8 KD PROTEIN C34E10.5 IN CHROMOSOME III.
0.12:85:31
25 CAENORHABDITIS ELEGANS.
P46580

25 F-THYRO1000956
PROBABLE G PROTEIN-COUPLEI) RECEPTOR APJ.
1.3e-68:165:84
HOMO SAPIENS (HUMAN).
P35414

30 F-THYRO1000964
TARNS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (P135 PROTEIN) (IER 2.9/ER2.6).
0.015:170:34
BOVINE HERPESVIRUS TYPE 1 (STRAIN JURA).
P29128

35 F-THYRÓ1000999
CRYPTDIN-RELATED PROTEIN 4C-2 PRECURSOR (CRS4C).
0.28:40:45
MUS MUSCULUS (MOUSE).
P50715

40 F-THYRO1001063
SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEP-TIDE IB-6; PEPTIDE P-H].
3.5e-05:232:32
50 HOMO SAPIENS (HUMAN).
P04280

45 F-THYRO1001071
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
0.00061:131:33
55 XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437

EP 1 130 094 A2

- 5 F-THYRO1001102
TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).
0.25:94:38
HOMO SAPIENS (HUMAN).
000268
- 10 F-THYRO1001113
SYNAPTOTAGMIN III (SYTIII).
2.0e-08:102:35
MUS MUSCULUS (MOUSE).
035681
- 15 F-THYRO1001128
GLYCOPROTEIN X PRECURSOR.
6.8e-07:182:31
EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).
P28968
- 20 F-THYRO1001205
NEUROGRANIN (NG) (PROTEIN KINASE C SUBSTRATE 7.5 KD PROTEIN) (RC3).
0.91:33:42
RATTUS NORVEGICUS (RAT).
Q04940
- 25 F-THYRO1001237
HYPOTHETICAL PROTEIN IN NIFH2 3 REGION (FRAGMENT).
4.0e-07:68:38
METHANOCOCCUS THERMOLITHOTROPHICUS.
P05410
- 30 F-THYRO1001242
SYNAPSINS IA AND IB (BRAIN PROTEIN 4.1).
1.0:104:35
HOMO SAPIENS (HUMAN).
P17600
- 35 F-THYRO1001266
SODIUM/GLUCOSE COTRANSPORTER 1 (NA(+)/GLUCOSE COTRANSPORTER 1) (HIGH AFFINITY SODIUM-GLUCOSE COTRANSPORTER).
4.3e-09:119:27
ORYCTOLAGUS CUNICULUS (RABBIT).
P11170
- 40 F-THYR01001327
HYPOTHETICAL 23.7 KD PROTEIN IN CYR1-OST1 INTERGENIC REGION.
1.7e-06:141:24
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P41544
- 45 F-THYRO1001456
HYPOTHETICAL 56.2 KD PROTEIN CY31.25C.
1.1e-11:88:48
MYCOBACTERIUM TUBERCULOSIS.
Q10555
- 50 F-THYRO1001457
PROTEIN KINASE C, MU TYPE (EC 2.7.1.-) (NPKC-MU).
2.1e-68:228:59

HOMO SAPIENS (HUMAN).
Q15139

5 F-THYRO1001471
COLLAGEN 1(X) CHAIN PRECURSOR.
3.9e-05:204:30
GALLUS GALLUS (CHICKEN).
P08125

10 F-THYRO1001478
COLLAGEN ALPHA 1(X) CHAIN PRECURSOR.
0.038:162:31
HOMO SAPIENS (HUMAN).
Q03692

15 F-THYRO1001495
!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!
4.8e-19:50:82
HOMO SAPIENS (HUMAN).
P39193

20 F-THYRO1001523
!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!
5.0e-13:66:62
25 HOMO SAPIENS (HUMAN).
P39195

25 F-THYRO1001529
SERINE PALMITOYLTRANSFERASE 2 (EC 2.3.1.50) (LONG CHAIN BASE BIOSYNTHESIS PROTEIN 2) (SPT
2).
1.6e-27:115:53
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q09925

35 F-THYRO1001593
PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-).
3.3e-92:225:77
HOMO SAPIENS (HUMAN).
P27448

40 F-THYRO1001608
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
1.2e-07:127:35
45 MUS MUSCULUS (MOUSE).
P05142

50 F-THYRO1001641
NUC-1 NEGATIVE REGULATORY PROTEIN PREG.
0.0039:98:31
NEUROSPORA CRASSA.
Q06712

55 F-THYRO1001700
INTERFERON-INDUCED, DOUBLE-STRANDED RNA-ACTIVATED PROTEIN KINASE (EC 2.7.1.-) (INTERFER-
ON-INDUCIBLE RNA-DEPENDENT PROTEIN KINASE) (P68 KINASE) (P1/EIF-2A PROTEIN KINASE).
3.3e-09:65:43
HOMO SAPIENS (HUMAN).
P19525

5 F-THYRO1001702
 MYELOID UPREGULATED PROTEIN.
 7.8e-62:161:78
 MUS MUSCULUS (MOUSE).
 035682

10 F-THYRO1001725
 PROTEIN KINASE C SUBSTRATE 80 KD PROTEIN (FRAGMENTS).
 0.00061:82:41
 RATTUS NORVEGICUS (RAT).
 P20468

15 F-THYRO1001770
 PROBABLE SERINE/THREONINE-PROTEIN KINASE YNL020C (EC 2.7.1.-).
 1.0e-20:165:35
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 P53974

20 F-THYRO1001803
 GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).
 3.6e-07:221:30
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 P08640

25 F-Y79AA1000030
 TRANSCRIPTIONAL ACTIVATOR FE65.
 4.5e-09:43:46
 RATTUS NORVEGICUS (RAT).
 P46933

30 F-Y79AA1000127
 FAS ANTIGEN LIGAND (APOPTOSIS ANTIGEN LIGAND) (APTL).
 1.3e-05:72:43
 HOMO SAPIENS (HUMAN).
 P48023

35 F-Y79AA1000207
 STANNIocalcin PRECURSOR (STC) (CORPUSCLES OF STANNIUS PROTEIN) (CS) (HYPOCALCIN) (TEL-EOCALCIN).
 1.0:100:27
 ANGUILLA AUSTRALIS (AUSTRALIAN EEL).
 P18301

40 F-Y79AA1000226
 HYPOTHETICAL 52.8 KD PROTEIN T05E11.5 IN CHROMOSOME IV.
 2.6e-07:188:28
 CAENORHABDITIS ELEGANS.
 P49049

45 F-Y79AA1000270
 VACUOLAR ATP SYNTHASE SUBUNIT AC45 PRECURSOR (EC 3.6.1.34) (V-ATPASE AC45 SUBUNIT).
 1.6e-102:233:87
 BOS TAURUS (BOVINE).
 P40682

50 F-Y79AA1000426
 INHIBIN BETA C CHAIN PRECURSOR (ACTIVIN BETA-C CHAIN).

1.1e-14:149:38
 HOMO SAPIENS (HUMAN).
 P55103

5 F-Y79AA1000521
 MALE SPECIFIC SPERM PROTEIN MST84DD.
 0.00079:60:36
 DROSOPHILA MELANOGASTER (FRUIT FLY).
 Q01645

10 F-Y79AA1000750
 EBNA-1 NUCLEAR PROTEIN.
 2.0e-09:131:38
 EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
 P03211

15 F-Y79AA1000776
 CORNIFIN (SMALL PROLINE-RICH PROTEIN I) (SPR-I) (SMALL PROLINE-RICH SQUAMOUS CELL MARKER)
 (SPRP).
 20 0.080:44:40
 SUS SCROFA (PIG).
 P35323

25 F-Y79AA1000777
 PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).
 4.2e-33:204:39
 THERMOMONOSPORA CURVATA.
 P49695

30 F-Y79AA1000876
 PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1) (PROLYL 4-HYDROXYLASE BETA SUB-
 UNIT) (CELLULAR THYROID HORMONE BINDING PROTEIN) (P55).
 4.6e-16:115:38
 BOS TAURUS (BOVINE).
 P05307

35 F-Y79AA1000888
 TRNA PSEUDOURIDINE SYNTHASE A (EC 4.2.1.70) (PSEUDOURIDYLATE SYNTHASE I) (PSEUDOURIDINE
 SYNTHASE I) (URACIL HYDROLYASE).
 40 2.0e-09:159:35
 TREPONEMA PALLIDUM.
 083802

45 F-Y79AA1000959
 HOMEobox PROTEIN HOX-B3 (HOX-2.7) (MH-23).
 8.8e-08:72:38
 MUS MUSCULUS (MOUSE).
 P09026

50 F-Y79AA1000967
 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123) (CAM KINASE I).
 1.1e-37:202:42
 RATTUS NORVEGICUS (RAT).
 Q63450

55 F-Y79AA1001013
 SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS : PEPTIDE P-D] (FRAGMENT).
 0.038:128:28

HOMO SAPIENS (HUMAN).
P10162

F-Y79AA1001056

HYPOTHETICAL 7.1 KD PROTEIN IN TK-VS INTERGENIC REGION.

0.41:42:30

BACTERIOPHAGE T4.

P13307

10 F-Y79AA1001062

TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN).

9.9e-13:132:38

HOMO SAPIENS (HUMAN).

Q13829

15 F-Y79AA1001090

ANKYRIN HOMOLOG PRECURSOR.

4.0e-19:176:34

CHROMATIUM VINOsum.

20 Q06527

F-Y79AA1001212

HYPOTHETICAL PROTEIN MJ0110.

0.095:55:34

25 METHANOCOCCUS JANNASCHII.

Q57574

F-Y79AA1001264

HYPOTHETICAL 39.9 KD PROTEIN T15H9.1 IN CHROMOSOME II PRECURSOR.

30 3.3e-53:177:55

CAENORHABDITIS ELEGANS.

Q10005

35 F-Y79AA1001272

ACROSIN PRECURSOR (EC 3.4.21.10).

6.3e-08:78:46

ORYCTOLAGUS CUNICULUS (RABBIT).

P48038

40 F-Y79AA1001328

DELTA-LIKE PROTEIN 1 PRECURSOR (DELTA1).

1.3e-08:118:39

RATTUS NORVEGICUS (RAT).

P97677

45 F-Y79AA1001426

BAND 3 ANION TRANSPORT PROTEIN.

1.7e-18:156:32

50 GALLUS GALLUS (CHICKEN).

P15575

F-Y79AA1001427

INDUCIBLE NITRATE REDUCTASE 2 (EC 1.6.6.1) (NR).

1.1e-49:131:51

55 GLYCINE MAX (SOYBEAN).

P39870

F-Y79AA1001430

EP 1 130 094 A2

RING CANAL PROTEIN (KELCH PROTEIN).
2.5e-24:157:40
DROSOPHILA MELANOGASTER (FRUIT FLY).
Q04652

5 F-Y79AA1001523
TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA (NUCLEAR COREPRESSOR KAP-1) (KRAB-ASSOCIATED PROTEIN 1).
6.2e-15:141:39

10 HOMO SAPIENS (HUMAN).
Q13263

F-Y79AA1001530
TUBULIN BETA-5 CHAIN.
15 8.0e-76:204:76
HOMO SAPIENS (HUMAN).
P04350

F-Y79AA1001592
20 PTB-ASSOCIATED SPLICING FACTOR (PSF).
0.42:104:33
HOMO SAPIENS (HUMAN).
P23246

F-Y79AA1001727
25 AMALGAM PROTEIN PRECURSOR.
1.9e-09:185:28
DROSOPHILA MELANOGASTER (FRUIT FLY).
P15364

30 F-Y79AA1001787
PROBABLE CALCIUM-TRANSPORTING ATPASE 9 (EC 3.6.1.38).
7.6e-43:210:45
35 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
Q12697

F-Y79AA1001793
40 CORNIFIN (SMALL PROLINE-RICH PROTEIN I) (SPR-I) (SMALL PROLINE-RICH SQUAMOUS CELL MARKER) (SPRP).
0.077:44:40
SUS SCROFA (PIG).
P35323

F-Y79AA1001795
45 HYPOTHETICAL BHLF1 PROTEIN.
0.00014:210:31
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03181

F-Y79AA1001799
50 MITOCHONDRIAL RNA SPLICING PROTEIN MSR4.
2.8e-18:107:44
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P23500

F-Y79AA1001803
55 SECRETOGRANIN III PRECURSOR (SGIII).
1.3e-68:182:76

MUS MUSCULUS (MOUSE).
P47867

5 F-Y79AA1001863
GLYCOPROTEIN J.
0.030:61:32
HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).
P06480

10 F-Y79AA1002022
WISKOTT-ALDRICH SYNDROME PROTEIN (WASP).
9.8e-08:127:37
HOMO SAPIENS (HUMAN).
P42768

15 F-Y79AA1002058
CCAAT/ENHANCER BINDING PROTEIN DELTA (C/EBP DELTA) (NUCLEAR FACTOR NF-IL6-BETA) (NF-IL6-BETA).
0.28:56:42
20 HOMO SAPIENS (HUMAN).
P49716

F-Y79AA1002121
D-BINDING PROTEIN (DBP) (ALBUMIN D BOX-BINDING PROTEIN).
25 0.71:57:36
MUS MUSCULUS (MOUSE).
Q60925

30 F-Y79AA1002129
TRANSCRIPTIONAL REGULATORY PROTEIN ALGP (ALGINATE REGULATORY PROTEIN ALGR3).
0.98:158:24
PSEUDOMONAS AERUGINOSA.
P15276

35 F-Y79AA1002213
HYPOTHETICAL 52.7 KD PROTEIN C38C10.2 IN CHROMOSOME III.
4.7e-39:218:41
CAENORHABDITIS ELEGANS.
Q03567

40 F-Y79AA1002334
HYPOTHETICAL PROTEIN MJ1345.
1.8e-08:164:26
45 METHANOCOCCUS JANNASCHII.
Q58741

F-Y79AA1002373
50 CORNIFIN (SMALL PROLINE-RICH PROTEIN I) (SPR-I) (SMALL PROLINE-RICH SQUAMOUS CELL MARKER) (SPRP).
0.083:44:40
SUS SCROFA (PIG).
P35323

F-Y79AA1002376
55 DYNEIN INTERMEDIATE CHAIN 2, CYTOSOLIC (DH IC-2).
3.0e-91:214:83
RATTUS NORVEGICUS (RAT).
Q62871

5 F-Y79AA1002378
 ZINC FINGER PROTEIN 38 (ZFP-38) (CTFIN51) (TRANSCRIPTION FACTOR RU49).
 1.0e-59:163:74
 MUS MUSCULUS (MOUSE).
 Q07231

10 F-Y79AA1002381
 CELL DIVISION CONTROL PROTEIN 28 (EC 2.7.1.-).
 9.5e-41:179:38
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 P00546

Homology search result 6

15 [0296] The result of the homology search in the GenBank(<http://www.ncbi.nlm.nih.gov/web/GenBank/>) using the clone sequences of the 5'-ends. except EST and STS sequences

20 Indicated are from the top,
 the name of the clone sequence,
 definition of the top hit data,
 the P-value: the length of the sequence used for comparison (nucleotide):similarity (%),
 the Accession No. of the top hit data.

25 [0297] Data were not shown for the clones in which the P-value was higher than 1.

25 F-BNGH41000020
 H.sapiens mitochondrial DNA, complete genome.
 6.0e-188:913:97
 X93334

30 F-BNGH41000087
 Human DNA sequence from clone 1049G16 on chromosome 20q12-13.2 Contains gene similar to GLU-COSAMINE-6-SULFATASE, a nuclear receptor coactivator gene, ESTs, STSs, GSSs, complete sequence.
 7.1e-32:176:99

35 AL034418

40 F-BNGH41000091
 Homo sapiens potassium channel h-eag.
 1.6e-79:687:76
 AJ001366

45 F-HEMBA1000006
 S.erythraea second and third ORF's of eryA gene, complete cds.
 0.95:243:64
 M63677

50 F-HEMBA1000121
 Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 796F18, WORKING DRAFT SEQUENCE.
 5.9e-70:450:89
 AL031291

55 F-HEMBA1000128
 Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-14, complete sequence.
 1.0:274:59
 Z98549

F-HEMBA1000275

EP 1 130 094 A2

Herpes simplex virus type 2 (strain HG52), complete genome.
0.036:625:55
Z86099

- 5 F-HEMBA1000300
Homo sapiens chromosome 17, clone hRPK.178_C_3, complete sequence.
1.4e-40:343:80
AC005702
- 10 F-HEMBA1000349
Homo sapiens chromosome 17, clone hRPK.235_I_10, complete sequence.
7.5e-65:451:72
AC005922
- 15 F-HEMBA1000443
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 222E13, WORKING DRAFT SE-
QUENCE.
8.1e-77:216:95
Z93241
- 20 F-HEMBA1000462
Caenorhabditis elegans cosmid C49H3.
3.7e-06:98:82
U42436
- 25 F-HEMBA1000477
Mus musculus BALB/c putative growth factor GDF7 (Gdf7) gene, partial cds.
9.1e-05:190:65
U08339
- 30 F-HEMBA1000590
Human DNA sequence from clone 453C12 on chromosome 20q12-13.12 Contains SDC4 (syndecan 4 (amphig-
lycan, ryudocan)) predicts a gene like the mouse transcription factor RBP-L, MATN4 (matrilin-4) STS, GSS, CpG
island, complete sequence.
- 35 3.0e-102:209:99
AL021578
- 40 F-HEMBA1000634
*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0539L10; HTGS phase 1,
WORKING DRAFT SEQUENCE, 15 unordered pieces.
2.0e-95:460:99
AC004480
- 45 F-HEMBA1000671
Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.
1.5e-28:259:69
AC006116
- 50 F-HEMBA1000713
Homo sapiens 10kD protein (BC10) mRNA, complete cds.
6.5e-126:442:97
AF053470
- 55 F-HEMBA1000732
Homo sapiens clone IMAGE Consortium 302831 latent transforming growth factor-beta binding protein 4 mRNA,
partial cds.
1.7e-45:258:94
AF054502

- 5 F-HEMBA1000745
Streptomyces coelicolor cosmid 3F9.
 3.5e-06:360:61
 AL023862
- 10 F-HEMBA1000835
Homo sapiens fibrillin mRNA, complete cds.
 1.3e-07:151:69
 L13923
- 15 F-HEMBA1000875
Human Krueppel-type zinc finger protein (ZNF169) gene, partial cds.
 2.6e-28:249:81
 U28322
- 20 F-HEMBA1000907
Spermatozopsis similis mRNA for 95 kD basal apparatus-protein.
 3.4e-09:599:60
 AJ001438
- 25 F-HEMBA1000940
Homo sapiens connexin46.6 (Cx46.6) gene, complete cds.
 1.7e-16:307:66
 AF014643
- 30 F-HEMBA1000962
Homo sapiens Chromosome 11q12.2 PAC clone pDJ519o13 containing human gene for ferritin heavy chain (FTH),
 complete sequence.
 0.00040:497:59
 AC004228
- 35 F-HEMBA1001184
Homo sapiens SH3 domain binding glutamic acid-rich-like protein (SH3BGRL) mRNA, complete cds.
 8.8e-23:404:67
 AF042081
- 40 F-HEMBA1001221
Human transmembrane protein mRNA, complete cds.
 2.4e-42:858:63
 U19878
- 45 F-HEMBA1001228
Human germline oligomeric matrix protein (COMP) mRNA, complete cds.
 1.9e-82:470:91
 L32137
- 50 F-HEMBA1001272
Human Ig gamma-2 heavy chain switch region.
 0.032:549:60
 U39934
- 55 F-HEMBA1001296
H.sapiens mRNA for PQ-rich protein.
 6.9e-07:73:98
 Z50194
- F-HEMBA1001297
Homo sapiens putative transcription factor CA150 mRNA, complete cds.

- 9.3e-14:143:81
AF017789
- 5 F-HEMBA1001390
Mus musculus polymerase I-transcript release factor mRNA, complete cds.
2.5e-56:464:81
AF036249
- 10 F-HEMBA1001563
Human DNA sequence from clone 71L16 on chromosome Xp11. Contains a probable Zinc Finger protein (pseudo) gene, an unknown putative gene, a pseudogene with high similarity to part of antigen KI-67, a putative Chondroitin 6-Sulfotransferase LIKE gene and a KIAA0267 LIKE putative Na(+)/H(+) exchanger protein gene. Contains a predicted CpG island, ESTs, STSs and GSSs and genomic markers DXS1003 and DXS1055, complete sequence.
3.1e-06:210:68
AL022165
- 15 F-HEMBA1001621
Human G protein-coupled receptor APJ gene, complete cds.
2.0e-98:516:95
U03642
- 20 F-HEMBA1001878
Homo sapiens U5 snRNP-specific 40 kDa protein mRNA, complete cds.
1.0e-170:810:98
AF090988
- 25 F-HEMBA1001886
Human repressor transcriptional factor (ZNF85) mRNA, complete cds.
3.3e-114:849:80
U35376
- 30 F-HEMBA1002048
HS_3058_B2_A11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3058 Col=22 Row=B, genomic survey sequence.
3.8e-11:244:66
AQ103440
- 35 F-HEMBA1002131
Homo sapiens mRNA for KIAA0584 protein, partial cds.
3.5e-44:709:66
AB011156
- 40 F-HEMBA1002163
Homo sapiens chromosome X, clone 592, WORKING DRAFT SEQUENCE, 8 unordered pieces.
2.3e-28:373:71
AC002489
- 45 F-HEMBA1002164
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 167A19, WORKING DRAFT SEQUENCE.
1.3e-127:493:99
AL031427
- 50 F-HEMBA1002167
Rattus norvegicus neuroligin I mRNA, complete cds.
8. 1e-155:850:91
U22952

F-HEMBA1002178

Homo sapiens mRNA for KIAA0584 protein, partial cds.

2.6e-46:794:65

AB011156

5

F-HEMBA1002195

Human lysosomal alpha-mannosidase (manB) gene, 5' flanking region and exon 1.

7.7e-35:255:86

U60885

10

F-HEMBA1002227

Homo sapiens mRNA for 80K-L protein, complete cds.

3.8e-137:382:95

D10522

15

F-HEMBA1002239

Homo sapiens Chromosome 16 BAC clone CIT987SK-A-485G10, complete sequence.

4.5e-43:452:74

AC003049

20

F-HEMBA1002316

Homo sapiens DNA sequence from PAC 29C18 on chromosome 22.

3.0e-22:609:67

Z97192

25

F-HEMBA1002420

Homo sapiens clone RG031N19, WORKING DRAFT SEQUENCE, 1 unordered pieces.

4.2e-142:322:98

AC005632

30

F-HEMBA1002421

Human heparan sulfate proteoglycan (HSPG) core protein, 3' end.

1.3e-165:778:98

J04621

35

F-HEMBA1002524

Homo sapiens clone UWGC:y55c025 from 6p21, complete sequence.

1.3e-153:313:96

AC004209

40

F-HEMBA1002551

Human potential CENP-C binding target sequence, 0.7 kb clone, partial sequence 2.

6.1e-16:108:97

U57994

45

F-HEMBA1002767

Homo sapiens chromosome 1p33-p34 beta-1,4-galactosyltransferase mRNA, complete cds.

1.4e-168:798:98

AF038660

50

F-HEMBA1002985

HS_3165_A2_C08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone
Plate=3165 Col=16 Row=E, genomic survey sequence.

1.7e-08:127:76

AQ142051

55

F-HEMBA1002992

RPCI11-67B15.TJ RPCI11 Homo sapiens genomic clone R-67815, genomic survey sequence.

- 2.7e-11:119:86
AQ201833
- 5 F-HEMBA1003047
Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds.
4.5e-187:873:99
AF034611
- 10 F-HEMBA1003072
Gallus gallus single-strand DNA-binding protein csdp mRNA, partial cds.
4.1e-50:515:73
U68380
- 15 F-HEMBA1003101
Homo sapiens tyrosylprotein sulfotransferase-2 mRNA, complete cds.
5.3e-139:671:98
AF049891
- 20 F-HEMBA1003120
Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.
3.3e-44:213:73
AC006116
- 25 F-HEMBA1003230
Homo sapiens UP50 mRNA, complete cds.
5.5e-183:856:98
AF093118
- 30 F-HEMBA1003294
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 495010, WORKING DRAFT SEQUENCE.
4.2e-38:558:69
AL031121
- 35 F-HEMBA1003315
Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9I9, complete sequence.
1.2e-61:737:68
AB013390
- 40 F-HEMBA1003392
Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds.
2.9e-183:851:99
AF074264
- 45 F-HEMBA1003399
Homo sapiens clone DJ0826E18, WORKING DRAFT SEQUENCE, 4 unordered pieces.
8.7e-16:215:74
AC005282
- 50 F-HEMBA1003487
H.sapiens DNA sequence.
0.0075:158:67
Z22340
- 55 F-HEMBA1003497
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 2705, WORKING DRAFT SEQUENCE.
1.1e-109:538:98
AL033529

- 5 F-HEMBA1003530
S.scrofa mRNA for BM88 antigen.
2.8e-47:644:69
X82027
- 10 F-HEMBA1003602
Human (lambda) DNA for immunoglobulin light chain.
2.5e-94:551:91
D86997
- 15 F-HEMBA1003732
Homo sapiens clone DJ0935K16, complete sequence.
6.1e-151:777:96
AC006011
- 20 F-HEMBA1003945
Homo sapiens clone 638 unknown mRNA, complete sequence.
1.8e-76:310:93
AF091085
- 25 F-HEMBA1004007
Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.
8.7e-133:718:94
AL031864
- 30 F-HEMBA1004067
Homo sapiens, clone hRPK.2_A_1, complete sequence.
2.7e-58:256:80
AC006197
- 35 F-HEMBA1004110
Homo sapiens intersectin short form mRNA, complete cds.
3.8e-159:779:96
AF064243
- 40 F-HEMBA1004250
Homo sapiens chromosome 5, BAC clone 182a8 (LBNL H161), complete sequence.
1.2e-183:863:99
AC005752
- 45 F-HEMBA1004391
H.sapiens gene for neural cell adhesion molecule L1.
0.51:426:59
Z29373
- 50 F-HEMBA1004444
Homo sapiens clone DJ0971C03, WORKING DRAFT SEQUENCE, 18 unordered pieces.
3.3e-147:463:93
AC004938
- 55 F-HEMBA1004454
Homo sapiens tetraspan NET-4 mRNA, complete cds.
0.00036:230:62
AF065389

- 5 F-HEMBA1004505
D.melanogaster mRNA for alpha 1,2 mannosidase.
5.5e-17:663:58
X82640
- 10 F-HEMBA1004785
Gallus gallus mRNA for chromobox protein (CHCB3), complete cds.
6.6e-19:322:68
AB005619
- 15 F-HEMBA1004797
Haemonchus contortus GT microsatellite DNA sequence.
3.0e-08:175:71
U84474
- 20 F-HEMBA1004952
Mus musculus recombinant quaking gene sequence.
4.8e-15:398:65
U44942
- 25 F-HEMBA1005070
Human mRNA for KIAA0310 gene, complete cds.
2.5e-65:370:93
AB002308
- 30 F-HEMBA1005084
Mouse transcriptional control element.
0.0024:189:63
M17284
- 35 F-HEMBA1005145
Pseudorabies virus glycoprotein gp50 gene, complete cds.
0.00022:395:60
AF092447
- 40 F-HEMBA1005230
Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.
2.8e-102:302:94
AC006116
- 45 F-HEMBA1005246
Homo sapiens CAGH44 mRNA, partial cds.
5.0e-29:429:66
U80741
- 50 F-HEMBA1005267
Homo sapiens chromosome 3, olfactory receptor pseudogene cluster 1, complete sequence, and myosin light chain kinase (MLCK) pseudogene, partial sequence.
1.0e-43:320:87
AF042089
- 55 F-HEMBA1005337
Plasmodium falciparum MAL3P6, complete sequence.
4.1e-08:84:89

Z98551

F-HEMBA1005430

5 F-HEMBA1005449

T.aestivum mRNA for a proline-rich protein.

0.00097:385:61

X52472

10 F-HEMBA1005489

Homo sapiens Xq28 genomic DNA in the region of the ALD locus containing the genes for creatine transporter (SLC6A8), CDM, adrenoleukodystrophy (ALD), Na+-isocitrate dehydrogenase gamma subunit (IDH), and translocon-associated protein delta (TRAP) genes, complete cds, plexin related protein (PLEXR) and serine kinase (SK) genes, partial cds, Xq281u1 gene and cytochrome C (CCp) pseudogene.

15 7.8e-16:405:62

U52111

F-HEMBA1005522

O.cuniculus rACNG mRNA for aorta CNG channel.

20 5.9e-47:344:85

X59668

F-HEMBA1005545

Human m3 muscarinic acetylcholine receptor (CHRM3) gene, complete cds.

25 5.1e-173:810:98

U29589

F-HEMBA1005698

30 F-HEMBA1005913

HS_2249_B1_E01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2249 Col=1 Row=J, genomic survey sequence.

0.17:215:61

AQ072649

35 F-HEMBA1005929

Homo sapiens chromosome 19, cosmid R31237, complete sequence.

7.0e-107:285:93

AC005581

40 F-HEMBA1005945

Oryctolagus cuniculus peroxisomal Ca-dependent solute carrier mRNA, complete cds.

1.8e-46:670:65

AF004161

45 F-HEMBA1006016

CIT-HSP-2334L16.TF CIT-HSP Homo Sapiens genomic clone 2334L16, genomic survey sequence.

2.1e-13:246:69

AQ038406

50 F-HEMBA1006171

F-HEMBA1006276

Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.

55 1.4e-144:416:93

AC005261

F-HEMBA1006299

F-HEMBA1006311

F-HEMBA1006335

Human DNA sequence from clone 496H19 on chromosome 6q24 Contains ESTs, complete sequence.

5 9.6e-61:370:91

AL023582

F-HEMBA1006357

Homo sapiens secretory carrier membrane protein (SCAMP2) mRNA, complete cds.

10 2.3e-26:389:67

AF005038

F-HEMBA1006430

Caenorhabditis elegans cosmid T12A2.

15 4.6e-23:283:72

U13019

F-HEMBA1006482

Homo sapiens h-sco1 (SCO1) mRNA, nuclear gene encoding mitochondrial protein, complete cds.

20 1.9e-144:575:98

AF026852

F-HEMBA1006517

25 F-HEMBA1006544

Homo sapiens suppressor of white-apricot homolog 2 (SWAP2) gene, exons 12 and 13.

2.3e-151:732:97

AF042809

30 F-HEMBA1006572

HS_3058_B2_A11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3058 Col=22 Row=B, genomic survey sequence.

1.9e-45:245:96

AQ103440

35 F-HEMBA1006658

Homo sapiens mRNA for KIAA0687 protein, partial cds.

3.6e-127:646:95

AB014587

40 F-HEMBA1006707

Human DNA sequence from clone 453C12 on chromosome 20q12-13.12 Contains SDC4 (syndecan 4 (amphiglycan, ryudocan)) predicts a gene like the mouse transcription factor RBP-L, MATN4 (matrilin-4) STS, GSS, CpG island, complete sequence.

45 1.7e-118:397:98

AL021578

F-HEMBA1006724

H.sapiens CpG island DNA genomic Mse1 fragment, clone 40c2, forward read cpg40c2.ft1k.

50 1.4e-53:282:97

Z55440

F-HEMBA1006749

Human DNA sequence from clone 453C12 on chromosome 20q12-13.12 Contains SDC4 (syndecan 4 (amphiglycan, ryudocan)) predicts a gene like the mouse transcription factor RBP-L, MATN4 (matrilin-4) STS, GSS, CpG island, complete sequence.

55 3.9e-116:457:98

AL021578

EP 1 130 094 A2

- 5 F-HEMBA1006770
Xenopus laevis elav-type ribonucleoprotein (etr-1) mRNA, complete cds.
1.6e-53:280:81
U16800
- 10 F-HEMBA1006902
Human DNA sequence from clone 453C12 on chromosome 20q12-13.12 Contains SDC4 (syndecan 4 (amphiglycan, ryudocan)) predicts a gene like the mouse transcription factor RBP-L, MATN4 (matrilin-4) STS, GSS, CpG island, complete sequence.
4.9e-122:462:98
AL021578
- 15 F-HEMBA1006912
- 20 F-HEMBA1006916
Homo sapiens Grb14 mRNA, complete cds.
1.6e-118:651:92
L76687
- 25 F-HEMBA1006960
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 110F11, WORKING DRAFT SEQUENCE.
0.20:298:60
AL033526
- 30 F-HEMBA1007013
Rattus norvegicus repeat element associated with the Rasgrf1 gene.
8.0e-07:531:59
AF056927
- 35 F-HEMBA1007057
Human DNA sequence from clone 522J7 on chromosome 22q13.3. Contains part of a 60S Ribosomal protein L5 pseudogene and a Peregrin (BR140) LIKE gene downstream of a putative CpG island. Contains ESTs, STSs and GSSs, complete sequence.
0.27:277:64
Z98885
- 40 F-HEMBA1007063
- 45 F-HEMBA1007226
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 310013, WORKING DRAFT SEQUENCE.
0.00033:488:63
AL031658
- 50 F-HEMBA1007241
Caenorhabditis elegans cosmid T15B7.
0.068:304:59
AF022985
- 55 F-HEMBA1007291
Homo sapiens chromosome 19, fosmid 37502, complete sequence.
6.2e-123:587:98
AC004755
- F-HEMBA1007332
Human HeLa mRNA isolated as a false positive in a two-hybrid-screen.
1.3e-30:172:97
U56430

EP 1 130 094 A2

- 5 F-HEMBB1000106
Human DNA sequence from clone 1170D6 on chromosome Xq22.3-23. Contains a pseudogene similar to U-SNRP_associated Cyclophilin (USA-CYP, EC 5.2.1.8), ESTs, an STS and a GSS, complete sequence.
0.033:332:61
AL030995
- 10 F-HEMBB1000276
Dictyostelium discoideum gene encoding a novel glycoprotein.
0.00070:440:60
AJ005262
- 15 F-HEMBB1000309
Homo sapiens zinc finger protein (MBLL) mRNA, complete cds.
7.6e-34:180:100
AF061261
- 20 F-HEMBB1000407
Human Chromosome 11 pac pDJ393o15, WORKING DRAFT SEQUENCE, 8 unordered pieces. 0.16:228:64
AC000384
- 25 F-HEMBB1000447
Homo sapiens JWA protein mRNA, complete cds.
1.4e-158:750:98
AF070523
- 30 F-HEMBB1000542
Human DNA sequence from PAC 509L4 on chromosome 6q22.1-6q22.33. Contains SSX3 like pseudogene, EST, STS.
4.3e-141:874:89
Z99496
- 35 F-HEMBB1000567
Human DNA for insulin-like growth factor II (IGF-2); exon 7 and additional ORF.
9.7e-122:572:99
X07868
- 40 F-HEMBB1000642
Caenorhabditis elegans cosmid K06A5.
0.00041:174:64
AF039038
- 45 F-HEMBB1000679
C.familiaris mRNA for TRAM-protein.
6.1e-100:756:80
X63678
- 50 F-HEMBB1000881
Danio rerio mRNA for MINDIN2, complete cds.
6.2e-40:581:66
AB006085
- 55 F-HEMBB1000905
Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.
4.9e-91:209:94
AC005089

- 5 F-HEMBB1001026
Human p76 mRNA, complete cds.
1.9e-06:410:61
U81006
- 10 F-HEMBB1001048
Human Hpast (HPAST) mRNA, complete cds.
6.8e-55:524:75
AF001434
- 15 F-HEMBB1001200
Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9
unordered pieces.
4.4e-12:794:59
AC004157
- 20 F-HEMBB1001407
Homo sapiens chromosome 17, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1
ordered pieces.
2.7e-43:281:91
AC004150
- 25 F-HEMBB1001530
HS_2255_B1_F05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens
genomic clone Plate=2255 Col=9 Row=L, genomic survey sequence.
2.1e-14:95:97
AQ131814
- 30 F-HEMBB1001547
S.cerevisiae chromosome VII reading frame ORF YGL236c.
1.1e-19:550:61
Z72758
- 35 F-HEMBB1001573
Homo sapiens 12p13.3 PAC RPCI5-951N9 (Roswell Park Cancer Institute Human PAC library) complete se-
quence.
2.7e-07:467:60
AC004672
- 40 F-HEMBB1001847
H.sapiens CpG island DNA genomic Mse1 fragment, clone 13d12, reverse read cpg13d12.rt1c.
1.1e-14:94:100
Z64565
- 45 F-HEMBB1001959
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 537K23, WORKING DRAFT SE-
QUENCE.
1.2e-82:492:90
AL034405
- 50 F-HEMBB1001978
Homo sapiens chromosome 10 clone CIT987SK-1057L21 map 10q25, complete sequence.
7.0e-23:239:76
AC005386
- 55 F-HEMBB1002039
Human DNA sequence from cosmid 315B17, between markers DXS366 and DXS87 on chromosome X contains
ESTs.

- 3.5e-49:605:71
Z73967
- 5 F-HEMBB1002041
R.norvegicus mRNA for leucocyte common antigen-related protein (3941 bp).
3.5e-09:501:60
X83546
- 10 F-HEMBB1002051
Homo sapiens E74-like factor 5 (ELF5) mRNA, complete cds.
3.1e-95:454:99
AF049703
- 15 F-HEMBB1002120
- 15 F-HEMBB1002162
Homo sapiens genethonin 1 mRNA, complete cds.
7.0e-67:328:99
AF062534
- 20 F-HEMBB1002228
Homo sapiens unknown mRNA, complete cds.
1.6e-39:208:98
AF047439
- 25 F-HEMBB1002245
Rattus norvegicus prostaglandin F2a receptor regulatory protein precursor, mRNA, complete cds.
3.7e-68:424:87
U26595
- 30 F-HEMBB1002302
RPCI11-18E11.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-18E11, genomic survey sequence.
2.7e-15:101:98
B88081
- 35 F-HEMBB1002427
Homo sapiens chromosome 9q34, clone 70C11, complete sequence.
2.9e-123:249:90
AC002319
- 40 F-HEMBB1002465
Mouse short chain acyl-CoA dehydrogenase mRNA, complete cds.
7.9e-18:545:61
L11163
- 45 F-HEMBB1002661
Drosophila melanogaster; Chromosome 2R; Region 44A1-44A2; P1 clone DS07435, WORKING DRAFT SE-
QUENCE, 2 unordered pieces.
1.9e-07:187:67
- 50 AC005445
- F-HEMBB1002663
- 55 F-HEMBB1002693
Homo sapiens full length insert cDNA, clone ZD85G07.
2.1e-20:136:93
AF086462

EP 1 130 094 A2

F-MAMMA1000046

CIT-HSP-2166017.TF CIT-HSP Homo sapiens genomic clone 2166O17, genomic survey sequence.

2.0e-60:345:92

B92334

5

F-MAMMA1000102

Human DNA sequence from cosmid B33F2 on chromosome 22 Contains ESTs.

3.0e-161:766:98

Z79996

10

F-MAMMA1000106

Rat gene for alpha 1B adrenergic receptor, promoter region and partial cds.

0.0025:247:64

D32045

15

F-MAMMA1000118

Canis familiaris beta1 adrenergic receptor (dogbeta1) gene, complete cds.

6.1e-06:545:60

U73207

20

F-MAMMA1000141

Homo sapiens 12q24.2 PAC RPCI1-128M12 (Roswell Park Cancer Institute Human PAC library) complete sequence.

1.5e-10:151:78

25

AC004024

F-MAMMA1000204

Homo Sapiens mRNA for LGMD2B protein.

2. le-166:781:98

30

AJ007670

F-MAMMA1000226

*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone B331O8; HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces.

35

2.9e-35:188:100

AC004064

F-MAMMA1000403

Human vascular addressin MAdCAM-1 mRNA, complete cds.

40

0.00043:538:59

U82483

F-MAMMA1000449

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 317C6, WORKING DRAFT SEQUENCE.

45

0.090:514:60

Z97651

F-MAMMA1000457

H.sapiens mRNA for NADH-cytochrome b5 reductase.

50

5.5e-36:469:68

Y09501

55

F-MAMMA1000473

Caenorhabditis elegans cosmid B0491, complete sequence.

0.0052:187:64

Z49907

F-MAMMA1000496

EP 1 130 094 A2

- Homo sapiens PAC clone DJ130H16 from 22q12.1-qter, complete sequence.
1.2e-81:318:92
AC004997
- 5 F-MAMMA1000528
P.falciparum complete gene map of plastid-like DNA (IR-B).
0.016:343:58
X95276
- 10 F-MAMMA1000591
Mus musculus UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase-T3 mRNA, complete cds.
1.2e-24:493:63
U70538
- 15 F-MAMMA1000614
*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0190L06; HTGS phase 1,
WORKING DRAFT SEQUENCE, 21 unordered pieces.
7.5e-13:615:60
AC004670
- 20 F-MAMMA1000652
Homo sapiens Chromosome 16 BAC clone CIT987SK-A-116A10, complete sequence.
1.6e-59:451:82
AC004638
- 25 F-MAMMA1000681
Homo sapiens mRNA for putative G-protein coupled receptor, EDG6.
1.2e-32:636:65
AJ000479
- 30 F-MAMMA1000706
*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0110D16; HTGS phase 1,
WORKING DRAFT SEQUENCE, 7 unordered pieces.
6.8e-06:428:62
AC004578
- 35 F-MAMMA1000788
HS_3080_A2_B03_MRCIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3080
Col=6 Row=C, genomic survey sequence.
4.9e-35:204:94
AQ128409
- 40 F-MAMMA1000810
Homo sapiens DNA sequence from PAC 510L9 on chromosome 6p24.1-p25.3.
5.8e-06:246:65
AL022098
- 45 F-MAMMA1000814
Anadara trapezia (alpha 3.15L) hemoglobin alpha-chain (HBA) gene, exons 2 and 3, intron 2, including hypervar-
iable microsatellite polymorphic repeat regions.
1.0e-12:176:75
L25098
- 50 F-MAMMA1000881
Rattus norvegicus serum and glucocorticoid-regulated kinase (sgk) mRNA, complete cds.
2.8e-07:283:63
L01624

EP 1 130 094 A2

F-MAMMA1000986

Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence.

1.8e-166:306:99

AF001550

5

F-MAMMA1000994

Mycobacterium tuberculosis H37Rv complete genome; segment 48/162.

0.75:260:61

AL021897

10

F-MAMMA1001043

H.sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2).

0.038:376:60

Z37976

15

F-MAMMA1001066

Homo sapiens DNA from chromosome 19-cosmid f24590 containing CAPNS and POL2RI, genomic sequence.

4.4e-15:162:72

AD001527

20

F-MAMMA1001094

Homo sapiens clone 243 unknown mRNA, complete sequence.

6.2e-181:844:99

AF091094

25

F-MAMMA1001141

Cams familiaris beta1 adrenergic receptor (dogbeta1) gene, complete cds.

1.3e-10:602:59

U73207

30

F-MAMMA1001150

M.musculus (Balb/c) mRNA for serine/threonine protein kinase.

7.7e-57:447:67

Z34524

35

F-MAMMA1001237

Rattus norvegicus monocarboxylate transporter MCT3 mRNA, complete cds.

1.5e-08:306:65

AF059258

40

F-MAMMA1001284

HS_3076_A1_F08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3076

Col=15 Row=K, genomic survey sequence.

5.2e-53:307:93

45

AQ120674

F-MAMMA1001310

1(2)09851 Drosophila melanogaster P lethal line Drosophila melanogaster genomic Sequence recovered from 3' end of P element, genomic survey sequence.

50

0.00072:209:66

AQ025672

F-MAMMA1001344

Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit homolog (CCA1) and putative protein 2 (PUT2) genes, partial cds, complete sequence.

5.2e-05:164:67

AF026198

F-MAMMA1001418

Human Na⁺/nucleoside cotransporter (hCNT1a) mRNA, complete cds.

5 6.0e-35:622:63

U62966

F-MAMMA1001532

Homo sapiens PAC clone DJ0728D04, complete sequence.

10 5.2e-46:538:74

AC004865

F-MAMMA1001609

Homo sapiens chromosome 10 clone CIT-HSP-1240G16 map 10q25.1, complete sequence. 0.00031:592:57

15 AC005886

F-MAMMA1001615

H.sapiens CpG island DNA genomic Mse1 fragment, clone 71h9, reverse read cpg71h9.rt1a.

20 1.2e-25:146:99

Z62710

F-MAMMA1001623

Homo sapiens 12q24.2 BAC RPCI11-407A16 (Roswell Park Cancer Institute Human BAC Library) complete sequence.

25 3.9e-69:471:85

AC006065

F-MAMMA1001634

Human DNA sequence from PAC 93C23 on chromosome X. Contains steroid 5-alpha-reductase pseudogene, ESTs and STS.

30 2.2e-22:228:79

AL008713

F-MAMMA1001893

HS_3067_B2_H09_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3067 Col=18 Row=P, genomic survey sequence.

35 2.5e-29:188:93

AQ138065

F-MAMMA1001901

Human DNA sequence from clone 354J5 on chromosome 6q21-22. Contains pseudogene similar to zinc finger protein (ZPR1), EST, STS, GSS, complete sequence.

40 2.0e-23:287:71

Z95118

45 F-MAMMA1001957

Drosophila melanogaster, chromosome 2L, region 21C5-21D1, P1 clone DS07610, complete sequence.

1.5e-14:192:66

AC004573

50 F-MAMMA1001978

Human immunoglobulin S(u) like sequence.

0.60:150:66

X15517

55 F-MAMMA1002070

Human PAC clone DJ515N1 from 22q11.2-q22, complete sequence.

3.9e-116:250:93

AC002073

F-MAMMA1002080

Mus musculus chromosome 11, clone mCIT.268_P_23, complete sequence.

5 1.1e-59:493:78

AC004807

F-MAMMA1002087

HS-1047-B2-A09-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 830
10 Col=18 Row=B, genomic survey sequence.

2.1e-31:174:98

B38457

F-MAMMA1002091

15 Homo sapiens CD39L2 (CD39L2) mRNA, complete cds.

1.6e-156:743:98

AF039916

F-MAMMA1002095

20 Rat alternatively spliced mRNA.

4.9e-126:691:91

M93017

F-MAMMA1002128

25 Mus musculus C2C12 unknown mRNA, partial cds.

5.0e-41:353:77

U31629

F-MAMMA1002142

30

F-MAMMA1002165

Homo sapiens connective tissue growth factor related protein WISP-2 (WISP2) mRNA, complete cds.

1.2e-34:219:90

AF100780

35

F-MAMMA1002205

Homo Sapiens Chromosome X clone bWXD691, complete sequence.

8.1e-33:535:67

AC004386

40

F-MAMMA1002224

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 229A8, WORKING DRAFT SEQUENCE.

1.2e-31:274:82

Z86090

45

F-MAMMA1002234

Canine mRNA for 68kDa subunit of signal recognition particle (SRP68).

9.8e-145:736:91

X53744

50

F-MAMMA1002586

Drosophila melanogaster cosmid clone 86E4.

0.0071:306:58

AL021086

55

F-MAMMA1002633

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 850H21, WORKING DRAFT SE-
QUENCE.

- 3.9e-33:297:79
AL031680
- 5 F-MAMMA1003126
Human Hpast (HPAST) mRNA, complete cds.
1.7e-82:801:74
AF001434
- 10 F-NT2RM1000407
Cloning vector pUC-GM-INT, complete sequence.
9.4e-141:673:98
AF025392
- 15 F-NT2RM1000462
, complete sequence.
1.5e-86:232:82
AC005300
- 20 F-NT2RM1000542
Mouse beta-galactosidase (BGAL) gene, complete cds.
4.4e-17:468:62
M57734
- 25 F-NT2RM1000580
Caenorhabditis elegans cosmid F09E5.
1.6e-08:352:61
U37429
- 30 F-NT2RM1000789
Homo sapiens mRNA for hTCF-4.
1.1e-94:299:92
Y11306
- 35 F-NT2RM1000855
Canis familiaris sec61 homologue mRNA, complete cds.
6.6e-110:671:87
M96629
- 40 F-NT2RM1000858
tricarboxylate carrier [rats, liver, mRNA Partial, 2986 nt].
2.0e-65:716:70
S70011
- 45 F-NT2RM1000899
S.pombe chromosome I cosmid c8C9.
0.0010:300:59
Z99168
- 50 F-NT2RM2000241
Homo sapiens chromosome 12p13.3 clone RPCI11-350L7, WORKING DRAFT SEQUENCE, 72 unordered pieces.
0.99:201:65
AC005844
- 55 F-NT2RM2000306
Homo sapiens DNA sequence from PAC 257I20 on chromosome 22q13.1-13.2. Contains cytochrome P450 pseudogenes CYP2D7P, CYP2D8P, CYP2D6(D), TCF20, NADH ubiquinone oxidoreductase B14 subunit, ESTs, CA repeat, STS, GSS.
1.1e-142:595:97

AL021878

F-NT2RM2000410

S.gregaria Abd-B gene.

5 0.076:172:66

X69161

F-NT2RM2000423

Arthrobacter sp. beta-galactosidase gene, complete cds.

10 4.2e-06:606:57

U78028

F-NT2RM2000497

Homo sapiens chromosome 17, clone hRPK.215_P_18, complete sequence.

15 1.2e-55:285:81

AC005969

F-NT2RM2000514

20 F-NT2RM2000565

Caenorhabditis elegans cosmid F28C5, complete sequence.

4.2e-18:539:62

Z68315

25 F-NT2RM2000582

P.zebra microsatellite locus DNA, 429bp.

0.00015:160:69

X99784

30 F-NT2RM2000589

Bos taurus myosin X, complete cds.

3.4e-139:817:88

U55042

35 F-NT2RM2000622

H.sapiens MFH-1 gene.

0.0010:466:57

Y08223

40 F-NT2RM2000632

Homo sapiens mRNA for TBP-associated factor 170 (TAFII170).

0.0052:331:59

AJ001017

45 F-NT2RM2000773

Oryctolagus cuniculus serum amyloid A-activating factor SAF-8 mRNA, partial cds.

2.9e-91:496:93

AF076786

50 F-NT2RM2001126

Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds.

1.6e-161:663:99

AF093419

55 F-NT2RM2001558

Homo sapiens protein kinase A binding protein AKAP110 mRNA, complete cds.

1.2e-164:770:98

AF093408

EP 1 130 094 A2

F-NT2RM2001626

F.rubripes GSS sequence, clone 060E22bA4, genomic survey sequence.

4.5e-46:606:68

Z88651

5

F-NT2RM2001643

HS-1053-B2-E09-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT775
Col=18 Row=J, genomic survey sequence.

2.5e-06:181:66

10 B41504

F-NT2RM2001738

S.capreolus ard2 gene and orf2, orf4 and orf5.

0.41:273:63

15 Y11036

F-NT2RM2001767

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 50O24, WORKING DRAFT SEQUENCE.

8.0e-18:130:92

20 AL034380

F-NT2RM2001792

Homo sapiens mRNA for serum lectin P35, complete cds.

2.5e-12:244:67

25 D49353

F-NT2RM2001818

F-NT2RM2001902

Drosophila melanogaster mRNA for p21 activated kinase related protein.

7.2e-74:683:75

AJ011578

30

F-NT2RM2001939

Human G protein-coupled receptor GPR-NGA gene, complete cds.

1.4e-140:702:96

U55312

35

F-NT2RM2001941

Human gene for muscarinic acetylcholine receptor HM1.

6.3e-20:488:62

X15263

40

F-NT2RM4000100

Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence.

7.7e-25:162:74

AC004827

45

F-NT2RM4000115

50

F-NT2RM4000198

F-NT2RM4000284

Human IgG Fc receptor hFcRn mRNA, complete cds.

7.3e-37:194:98

U12255

55

F-NT2RM4000295

EP 1 130 094 A2

Streptomyces chrysomallus actinomycin synthetase II (acmB) gene, complete cds.

1.6e-05:642:59

AF047717

5 F-NT2RM4000326

Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterranean Fever gene disease.

1.0e-127:340:92

AJ003147

10 F-NT2RM4000417

Oncorhynchus kisutch microsatellite OKi20 DNA.

0.44:144:66

AF055444

15 F-NT2RM4000444

S.salar mRNA for transport-associated protein Tap2A.

1.7e-27:577:62

Z83328

20 F-NT2RM4000587

Homo sapiens chromosome 19, cosmid R28058, complete sequence.

7.7e-16:388:64

AC005615

25 F-NT2RM4000593

F-NT2RM4000648

M.musculus mRNA for K-glycan.

30 1.4e-50:610:70

X83577

F-NT2RM4000761

Human mitochondrial DNA, fragment M1, encoding transfer RNAs, cytochrome oxidase I, and 2 URFs.

35 4.8e-167:787:98

M10546

F-NT2RM4000965

S.scrofa mRNA for calcium release channel (CRC).

40 0.044:356:60

X62880

F-NT2RM4000997

45 F-NT2RM4001321

HS-1053-B2-E09-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 775 Col=18 Row=J, genomic survey sequence.

1.3e-06:181:67

B41504

50 F-NT2RM4001325

Homo sapiens mRNA for chondroitin 6-sulfotransferase, complete cds.

6.6e-12:384:64

AB012192

55 F-NT2RM4001377

Homo sapiens mRNA for KIAA0638 protein, partial cds.

9.7e-155:719:99

EP 1 130 094 A2

AB014538

F-NT2RM4001735

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 483K16, WORKING DRAFT SEQUENCE.

1.3e-162:679:96

AL034374

F-NT2RM4001768

Human HepG2 partial cDNA, clone hrnd3a07m5.

2.7e-52:271:98

D17020

F-NT2RM4001843

F-NT2RM4002352

Homo sapiens hLRp105 mRNA for LDL receptor related protein 105, complete cds.

1.4e-155:761:97

AB009462

F-NT2RP1000002

Mouse cAMP-dependent protein kinase beta subunit gene, exon 1.

1.7e-06:252:65

M21096

F-NT2RP1000050

Human HepG2 partial cDNA, clone hmd3g02m5.

7.1e-18:115:97

D17047

F-NT2RP1000181

Homo sapiens Chromosome 11q12.2 PAC clone pDJ519o13 containing human gene for ferritin heavy chain (FTH), complete sequence.

4.2e-139:427:98

AC004228

F-NT2RP1000239

Homo sapiens clone DT1P1E11 mRNA, CAG repeat region.

1.4e-90:524:91

U92989

F-NT2RP1000261

Homo sapiens hPMS1 gene, promoter region and exon 1.

2.5e-14:132:85

AB006462

F-NT2RP1000271

Homo sapiens DNA-binding protein mRNA, complete cds.

4.3e-139:678:97

AF038951

F-NT2RP1000300

Homo sapiens, complete sequence.

0.012:146:69

AC005854

F-NT2RP1000325

H.sapiens gene for phosphate carrier.

EP 1 130 094 A2

- 4.2e-110:438:98
X77337
- 5 F-NT2RP1000448
Streptomyces coelicolor cosmid 1A6.
0.79:209:61
AL023496
- 10 F-NT2RP1000465
Mus musculus nuclear protein NIP45 mRNA, complete cds.
2.2e-29:489:68
U76759
- 15 F-NT2RP1000468
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 537K23, WORKING DRAFT SE-
QUENCE.
1.6e-49:306:91
AL034405
- 20 F-NT2RP1000551
Homo sapiens putative interferon-related protein (SM15) mRNA, partial cds.
7.5e-139:742:93
U09585
- 25 F-NT2RP1000579
Human succinate dehydrogenase flavoprotein subunit (SDH) mRNA, complete cds.
3.6e-140:798:91
L21936
- 30 F-NT2RP1000613
Sequence 1 from patent US 5589579.
8.1e-10:468:58
I32995
- 35 F-NT2RP1000679
Homo sapiens chromosome 17, clone hRPC.4_G_17, complete sequence.
1.3e-112:448:89
AC003688
- 40 F-NT2RP1000740
H.sapiens CpG island DNA genomic Mse1 fragment, clone 34a2, reverse read cpg34a2.rt1a.
9.3e-14:211:73
Z60772
- 45 F-NT2RP1000903
HS_2256_B1_E10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2256
Col=19 Row=J, genomic survey sequence.
9.0e-21:197:84
AQ084622
- 50 F-NT2RP1000981
F-NT2RP1001004
Danio rerio mRNA for MINDIN2, complete cds.
4.1e-22:472:63
AB006085
- 55 F-NT2RP1001020
Mus musculus clone OST66, genomic survey sequence.

EP 1 130 094 A2

- 1.5e-47:352:81
AF046696
- 5 F-NT2RP1001031
CIT-HSP-2330P23.TR CIT-HSP Homo sapiens genomic clone 2330P23, genomic survey sequence.
8.0e-26:145:99
AQ035969
- 10 F-NT2RP1001563
Homo sapiens clone DJ1125K23, WORKING DRAFT SEQUENCE, 21 unordered pieces. 0.096:405:59
AC004971
- 15 F-NT2RP2000092
Human zinc finger protein ZNF136.
1.8e-54:652:70
U09367
- 20 F-NT2RP2000178
Streptomyces coelicolor cosmid 3F9.
0.92:217:64
AL023862
- 25 F-NT2RP2000240
Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence.
2.9e-96:534:90
AF001550
- 30 F-NT2RP2000394
Gallus gallus p52 pro-apototic protein mRNA, complete cds.
2.9e-19:380:65
AF029071
- 35 F-NT2RP2000447
Homo sapiens clone DJ1129D05, complete sequence.
1.3e-109:289:98
AC005630
- 40 F-NT2RP2000479
Human DNA sequence from PAC 130G2 on chromosome 6p22.2-22.3. Contains ribosomal protein L29 pseudo-gene, ESTs and STSs.
0.0039:219:63
AL008627
- 45 F-NT2RP2000514
Homo sapiens roundabout 2 (robo2) mRNA, partial cds.
3.7e-89:461:95
AF040991
- 50 F-NT2RP2000533
Mus musculus cornichon mRNA, complete cds.
1.4e-113:677:89
AF022811
- 55 F-NT2RP2000610
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 537K23, WORKING DRAFT SEQUENCE.
4.3e-25:177:89
AL034405

EP 1 130 094 A2

- 5 F-NT2RP2000616
RPCI11-75J11.TK MCI11 Homo sapiens genomic clone R-75J11, genomic survey sequence.
8.4e-34:135:91
AQ268877
- 10 F-NT2RP2000649
Homo sapiens CAAX prenyl protease (STE24) mRNA, complete cds.
1.2e-165:802:97
AF064867
- 15 F-NT2RP2000663
Human DNA sequence from cosmid U61B11, between markers DDX366 and DDX87 on chromosome X contains ESTs.
1.6e-106:365:97
Z73913
- 20 F-NT2RP2000694
Homo sapiens 5T4 oncofetal trophoblast glycoprotein gene.
4.2e-112:561:96
AJ012159
- 25 F-NT2RP2000712
HS_3071_A2_D05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071 Col=10 Row=G, genomic survey sequence.
7.6e-78:389:97
AQ166085
- 30 F-NT2RP2000739
Human mRNA for KIAA0326 gene, partial cds.
6.4e-24:574:62
AB002324
- 35 F-NT2RP2000818
Drosophila melanogaster, chromosome 2R, region 38A5-38B4, BAC clone BACR48M05, complete sequence.
0.00047:304:61
AC005719
- 40 F-NT2RP2000903
Homo sapiens 5T4 oncofetal trophoblast glycoprotein gene.
2.6e-110:541:97
AJ012159
- 45 F-NT2RP2001200
Homo sapiens mRNA for KIAA0676 protein, partial cds.
3.3e-1 10:540:96
AB014576
- 50 F-NT2RP2001223
HS-1054-B2-C02-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 776 Col=4 Row=F, genomic survey sequence.
7.2e-10:128:77
B41982
- 55 F-NT2RP2001276
Mouse regulatory protein (npdc-1) mRNA, complete cds.
1.2e-38:296:81
L03814

- 5 F-NT2RP2001388
RPCI11-30G23.TV RPCI-11 Homo sapiens genomic clone RPCI-11-30G23, genomic survey sequence.
0.32:53:94
B87787
- 10 F-NT2RP2001469
M.musculus tex292 mRNA (5'region).
4.2e-10:120:83
X80434
- 15 F-NT2RP2001480
Homo sapiens thrombospondin 3 (THBS3) gene, complete cds.
9.0e-140:686:96
L38969
- 20 F-NT2RP2001495
Human transporter protein (g17) mRNA, complete cds.
1.9e-35:581:64
U49082
- 25 F-NT2RP2001514
Drosophila melanogaster DNA sequence (P1 DS06882 (D310)), complete sequence.
3.7e-22:475:62
AC005115
- 30 F-NT2RP2001529
Homo sapiens mRNA for ZIP-kinase, complete cds.
4.6e-152:757:96
AB007144
- 35 F-NT2RP2001538
Sequence 11 from patent US 5624818.
1.4e-88:528:88
I41141
- 40 F-NT2RP2001562
Homo sapiens GLE1 (GLE1) mRNA, complete cds.
2.3e-117:572:97
AF058922
- 45 F-NT2RP2001662
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 460J8, WORKING DRAFT SEQUENCE.
6.1e-107:365:91
AL031662
- 50 F-NT2RP2001769
A.sativa Aspk11 mRNA.
4.7e-17:537:60
X79992
- 55 F-NT2RP2001817
Candida albicans SIR2 (SIR2) gene, complete cds.
4.6e-10:285:61

AF045774

F-NT2RP2001878

Mus musculus repeat element upstream of the Rasgrf1/Cdc25Mm gene.

5 5.0e-06:554:60

AF021791

F-NT2RP2001903

M.musculus mRNA for m-calpain.

10 3.1e-06:337:60

Y10139

F-NT2RP2001915

Homo sapiens chromosome 17, clone hRPK.63_A_1, complete sequence.

15 6.8e-28:488:65

AC005670

F-NT2RP2001921

Homo sapiens clone NH0332L11, complete sequence.

20 1.1e-77:148:99

AC005538

F-NT2RP2001948

Sequence 2 from patent US 5541311.

25 0.59:284:57

I24091

F-NT2RP2001956

Feline c-sis proto-oncogene, segment 4.

30 0.99:101:69

M25356

F-NT2RP2002015

HS-1053-B2-E09-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 775

35 Col=18 Row=J, genomic survey sequence.

3.0e-06:181:65

B41504

F-NT2RP2002063

Homo sapiens chromosome 4 clone B207D4 map 4q25, complete sequence.

40 1.3e-108:418:94

AC004050

F-NT2RP2002188

Rattus norvegicus neuroligin 3 mRNA, complete cds.

45 1.0e-125:700:90

U41663

F-NT2RP2002232

50 F-NT2RP2002304

Human FMR1 gene, 5' end.

0.12:93:67

L19476

55 F-NT2RP2002409

Myxococcus xanthus response regulator FrzZ (frzZ) gene, partial cds; alanine dehydrogenase (aldA), putative ECF sigma factor RpoE1 (rpoE1), and response regulator homolog (frzS) genes, complete cds; and unknown

- genes.
 9.0e-10:553:59
 AF049107
- 5 F-NT2RP2002510
 Mus musculus (129SV) DNA, unmapped BAC 10817, complete sequence.
 4.2e-27:573:62
 AC004093
- 10 F-NT2RP2002527
 Homo sapiens Chromosome 11q12.2 PAC clone pDJ519o13 containing human gene for ferritin heavy chain (FTH),
 complete sequence.
 3.2e-110:439:99
 AC004228
- 15 F-NT2RP2002533
 Homo sapiens putative tumor suppressor gene 26 protein alpha 2 delta calcium channel subunit mRNA, complete
 cds.
 6.4e-141:726:95
 AF040709
- 20 F-NT2RP2002564
 Homo sapiens PAC clone DJ0979P20 from 7q33-q35, complete sequence.
 2.6e-112:403:98
 AC004941
- 25 F-NT2RP2002674
 HS_3122_B2_A02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3122
 Col=4 Row=B, genomic survey sequence.
 4.8e-13:86:100
 AQ182907
- 30 F-NT2RP2002721
- 35 F-NT2RP2002824
 Arabidopsis thaliana BAC T19D16 genomic sequence.
 1.3e-12:135:69
 U95973
- 40 F-NT2RP2002942
 Homo sapiens mRNA for KIAA0806 protein, complete cds.
 6.1e-145:758:94
 AB018349
- 45 F-NT2RP2002974
 Mus musculus mRNA for Six5, partial cds.
 8.0e-84:588:82
 D83146
- 50 F-NT2RP2002976
 H.sapiens gene for phospholipase C beta 3, exon 14.
 0.93:210:61
 Z37557
- 55 F-NT2RP2003042
 G.gallus mRNA for lecithin-cholesterol acyltransferase.
 9.1e-26:462:65
 X91011

F-NT2RP2003138

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 460J8, WORKING DRAFT SEQUENCE.

3.9e-142:702:96

AL031662

5

F-NT2RP2003179

Homo sapiens mRNA for KIAA0537 protein, complete cds.

3.3e-42:587:70

AB011109

10

F-NT2RP2003210

Mus musculus fatty acid transport protein 4 mRNA, partial cds.

2.6e-112:726:85

AF072759

15

F-NT2RP2003302

Human zinc finger protein ZNF136.

5.5e-63:691:69

U09367

20

F-NT2RP2003369

Homo sapiens chromosome 7q22 sequence, complete sequence.

2.0e-49:249:95

AF053356

25

F-NT2RP2003383

Homo sapiens chromosome 1 atrophin-1 related protein (DRPLA) mRNA, complete cds.

1.5e-159:817:95

AF016005

30

F-NT2RP2003390

Homo sapiens SEC63 (SEC63) mRNA, complete cds.

7.0e-115:554:98

AF100141

35

F-NT2RP2003469

Genomic sequence from Human 9q34, complete sequence.

5.6e-38:210:97

AC001644

40

F-NT2RP2003545

Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds.

2.2e-48:579:71

AF024636

45

F-NT2RP2003593

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 971N18, WORKING DRAFT SEQUENCE.

1.8e-90:326:99

50

AL021396

F-NT2RP2003599

F-NT2RP2003655

M.musculus tex261 mRNA.

5.3e-77:513:85

X81058

EP 1 130 094 A2

- 5 F-NT2RP2003664
Homo sapiens mRNA for leptin receptor gene-related protein.
1.7e-132:630:98
Y12670
- 10 F-NT2RP2003931
Homo sapiens chromosome 19, overlapping cosmids R27918 and R33775, complete sequence.
1.3e-114:411:97
AC004447
- 15 F-NT2RP2003940
Human ZNF43 mRNA.
1.4e-97:693:82
X59244
- 20 F-NT2RP2003950
Sequence 1 from patent US 5648238.
6.9e-13:143:79
I55887
- 25 F-NT2RP2004069
F-NT2RP2004108
Human zinc finger protein ZNF136.
1.5e-67:548:78
U09367
- 30 F-NT2RP2004141
Rattus norvegicus leukocyte common antigen receptor (LAR) gene, trans-spliced alternative untranslated exon.
8.0e-10:487:62
U87960
- 35 F-NT2RP2004179
Homo sapiens chromosome 11 from 11p15.5 region, complete sequence.
0.56:600:57
AF015416
- 40 F-NT2RP2004205
Homo sapiens chromosome 16, cosmid clone RT81 (LANL), complete sequence.
0.32:431:55
AC005356
- 45 F-NT2RP2004447
Homo sapiens Chromosome 11q13 BAC Clone 18h3, WORKING DRAFT SEQUENCE, 7 ordered pieces.
2.0e-23:252:79
AC000353
- 50 F-NT2RP2004495
Human transporter protein (g17) mRNA, complete cds.
3.6e-25:497:61
U49082
- 55 F-NT2RP2004524
Genomic sequence from Human 9q34, complete sequence.
5.9e-60:203:98
AC001644
- F-NT2RP2004556

EP 1 130 094 A2

HS_3022_A1_A11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3022
Col=21 Row=A, genomic survey sequence.
1.3e-51:419:79
AQ119143

- 5 F-NT2RP2004606
cDNA encoding NIC(Natural Inhibitor of Collagenase).
1.2e-113:617:92
E00985
- 10 F-NT2RP2004648
Felis catus lysosomal beta-galactosidase (Bgal) mRNA, complete cds.
1.5e-15:403:64
AF006749
- 15 F-NT2RP2004670
Rattus norvegicus vesicula-associate calmodulin-binding protein mRNA, complete cds.
1.1e-73:493:85
L22557
- 20 F-NT2RP2004794
Mus musculus mRNA for B-IND1 protein.
5.6e-12:109:86
Z97207
- 25 F-NT2RP2004837
Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.
2.8e-39:352:78
AC006030
- 30 F-NT2RP2004847
CIT-HSP-2357D24.TR CIT-HSP *Homo sapiens* genomic clone 2357D24, genomic survey sequence.
2.5e-35:196:96
AQ074738
- 35 F-NT2RP2005027
Human glucose transporter-like protein-III (GLUT3), complete cds.
2.2e-145:713:96
M20681
- 40 F-NT2RP2005069
Rat vacuolar protein sorting homolog r-vps33b mRNA, complete cds.
9.4e-51:200:90
U35245
- 45 F-NT2RP2005163
Mouse DNA fragment that hybridizes to HSV-1 SmaI A fragment.
1.4e-08:231:67
M11041
- 50 F-NT2RP2005181
Mus musculus cationic amino acid transporter (CAT3) mRNA, complete cds.
1.6e-96:575:85
U70859
- 55 F-NT2RP2005247
Mus musculus ret finger protein mRNA, complete cds.
1.8e-13:310:66

L46855

- 5 F-NT2RP2005378
RPCI11-21D23.TP RPCI-11 Homo sapiens genomic clone RPCI-11-21D23, genomic survey sequence.
3.0e-12:131:80
B85846
- 10 F-NT2RP2005391
S.muris mRNA for microneme antigen.
2.5e-10:345:61
Z26947
- 15 F-NT2RP2005425
Homo sapiens mRNA for KIAA0803 protein, partial cds.
1.0e-116:566:97
AB018346
- 20 F-NT2RP2005463
- 25 F-NT2RP2005514
- F-NT2RP2005535
Homo sapiens DNA-binding protein mRNA, complete cds.
2.3e-125:726:90
AF038951
- 30 F-NT2RP2005541
CIT-HSP-2386E2.TF.1 CIT-HSP Homo sapiens genomic clone 2386E2, genomic survey sequence.
6.2e-20:152:88
AQ240341
- 35 F-NT2RP2005597
D.melanogaster mRNA for rotated abdomen protein.
0.088:270:57
X95956
- 40 F-NT2RP2005632
Gallus gallus chicken brain factor-2 (CBF-2) mRNA, complete cds.
2.0e-07:207:67
U47276
- 45 F-NT2RP2005666
Homo sapiens chromosome 11 clone CIT-HSP-1337H24, WORKING DRAFT SEQUENCE, 9 unordered pieces.
1.0:328:57
AC005849
- 50 F-NT2RP2005774
Human zinc finger protein ZNF136.
4.0e-44:451:74
U09367
- F-NT2RP2005878
Mus musculus putative steroid dehydrogenase (KIK-I) mRNA, complete cds.
5.1e-16:382:63
AF064635
- F-NT2RP2005883
Human DNA sequence from clone 248E1 on chromosome 6q23.1-23.3 Contains DOPAMINE-BETA-MONOXY-

EP 1 130 094 A2

GENASE PRECURSOR, EF-1-ALPHA-2 pseudogene EST GSS and CA repeat, complete sequence.

1.5e-30:191:95

AL023578

5 F-NT2RP2005887

Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.

1.8e-50:394:79

AC006030

10 F-NT2RP2005941

Human DNA sequence from cosmid CFAT5, chromosome region 11p13 contains PAX6 exons 1-4, EST and CpG Islands.

9.5e-93:468:96

Z95332

15 F-NT2RP2005994

Homo sapiens chromosome 4 clone B207D4 map 4q25, complete sequence.

1.6e-139:692:96

AC004050

20 F-NT2RP2006004

CIT-HSP-2366J21.TF CIT-HSP Homo sapiens genomic clone 2366J21, genomic survey sequence.

6.6e-39:206:98

AQ080257

25 F-NT2RP2006042

Human mRNA for KIAA0144 gene, complete cds.

1.7e-10:220:69

D63478

30 F-NT2RP2006092

Homo sapiens chromosome 5, BAC clone 319C17 (LBNL H159), complete sequence.

3.6e-121:562:82

AC005214

35 F-NT2RP2006099

Human Chromosome 11 pac pDJ392a17, complete sequence.

8.7e-76:383:92

AC000385

40 F-NT2RP2006134

Homo sapiens Chromosome 22q11.2 Cosmid Clone 91c In DGCR Region, complete sequence. 0.055:125:71

AC000091

45 F-NT2RP2006269

D.melanogaster mRNA for rotated abdomen protein.

5.4e-05:357:58

X95956

50 F-NT2RP2006512

Sequence 1 from Patent EP 0285405.

3.7e-102:659:85

I05465

55 F-NT2RP3000011

RPCI11-43E12.TJ RPCI11 Homo sapiens genomic clone R-43E12, genomic survey sequence.

1.8e-10:113:84

AQ195722

EP 1 130 094 A2

F-NT2RP3000022

Human DNA sequence from clone 341E18 on chromosome 6p11.2-12.3. Contains a Serine/Threonine Protein Kinase gene (presumptive isolog of a Rat gene) and a novel alternatively spliced gene. Contains a putative CpG island, ESTs and GSSs, complete sequence.

5 6.7e-116:284:99

AL031178

F-NT2RP3000059

R.norvegicus mRNA for leucocyte common antigen-related protein (3941 bp).

10 0.0031:511:59

X83546

F-NT2RP3000063

Homo sapiens chromosome 19, fosmid 37502, complete sequence.

15 0.20:544:57

AC004755

F-NT2RP3000125

HS_3025_A1_D11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3025 Col=21 Row=G, genomic survey sequence.

20 1.0e-21:161:88

AQ101452

F-NT2RP3000148

25 Human Chromosome 16 BAC clone CIT987SK-A-635H12, complete sequence.

5.2e-40:257:77

AC002310

F-NT2RP3000169

30 Homo sapiens MRS1 mRNA, complete cds.

3.4e-106:501:99

AF093239

F-NT2RP3000171

35 Mus musculus mRNA for B-IND1 protein.

1.8e-97:571:89

Z97207

F-NT2RP3000172

40 Rattus norvegicus vesicula-associate calmodulin-binding protein mRNA, complete cds.

2.0e-123:702:86

L22557

F-NT2RP3000201

45 Homo sapiens mRNA for KIAA0687 protein, partial cds.

9.2e-170:792:98

AB014587

F-NT2RP3000232

50 HS_3238_B2_D04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3238 Col=8 Row=H, genomic survey sequence.

9.2e-24:174:88

AQ219879

55 F-NT2RP3000304

Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds.

3.3e-171:797:98

AF074264

EP 1 130 094 A2

F-NT2RP3000378

Mus musculus (clone pVZmSin3A9) mSin3A9 mRNA, complete cds.

5 5.8e-137:774:89

L38621

5

F-NT2RP3000427

Mouse cAMP-dependent protein kinase beta subunit gene, exon 1.

10 1.5e-18:390:65

M21096

10

F-NT2RP3000436

cDNA encoding a human novel protein disulfide isomerase like enzyme, EP52.

15 4.5e-05:353:59

E13330

15

F-NT2RP3000444

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 117715, WORKING DRAFT SEQUENCE.

20 9.7e-75:203:97

AL022315

20

F-NT2RP3000460

Canis familiaris sec61 homologue mRNA, complete cds.

25 7.1e-131:643:88

M96629

25

F-NT2RP3000481

Homo sapiens RanBP7/importin 7 mRNA, complete cds.

30 1.7e-162:770:98

AF098799

30

F-NT2RP3000616

Homo sapiens KIAA0405 mRNA, complete cds.

35 4.7e-31:579:62

AB007865

35

F-NT2RP3000645

Human chromosome 12p13 sequence, complete sequence.

40 5.9e-07:484:61

U47924

40

F-NT2RP3000652

Human ZNF43 mRNA.

45 4.4e-131:853:84

X59244

45

F-NT2RP3000676

Homo sapiens mRNA for KIAA0446 protein, complete cds.

50 2.7e-86:420:98

AB007915

50

F-NT2RP3000677

Human estrogen receptor-related protein (variant ER from breast cancer) mRNA, complete cds.

55 2.9e-21:125:100

M69296

55

F-NT2RP3000721

HS_2221_A2_C01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2221

Col=2 Row=E, genomic survey sequence.

0.94:254:60
AQ253443

F-NT2RP3000789

5 Mus musculus coding region determinant binding protein mRNA, complete cds.
5.4e-139:827:87
AF061569

F-NT2RP3000818

10 Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 94M16, WORKING DRAFT SEQUENCE.
3.0e-28:218:86
Z97201

F-NT2RP3000820

15 Mus musculus WSB-1 mRNA, complete cds.
1.1e-77:477:87
AF033186

F-NT2RP3000838

20 Homo sapiens mRNA for KIAA0638 protein, partial cds.
2.6e-77:682:79
AB014538

F-NT2RP3000871

25 Homo sapiens retinoblastoma-interacting protein (RBBP8) mRNA, complete cds.
5.8e-07:350:60
AF043431

F-NT2RP3000907

30 Drosophila melanogaster DNA sequence (P1 DS06882 (D310)), complete sequence.
1.7e-13:330:62
AC005115

F-NT2RP3000921

35 cDNA GA3-43 encoding novel polypeptide which appear when differentiate from embryo-tumor cell P19 to nerve cell.
6.8e-68:812:69
E12950

F-NT2RP3001012

40 cDNA encoding novel rat protein TIP120 which is formed of complex with TBP (TATA binding protein).
2.4e-129:692:92
E12829

F-NT2RP3001044

45 Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.
3.7e-60:393:79
AC006030

F-NT2RP3001061

50 F.rubripes GSS sequence, clone 154E17aC12, genomic survey sequence.
1.8e-07:239:62
AL018519

F-NT2RP3001159

55 Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete sequence.
4.4e-24:156:72

AC004770

F-NT2RP3001170

Homo sapiens mRNA for KIAA0784 protein, partial cds.

5 2.3e-181:859:98

AB018327

F-NT2RP3001195

Genomic sequence from Human 9q34, complete sequence.

10 3.8e-53:253:92

AC001644

F-NT2RP3001240

Canis familiaris sec61 homologue mRNA, complete cds.

15 1.4e-133:740:87

M96629

P-NT2RP3001271

Homo sapiens chromosome 19, cosmid F20237, complete sequence.

20 0.082:370:60

AC005775

F-NT2RP3001322

Homo sapiens mRNA for KIAA0566 protein, partial cds.

25 1.9e-38:728:63

AB011138

F-NT2RP3001388

Rattus norvegicus synaptotagmin XI mRNA, complete cds.

30 1.2e-103:701:83

AF000423

F-NT2RP3001542

Human Chromosome 11 Cosmid cSRL34e5, complete sequence.

35 8.6e-17:293:65

U73643

F-NT2RP3001560

Mouse mRNA for thymic epithelial cell surface antigen, complete cds.

40 7.8e-135:742:91

D67067

F-NT2RP3001592

Human Cdk-inhibitor p57KIP2 (KIP2) mRNA, complete cds.

45 7.2e-12:188:71

U22398

F-NT2RP3001650

Homo sapiens PAC clone DJ0722F20 from 7q31.1-q31.3, complete sequence.

50 1.9e-26:374:72

AC005281

F-NT2RP3001685

Homo sapiens 12q13.1 Cosmid C174F5 (Lawrence Livermore LL12NC01 or LL12NC02 human cosmid libraries)
complete sequence.

55 4.6e-73:284:98

AC004550

- 5 F-NT2RP3001738
Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete sequence.
1.8e-21:186:67
AC004770
- 10 F-NT2RP3001754
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 50024, WORKING DRAFT SEQUENCE.
5.0e-21:131:96
AL034380
- 15 F-NT2RP3001858
Homo sapiens mRNA for KIAA0584 protein, partial cds.
5.9e-39:770:63
AB011156
- 20 F-NT2RP3001976
M.domesticus (C57B1/6J) mRNA for zinc finger protein 30.
2.0e-37:536:70
Z30174
- 25 F-NT2RP3002015
Homo sapiens huntingtin gene, partial exon.
0.024:175:65
L49359
- 30 F-NT2RP3002160
Homo sapiens chromosome 9q34, clone 70C11, complete sequence.
1.6e-95:249:91
AC002319
- 35 F-NT2RP3002281
Homo sapiens mRNA for KIAA0765 protein, partial cds.
1.6e-149:713:98
AB018308
- 40 F-NT2RP3002286
Mus musculus EGF repeat transmembrane protein mRNA, complete cds.
2.0e-136:756:92
U57368
- 45 F-NT2RP3002311
Mouse beta-galactosidase (BGAL) gene, complete cds.
1.0e-29:624:63
M57734
- 50 F-NT2RP3002324
Human DNA sequence from cosmid RJ14 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains ESTs and CpG island.
5.7e-122:655:93
Z69890
- 55 F-NT2RP3002342
Human transporter protein (g17) mRNA, complete cds.
9.8e-36:565:65
U49082
- F-NT2RP3002353

EP 1 130 094 A2

- Streptomyces phaeochromogenes plasmid pJV1, complete sequence.
0.15:466:60
U23762
- 5 F-NT2RP3002409
Homo sapiens mRNA for KIAA0719 protein, complete cds.
2.0e-189:897:98
AB018262
- 10 F-NT2RP3002411
Mus musculus putative steroid dehydrogenase (KIK-I) mRNA, complete cds.
7.8e-122:796:84
AF064635
- 15 F-NT2RP3002448
R.norvegicus mRNA for leucocyte common antigen-related protein (3941 bp).
4.0e-11:403:64
X83546
- 20 F-NT2RP3002571
Bos taurus mRNA for lyncein.
8.7e-114:652:90
Y17923
- 25 F-NT2RP3002664
H.sapiens CpG island DNA genomic Mse1 fragment, clone 34a2, reverse read cpg34a2.rt1a.
6.1e-14:211:72
Z60772
- 30 F-NT2RP3002721
Homo sapiens citrate synthase mRNA, complete cds.
7.5e-179:873:96
AF047042
- 35 F-NT2RP3002737
Homo sapiens mRNA for HNSPC, complete cds.
1.4e-42:409:75
D82346
- 40 F-NT2RP3002738
Rattus norvegicus mRNA for Crk-associated substrate, p130, complete cds.
8.9e-122:812:83
D29766
- 45 F-NT2RP3002790
Human Cdk-inhibitor p57KIP2 (KIP2) mRNA, complete cds.
2.2e-15:626:62
U22398
- 50 F-NT2RP3002836
Homo sapiens mRNA for KIAA0463 protein, partial cds.
6.8e-152:717:99
AB007932
- 55 F-NT2RP3002887
R.norvegicus mRNA for leucocyte common antigen-related protein (3941 bp).
2.0e-05:491:59
X83546

EP 1 130 094 A2

F-NT2RP3002900

Cricetulus griseus COP-coated vesicle membrane protein CHOp24 mRNA, partial cds.

7.3e-13:327:66

U26264

5

F-NT2RP3002958

Mus musculus IgK chain (6S) intron with insertion/deletion mutations.

5.6e-22:403:66

L12153

10

F-NT2RP3002983

Homo sapiens genomic DNA, chromosome 21q11.1, segment 18/28, WORKING DRAFT SEQUENCE.

1.2e-118:339:99

AP000047

15

F-NT2RP3003000

Homo sapiens T-type calcium channel alpha-1 subunit mRNA, complete cds.

7.9e-88:555:88

AF051946

20

F-NT2RP3003076

Streptomyces coelicolor cosmid 2A11.

0.15:505:59

AL031184

25

F-NT2RP3003354

Homo sapiens secretory carrier membrane protein (SCAMP2) mRNA, complete cds.

1.2e-34:625:64

AF005038

30

F-NT2RP3003448

CIT-HSP-721P7.TV CIT-HSP Homo sapiens genomic clone 721P7, genomic survey sequence.

1.2e-16:126:89

B50017

35

F-NT2RP3003469

Homo sapiens chromosome 19, cosmid F23990, complete sequence.

2.0e-18:126:94

AC005262

40

F-NT2RP3003473

Homo sapiens chromosome 17, clone hRPK.1003_J_3, complete sequence.

7.1e-68:474:71

AC005181

45

F-NT2RP3003527

Homo sapiens mRNA for protein kinase Dyrk1B.

1.4e-160:769:98

Y17999

50

F-NT2RP3003532

Mus musculus cell surface molecule OX-2 mRNA, complete cds.

1.3e-96:712:80

AF004023

55

F-NT2RP3003535

Drosophila melanogaster (P1 DS02368 (D205)) DNA sequence, complete sequence. 0.027:155:65

AC004313

- 5 F-NT2RP3003559
H.sapiens CpG island DNA genomic Mse1 fragment, clone 171h5, reverse read cpg171h5.rt1a.
3.9e-50:261:97
Z59762
- 10 F-NT2RP3003614
Mus musculus semaphorin VIa mRNA, complete cds.
1.7e-131:811:86
AF030430
- 15 F-NT2RP3003729
Homo sapiens chromosome 10 clone LA10NC01_15_E_11 map 10q26.3, WORKING DRAFT SEQUENCE, 3 un-
ordered pieces.
1.4e-97:259:91
AC006171
- 20 F-NT2RP3003849
- 25 F-NT2RP3003874
M.musculus mRNA for myosin I heavy chain.
2.9e-151:863:89
X69987
- 30 F-NT2RP3003939
T24C19TF TAMU Arabidopsis thaliana genomic clone T24C19, genomic survey sequence.
1.4e-19:293:68
B29025
- 35 F-NT2RP3003963
CIT-HSP-2050C19.TF CIT-HSP Homo sapiens genomic clone 2050C19, genomic survey sequence.
1.3e-16:111:95
B80539
- 40 F-NT2RP3004000
Homo sapiens klotho gene, exon 1.
0.042:430:60
AB009666
- 45 F-NT2RP3004025
Human DNA sequence from Fosmid 49D8 on chromosome 22, complete sequence.
0.062:197:65
Z82186
- 50 F-NT2RP3004067
Human mRNA for KIAA0375 gene, complete cds.
1.7e-33:556:66
AB002373
- 55 F-NT2RP3004075
jd187 Trypanosome Shotgun M13 genomic Trypanosoma brucei brucei genomic clone 5H9, genomic survey se-
quence.
1.5e-12:438:61
B13419
- 60 F-NT2RP3004083
- 65 F-NT2RP3004090
Dog alpha-L-iduronidase (IDUA) gene, exons 7-12.

1.4e-06:469:60
L01060

5 F-NT2RP30041 19
Human mRNA for KIAA0215 gene, complete cds.
1.3e-72:640:75
D86969

10 F-NT2RP3004130

15 F-NT2RP3004133
Pseudomonas aeruginosa phage phi CTX DNA, complete genome.
0.0018:421:60
Y13918

20 F-NT2RP3004202

25 F-NT2RP3004294
Xenopus laevis ER1 mRNA, complete cds.
5.0e-77:335:78
AF015454

30 F-NT2RP3004309
Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete sequence.
9.6e-25:231:65
AC004770

35 F-NT2RP3004321
Homo sapiens chromosome 11 from 11p15.5 region, complete sequence.
3.7e-80:279:95
AF015416

40 F-NT2RP3004345
Human Cdk-inhibitor p57KIP2 (KIP2) mRNA, complete cds.
7.2e-12:188:71
U22398

45 F-NT2RP3004355
HS_3212_A1_C08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone
Plate=3212 Col=15 Row=E, genomic survey sequence.
0.061:266:65
AQ176625

50 F-NT2RP3004374
HS-1053-B2-E09-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 775
Col=18 Row=J, genomic survey sequence.
1.3e-06:181:67
B41504

55 F-NT2RP3004406
CIT-HSP-2340N18.TF CIT-HSP Homo sapiens genomic clone 2340N18, genomic survey sequence.
9.9e-74:359:99
AQ058326

F-NT2RP3004481
Mus musculus bassoon gene, exon 6 to 11.
0.0060:528:59

Y17038

F-NT2RP3004552

Mouse mRNA for seizure-related gene product 6 type 2 precursor, complete cds.

5 7.6e-40:731:64

D64009

F-NT2RP3004557

Human Ki nuclear autoantigen mRNA, complete cds.

10 8.1e-120:626:94

U11292

F-NT2RP3004625

Homo sapiens I-1 receptor candidate protein mRNA, complete cds.

15 9.8e-151:710:98

AF082516

F-NT2RP3004640

Bos taurus tuftelin mRNA, complete cds.

20 8.2e-104:565:87

AF105228

F-NT2RP3004647

Homo sapiens mRNA for KIAA0446 protein, complete cds.

25 2.1e-109:524:98

AB007915

F-NT2RP4000108

Human gene for neurofilament subunit NF-L.

30 7.0e-158:862:93

X05608

F-NT2RP4000634

Sequence 11 from patent US 5753446.

35 2.9e-155:828:92

AR008281

F-NT2RP4000962

Mus musculus clone OST66, genomic survey sequence.

40 6.0e-48:352:81

AF046696

F-NT2RP4001001

Homo sapiens chromosome 5, Bac clone 58g14 (LBNL H76), complete sequence.

45 4.8e-47:360:84

AC005915

F-NT2RP4001009

Homo sapiens CAAX prenyl protease (STE24) mRNA, complete cds.

50 5.9e-175:828:98

AF064867

F-NT2RP4001467

Human placental cDNA coding for 5'nucleotidase (EC 3.1.3.5).

55 3.3e-159:742:98

X55740

F-NT2RP4001877

EP 1 130 094 A2

- 1.7e-27:401:69
AC005637
- 5 F-NT2RP4001879
- F-NT2RP4002187
Mus musculus putative steroid dehydrogenase (KIK-I) mRNA, complete cds.
4.2e-115:777:83
AF064635
- 10 F-NT2RP4002451
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 111B22, WORKING DRAFT SEQUENCE.
6.1e-86:452:96
Z98200
- 15 F-NT2RP4002715
Homo sapiens clone NH0523H20, complete sequence.
3.6e-59:410:77
AC005041
- 20 F-NT2RP4002750
Mus musculus cationic amino acid transporter (CAT3) mRNA, complete cds.
3.4e-105:586:87
U70859
- 25 F-OVARC1000003
B.taurus mRNA for sodium dependent phosphate transporter.
9.0e-125:823:83
X81699
- 30 F-OVARC1000090
RPCI11-25E14.TP RPCI-11 Homo sapiens genomic clone RPCI-11-25E14, genomic survey sequence.
1.9e-06:151:74
B86784
- 35 F-OVARC1000105
S.cerevisiae UBC6 gene.
4.6e-25:525:64
X73234
- 40 F-OVARC1000137
Human SNARE protein Ykt6 (YKT6) mRNA, complete cds.
1.2e-33:184:98
U95735
- 45 F-OVARC1000208
Homo sapiens Chromosome 16 BAC clone ClT987SK-A-761H5, complete sequence.
1.7e-79:362:91
AC002544
- 50 F-OVARC1000255
Porcine protein-tyrosine kinase (syk) mRNA, complete cds.
4.9e-116:424:88
M73237
- 55 F-OVARC1000275
Homo sapiens chromosome 21q22.3, PAC clones 314N7, 225L15, BAC clone 7B7, complete sequence bases 1..
333303.

0.32:314:61
AJ011930

F-OVARC1000298

5 Homo sapiens clone RG031N19, WORKING DRAFT SEQUENCE, 1 unordered pieces.
2.5e-121:306:98
AC005632

F-OVARC1000307

10 Bovine herpesvirus type 1 genes for UL[27,28,29,30,31].
0.017:162:67
X94677

F-OVARC1000313

15 Homo sapiens mRNA for KIAA0573 protein, partial cds.
1.7e-119:585:97
AB011145

F-OVARC1000331

20 Sequence 2 from patent US 5756332.
1.9e-48:290:91
AR009648

F-OVARC1000410

25 Homo sapiens mRNA for angiopoietin-like factor.
4.6e-26:538:62
Y16132

F-OVARC1000439

30 F-OVARC1000467
HS_3008_A2_D12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone
Plate=3008 Col=24 Row=G, genomic survey sequence.
2.0e-11:132:82
AQ116995

F-OVARC1000529

35 HS_3092_B2_C11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3092
Col=22 Row=F, genomic survey sequence.
8.2e-12:115:84
AQ127947

F-OVARC1000553

40 Homo sapiens chromosome 19, cosmid R26894, complete sequence.
6.5e-92:221:96
AC005594

F-OVARC1000775

45 Human chromosome 3p21.1 gene sequence.
6.9e-69:380:95
L13435

F-OVARC1000811

50 Homo sapiens chromosome 16, cosmid clone 432A1 (LANL), complete sequence.
6.7e-77:500:86
AC004235

F-OVARC1000853

EP 1 130 094 A2

HS_3234_A1_F05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3234

Col=9 Row=K, genomic survey sequence.

4.6e-05:111:71

AQ191345

5

F-OVARC1000873

Human DNA sequence from clone 1049G16 on chromosome 20q12-13.2 Contains gene similar to GLUCOSAMINE-6-SULFATASE, a nuclear receptor coactivator gene, ESTs, STSs, GSSs, complete sequence.

8.2e-42:234:96

10

AL034418

F-OVARC1000916

Sequence 3 from patent US 5674748.

2.0e-55:422:84

15

I68139

F-OVARC1000956

Human DNA sequence from cosmid L241B9, Huntington's Disease Region, chromosome 4p16.3 contains polymorphic VNTR pYNZ32.

20

1.2e-107:540:97

Z69708

F-OVARC1000995

H.sapiens genomic DNA (chromosome 3; clone NL1106D).

25

4.3e-28:166:95

X87478

F-OVARC1001030

Human mRNA for KIAA0339 gene, complete cds.

30

2.1e-10:334:64

AB002337

F-OVARC1001049

*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0190L06; HTGS phase 1, WORKING DRAFT SEQUENCE, 21 unordered pieces.

5.4e-12:420:62

AC004670

35

F-OVARC1001086

Homo sapiens cyclin T2a mRNA, complete cds.

1.9e-164:761:99

AF048731

40

F-OVARC1001132

Homo sapiens genomic DNA, chromosome 21q11.1, segment 9/28, WORKING DRAFT SEQUENCE.

1.5e-89:328:75

AP000038

45

F-OVARC1001163

Caenorhabditis elegans cosmid F40E10, complete sequence.

3.8e-26:337:71

Z69792

50

F-OVARC1001222

CIT-HSP-2010I15.TR CIT-HSP Homo sapiens genomic clone 2010I15, genomic survey sequence.

1.2e-08:171:70

B57734

- 5 F-OVARC1001260
- 10 F-OVARC1001336
B.taurus mRNA for sodium dependent phosphate transporter.
5.4e-83:622:80
X81699
- 15 F-OVARC1001338
HS_2181_B2_E11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2181
Col=22 Row=J, genomic survey sequence.
2.3e-17:144:86
AQ022764
- 20 F-OVARC1001569
Mus musculus bone morphogenetic factor 11 (Bmp11) gene, exon 1.
2.9e-06:241:63
AF100904
- 25 F-OVARC1001570
Homo sapiens *** SEQUENCING IN PROGRESS ***, WORKING DRAFT SEQUENCE.
1.6e-10:235:64
AJ011929
- 30 F-OVARC1001596
Homo sapiens chromosome 17, clone hRPK.372_K_20, complete sequence.
2.2e-45:498:73
AC005951
- 35 F-OVARC1001607
Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds.
1.7e-38:323:80
U15128
- 40 F-OVARC1001725
Homo sapiens patched related protein TRC8 (TRC8) gene, exon 1 and partial cds.
3.5e-172:821:98
AF064800
- 45 F-OVARC1001727
Human DNA sequence from clone 48A11 on chromosome 20p12 Contains EST, STS, GSS, complete sequence.
2.2e-132:633:98
AL031132
- 50 F-OVARC1001807
Human TR3 orphan receptor mRNA, complete cds.
7. 1e-90:566:87
L13740
- 55 F-OVARC 1001833
Rattus norvegicus cis-Golgi matrix protein GM130 mRNA, complete cds.
5.2e-46:364:79
U35022
- F-OVARC1001952
Homo sapiens FGFR-4 gene.
1.7e-14:392:62
Y13901

EP 1 130 094 A2

F-OVARC1001991

Human Chromosome 11 Cosmid cSRL34e5, complete sequence.

2.3e-06:298:64

U73643

5

F-OVARC1002058

, complete sequence.

1.3e-108:617:92

AC005500

10

F-OVARC1002178

Herpes simplex virus type 2 (strain HG52), complete genome.

0.43:234:63

Z86099

15

F-PLACE1000033

Mus musculus otogelin mRNA, complete cds.

5.9e-18:579:59

U96411

20

F-PLACE1000231

Rattus norvegicus WAP four-disulfide core domain protein (ps20) mRNA, complete cds.

1.1e-18:273:68

AF037272

25

F-PLACE1000258

Human KRAB zinc finger protein (ZNP177) mRNA, complete cds.

1.2e-13:241:70

U37263

30

F-PLACE1000442

Human zinc finger protein ZNF136.

2.3e-87:774:76

U09367

35

F-PLACE1000560

Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158), complete sequence.

4.1e-107:318:96

AC005368

40

F-PLACE1000740

Rat notch 2 mRNA.

1.1e-37:399:74

M93661

45

F-PLACE1000907

RPCI11-73M20.TJ RPCI11 Homo sapiens genomic clone R-73M20, genomic survey sequence.

3.5e-21:147:92

AQ269030

50

F-PLACE1000912

F-PLACE1000914

Homo sapiens chromosome 17, clone HCIT145P4, WORKING DRAFT SEQUENCE, 8 unordered pieces.

55

1.8e-74:206:93

AC002093

F-PLACE1000927

EP 1 130 094 A2

- Cowpox virus strain GRI-90 DNA (49 kb fragment).
6.8e-75:683:74
Y15035
- 5 F-PLACE1000986
RPCI11-75H23.TK RPCI11 Homo sapiens genomic clone R-75H23, genomic survey sequence.
1.0:316:57
AQ268409
- 10 F-PLACE1001016
Human dihydropyridine-sensitive L-type calcium channel alpha-1 subunit (CACNL1A3) mRNA, complete cds.
0.28:432:59
L33798
- 15 F-PLACE1001100
RPCI11-32N5.TK RPCI-11 Homo sapiens genomic clone RPCI-11-32N5, genomic survey sequence.
0.48:145:64
AQ047336
- 20 F-PLACE1001114
Lysobacter enzymogenes beta-lactamase gene sequence.
0.033:349:60
M97392
- 25 F-PLACE1001123
F.rubripes GSS sequence, clone 084A20aC12, genomic survey sequence.
9.7e-05:138:64
AL015804
- 30 F-PLACE1001183
Homo sapiens BAC clone RG318C11 from 7p14-p15, complete sequence.
0.15:576:59
AC005091
- 35 F-PLACE1001229
F.rubripes GSS sequence, clone 144D13aC10, genomic survey sequence.
2.2e-21:271:70
AL017986
- 40 F-PLACE1001231
Rattus norvegicus sodium-dependent multi-vitamin transporter (SMVT) mRNA, complete cds.
6.4e-102:677:84
AF026554
- 45 F-PLACE1001340
Homo sapiens mRNA for KIAA0719 protein, complete cds.
1.3e-130:636:97
AB018262
- 50 F-PLACE1001401
CIT-HSP-2323H22.TR CIT-HSP Homo sapiens genomic clone 2323H22, genomic survey sequence.
6.4e-13:165:76
AQ028562
- 55 F-PLACE1001407
Human DNA sequence from clone 496H19 on chromosome 6q24 Contains ESTs, complete sequence.
2.4e-28:228:85
AL023582

EP 1 130 094 A2

- 5 F-PLACE1001464
Human placental cDNA coding for 5 nucleotidase (EC 3.1.3.5).
5.0e-151:742:96
X55740
- 10 F-PLACE1001500
CIT-HSP-2368L16.TR CIT-HSP Homo sapiens genomic clone 2368L16, genomic survey sequence.
1.1e-25:150:97
AQ078655
- 15 F-PLACE1001516
Homo sapiens Chromosome 16 BAC clone CIT987SK-A-575C2, complete sequence.
1.2e-139:676:98
AC002425
- 20 F-PLACE1001536
Human Chromosome X clone bWXD173, WORKING DRAFT SEQUENCE, 2 ordered pieces.
1.7e-142:513:97
AC004387
- 25 F-PLACE1001564
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 287G14, WORKING DRAFT SE-
QUENCE.
2.9e-104:373:89
AL033377
- 30 F-PLACE1001655
Homo sapiens Shab-related delayed-rectifier K+ channel alpha subunit (KCNS3) mRNA, complete cds.
1.3e-123:585:98
AF043472
- 35 F-PLACE1001788
Homo sapiens mRNA for HYA22, complete cds.
9.9e-21:234:75
D88153
- 40 F-PLACE1001795
Drosophila melanogaster; Chromosome 3L; Region 83F1-83F2; P1 clone DS07437, WORKING DRAFT SE-
QUENCE, 3 unordered pieces.
1.4e-05:218:64
AC005985
- 45 F-PLACE1001836
Homo sapiens BAC clone GS155M11 from 7q21-q22, complete sequence.
4.9e-79:577:82
AC004022
- 50 F-PLACE1001918
Arabidopsis thaliana BAC T19D16 genomic sequence.
3.7e-24:417:63
U95973
- 55 F-PLACE1001949
S.cerevisiae chromosome XV reading frame ORF YOR291w.
3.6e-16:255:70
Z75199
- F-PLACE1002080

EP 1 130 094 A2

Homo sapiens antigen NY-CO-9 (NY-CO-9) mRNA, partial cds.
7.5e-129:622:98
AF039691

- 5 F-PLACE1002095
Homo sapiens chromosome 5, P1 clone 1130f1 (LBNL H40), complete sequence.
2.3e-48:551:71
AC004219
- 10 F-PLACE1002153
Homo sapiens TACC2 protein (TACC2) mRNA, partial cds.
8.3e-161:764:98
AF095791
- 15 F-PLACE1002329
Sequence 12 from Patent WO 9000403.
6.9e-05:380:63
I09634
- 20 F-PLACE1002355
Homo sapiens protease-activated receptor 4 mRNA, complete cds.
2.8e-17:190:77
AF055917
- 25 F-PLACE1002374
Human mRNA for pro-cathepsin L(major excreted protein MEP).
6.2e-162:716:94
X12451
- 30 F-PLACE 1002518
HS_3091_A1_F08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3091
Col=15 Row=K, genomic survey sequence.
3.2e-74:316:94
AQ123005
- 35 F-PLACE1002547
Homo sapiens mRNA for KIAA0719 protein, complete cds.
2.6e-171:819:98
AB018262
- 40 F-PLACE1002726
CIT-HSP-2369G10.TR CIT-HSP Homo sapiens genomic clone 2369G10, genomic survey sequence.
4.8e-18:135:88
AQ075115
- 45 F-PLACE1002905
Drosophila melanogaster DNA sequence (P1 DS00906 (D99)), complete sequence.
3.7e-06:235:66
AC004154
- 50 F-PLACE1002911
Bovine herpesvirus 1 complete genome.
0.93:264:63
AJ004801
- 55 F-PLACE1002967
Homo sapiens IgE receptor beta chain (HTm4) mRNA, complete cds.
0.0041:302:60

L35848

F-PLACE1003135

Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds.

5 4.7e-49:450:75

AF024636

F-PLACE1003163

Homo sapiens DBI-related protein mRNA, complete cds.

10 4.7e-152:722:98

AF069301

F-PLACE1003407

Homo sapiens putative transmembrane protein (CLN5) mRNA, complete cds.

15 6.3e-141:682:97

AF068227

F-PLACE1003428

Human DNA sequence from clone 55C23 on chromosome 6q22.3-23.3 contains vanin-like genes VNN1 and VNN2, ESTs, GSSs,, complete sequence.

20 1.2e-116:286:100

AL032821

F-PLACE1003438

Pseudomonas alcaligenes outer membrane Xcp-secretion system gene cluster.

25 0.13:468:60

AF092918

F-PLACE1003460

HS_3234_A1_F05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3234 Col=9 Row=K, genomic survey sequence.

30 5.8e-05:111:71

AQ191345

F-PLACE1003529

Homo sapiens clone DJ0981O07, complete sequence.

35 5.8e-134:457:97

AC006017

F-PLACE1003573

Sequence 2 from patent US 5792648.

40 0.93:186:62

AR022348

F-PLACE1003598

Mus musculus mismatch repair protein (MSH6) gene, exon 1.

45 3.3e-07:311:63

AF031085

F-PLACE1003644

Homo sapiens Chromosome 11q23 PAC clone pDJ149k2 containing PLZF gene encoding kruppel-like zinc finger protein, complete sequence.

50 1.8e-06:138:74

AC001234

F-PLACE1003737

Homo sapiens Xp22-83 BAC GSHB-324M7 (Genome Systems Human BAC Library) complete sequence.

55 1.4e-165:791:98

- AC005859
- 5 F-PLACE1003772
Human p300/CBP-associated factor (P/CAF) mRNA, complete cds.
2.2e-07:448:61
U57317
- 10 F-PLACE1003839
Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12, complete sequence.
2.0e-106:525:97
AC004131
- 15 F-PLACE1003845
Caenorhabditis elegans cosmid D2096.
9.8e-26:386:69
U40800
- 20 F-PLACE1003852
Homo sapiens mRNA for KIAA0758 protein, partial cds.
7.4e-171:814:98
AB018301
- F-PLACE1004028
- 25 F-PLACE1004078
Homo sapiens PAC clone DJ0722F20 from 7q31.1-q31.3, complete sequence.
2.0e-116:274:98
AC005281
- 30 F-PLACE1004166
HS_3223_A1_H09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3223
Col=17 Row=O, genomic survey sequence.
0.77:304:58
AQ193346
- 35 F-PLACE1004168
- 40 F-PLACE1004199
CIT-HSP-2328F14.TR CIT-HSP Homo sapiens genomic clone 2328F14, genomic survey sequence.
9.4e-16:186:76
AQ042262
- 45 F-PLACE1004279
Homo sapiens putative renal organic anion transporter 1 (hROAT1) mRNA, complete cds.
1.2e-18:456:62
AF057039
- F-PLACE1004282
- 50 F-PLACE1004305
Homo sapiens mRNA for KIAA0740 protein, complete cds.
2.7e-121:612:96
AB018283
- 55 F-PLACE1004441
Human G protein-coupled receptor (GPR1) gene, complete cds.
2.4e-104:537:95
U13666

- 5 F-PLACE1004450
Pleuronectes americanus aminopeptidase N (ampN) mRNA, complete cds.
3.1e-20:601:60
AF012465
- 10 F-PLACE1004482
HS_3032_B1_C03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3032 Col=5 Row=F, genomic survey sequence.
1.1e-86:423:98
AQ129106
- 15 F-PLACE1004492
Human DNA sequence from PAC 434P1 on chromosome 22. Contains inward rectifier potassium channel 4, (potassium channel, inwardly rectifying, subfamily J, member 4) (hippocampal inward rectifier) (HIR) (HRK1) (HIRK2) (KIR2.3), ESTs similar to lumen protein retaining receptor 2 (KDEL receptor 2), DEAD-box protein P72, ESTs, CpG islands.
0.17:180:67
Z97056
- 20 F-PLACE1004519
Human DNA sequence from clone 24o18 on chromosome 6p21.31-22.2 Contains zinc finger protein pseudogene, VNO-type olfactory receptor pseudogene, nuclear envelope pore membrane protein, EST, STS, GSS, complete sequence.
1.1e-75:432:84
AL021808
- 25 F-PLACE1004520
Human pregnancy-specific beta-1-glycoprotein mRNA PSG95, complete cds.
4.1e-109:606:92
M34715
- 30 F-PLACE1004630
Homo sapiens mRNA for osteoblast specific cysteine-rich protein, complete cds.
6.2e-138:749:92
AB008375
- 35 F-PLACE1004637
HS-1061-B1-E10-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 783 Col=19 Row=J, genomic survey sequence.
0.013:92:75
B45487
- 40 F-PLACE1004648
- 45 F-PLACE1004816
Homo sapiens mRNA for Hakata antigen, complete cds.
3.8e-98:590:90
D88587
- 50 F-PLACE1004887
Dog alpha-L-iduronidase (IDUA) gene, exons 7-12.
1.2e-06:469:60
L01060
- 55 F-PLACE1005003
Human SNC19 mRNA sequence.
4.8e-20:472:63
U20428

EP 1 130 094 A2

- 5 F-PLACE1005005
Homo sapiens chromosome 21q22.3, PAC clones 314N7, 225L15, BAC clone 7B7, complete sequence bases 1..
333303.
7.8e-143:650:97
AJ011930
- 10 F-PLACE1005031
Bovine chlorine channel protein (p64) mRNA, complete cds.
7.1e-62:463:83
L16547
- 15 F-PLACE1005239
Homo sapiens mRNA for HIRIP3 protein, clone pH4-31.
2.2e-14:115:85
AJ223349
- 20 F-PLACE1005250
Mus musculus maternal transcript Maid (Maid) mRNA, complete cds.
3.3e-40:370:77
U50734
- 25 F-PLACE1005383
Homo sapiens UP50 mRNA, complete cds.
2.7e-126:633:96
AF093118
- 30 F-PLACE1005410
Rattus rattus sec61 homologue mRNA, complete cds.
1.9e-115:771:85
M96630
- 35 F-PLACE1005426
Homo sapiens chromosome 19, CIT-HSP BAC 490g23 (BC338531), complete sequence.
7.2e-113:391:96
AC005392
- 40 F-PLACE1005519
Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds.
1.0e-53:521:74
AF024636
- 45 F-PLACE1005539
c-erbB=proto-oncogene {exon 1, promoter} [chickens, Genomic, 700 nt].
3.6e-05:434:62
S66408
- 50 F-PLACE1005544
Mus musculus junctional adhesion molecule (Jam) mRNA, complete cds.
3.3e-56:575:74
U89915
- 55 F-PLACE1005569
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 159A1, WORKING DRAFT SEQUENCE.
1.1e-118:381:96
AL034397
- F-PLACE1005601
Human PAC clone DJ515N1 from 22q11.2-q22, complete sequence.

- 3.9e-143:697:98
AC002073
- 5 F-PLACE1005660
- F-PLACE1005669
Fruit fly (*D.melanogaster*) Glued mRNA, complete cds.
3.4e-14:275:66
J02932
- 10 F-PLACE1005682
Mus musculus Ankhzn mRNA, complete cds.
0.75:347:57
AB011370
- 15 F-PLACE1005725
Homo sapiens huntingtin (HD) gene, exon 1.
1.4e-06:425:62
L27350
- 20 F-PLACE1005736
- F-PLACE1005745
HS_3039_B1_F12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3039
25 Col=23 Row=L, genomic survey sequence.
1.0:283:59
AQ155068
- 30 F-PLACE1005768
Human DNA sequence from Fosmid 24E5 on chromosome 22q11.2-qter contains parvalbumin, ESTs, STS.
1.5e-141:719:96
Z82185
- 35 F-PLACE1005815
Sequence 1 from patent US 5571905.
0.088:199:62
I28535
- 40 F-PLACE1005878
Bovine chlorine channel protein (p64) mRNA, complete cds.
2.5e-54:394:84
L16547
- 45 F-PLACE1005927
HS_3138_B2_B03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3138
Col=6 Row=D, genomic survey sequence.
8.0e-32:162:95
AQ183333
- 50 F-PLACE1006071
1.6e-180:877:96
AF028816
- 55 F-PLACE1006073
Homo sapiens mRNA for glucuronyltransferase I, complete cds.
1.7e-94:464:98
AB009598

5 F-PLACE1006079
 Homo sapiens distal-less homeobox protein (DLX3) gene, complete cds.
 5.2e-107:423:96
 AF028233

10 F-PLACE1006093
 jd187 Trypanosome Shotgun M13 genomic Trypanosoma brucei brucei genomic clone 5H9, genomic survey sequence.
 0.00018:316:60
 B13419

15 F-PLACE1006208
 Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.
 1.4e-12:421:64
 L14320

20 F-PLACE1006219
 Caenorhabditis elegans cosmid D2096.
 6.4e-25:386:69
 U40800

25 F-PLACE1006277
 Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 159A1, WORKING DRAFT SEQUENCE.
 7.2e-135:381:97
 AL034397

30 F-PLACE1006290
 Caenorhabditis elegans cosmid F09E5.
 1.4e-08:354:61
 U37429

35 F-PLACE1006443
 Homo sapiens chromosome 17, clone HCIT145P4, WORKING DRAFT SEQUENCE, 8 unordered pieces.
 2.9e-80:168:95
 AC002093

40 F-PLACE1006515
 Homo sapiens mRNA for KIAA0576 protein, partial cds.
 4.2e-140:655:99
 AB011148

45 F-PLACE1006716
 Human DNA sequence from PAC 151B14 on chromosome 22q12-qter contains somatostatin receptor subtype 3 (SSTR3), tRNA, ESTs, CpG island and STS.
 2.2e-51:621:70
 Z86000

50 F-PLACE1006786
 CITBI-E1-2502A9.TR CITBI-E1 Homo sapiens genomic clone 2502A9, genomic survey sequence.
 0.43:237:64
 AQ264473

55 F-PLACE1006809
 HS_2255_B1_F05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2255
 Col=9 Row=L, genomic survey sequence.
 2.1e-14:95:97
 AQ131814

EP 1 130 094 A2

5 F-PLACE1006959
HS_3247_B1_E03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3247
Col=5 Row=J, genomic survey sequence.
1.1e-09:199:70
AQ220414

10 F-PLACE1007028
Homo sapiens Chromsome 11p15.5 PAC clone pDJ754h15 containing cdk-inhibitor p57/KIP2 (CDKN1C) gene,
complete sequence.
2.0e-24:658:62
AC005950

15 F-PLACE1007040
Mus musculus neuronal intermediate filament protein (alpha-internexin) gene, complete cds.
8.8e-09:585:62
L27220

20 F-PLACE1007077

25 F-PLACE1007081
RPCI11-31D7.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-31D7, genomic survey sequence.
2.3e-42:228:97
AQ016433

30 F-PLACE1007096

35 F-PLACE1007296
Human mRNA for a presumptive KDEL receptor.
1.3e-71:542:83
X55885

40 F-PLACE1007591
Homo sapiens full length insert cDNA clone YP44A02.
1.1e-18:141:90
AF085890

45 F-PLACE1007626
Homo sapiens unknown mRNA, complete cds.
7.8e-104:516:97
AF047439

50 F-PLACE1007702
Homo sapiens chromosome 17, clone 363G12, WORKING DRAFT SEQUENCE, 11 unordered pieces.
7.5e-50:439:77
AC002348

55 F-PLACE1007845
Caenorhabditis elegans cosmid F09E5.
4.4e-08:355:62
U37429

60 F-PLACE1007881
CITBI-E1-2517N6.TF CITBI-E1 Homo sapiens genomic clone 2517N6, genomic survey sequence.
1.4e-14:104:95
AQ279407

65 F-PLACE1007971
HS_3237_B2_F09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3237

EP 1 130 094 A2

Col=18 Row=L, genomic survey sequence.

1.2e-12:169:76

AQ206052

5 F-PLACE1008282

Homo sapiens clone DJ0042M02, WORKING DRAFT SEQUENCE, 20 unordered pieces.

4.5e-101:192:100

AC005995

10 F-PLACE1008297

Mycoplasma genitalium random genomic clone hg1, partial cds.

0.099:193:60

U02109

15 F-PLACE1008359

Homo sapiens DNA for (CGG)n trinucleotide repeat region, isolate CL16-1 (Chr.16).

0.53:185:65

AJ001218

20 F-PLACE1008469

Homo sapiens chromosome 17, clone HCIT145P4, WORKING DRAFT SEQUENCE, 8 unordered pieces.

1.2e-93:213:98

AC002093

25 F-PLACE1008549

Homo sapiens E74-like factor 5 (ELF5) mRNA, complete cds.

5.7e-144:693:98

AF049703

30 F-PLACE1008657

Bovine mRNA for adseverin, complete cds.

5.6e-140:782:90

D26549

35 F-PLACE1008716

Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds.

1.1e-133:648:97

U15128

40 F-PLACE1008744

Sequence 1 from patent US 5691147.

8.4e-91:475:95

I76197

45 F-PLACE1008984

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 167A19, WORKING DRAFT SEQUENCE.

4.2e-103:493:99

AL031427

50

F-PLACE1008985

Mus musculus synaptotagmin VIII mRNA, partial cds.

1.1e-23:289:72

U20107

55

F-PLACE1009067

H.sapiens CpG island DNA genomic Mse1 fragment, clone 52e12, forward read cpg52e12.ft1a.

1.2e-28:164:96

Z61442

F-PLACE1009196

5 F-PLACE1009279

H.sapiens mRNA for serine protease.

6.0e-10:327:64

Y07921

10 F-PLACE1009527

Human DNA-binding protein ABP/ZF mRNA, complete cds.

2.0e-19:125:96

U82613

15 F-PLACE1009546

S.lividans mercury resistance operon.

0.56:358:59

X65467

20 F-PLACE1009600

Mouse mRNA for tetracycline transporter-like protein, complete cds.

2.1e-128:718:91

D88315

25 F-PLACE1009735

Homo sapiens clone NH0523H20, complete sequence.

2.9e-128:613:99

AC005041

30 F-PLACE1009982

F-PLACE1010011

, complete sequence.

2.1e-26:234:83

35 AC005409

F-PLACE1010078

Saccharomyces cerevisiae chromosome XII cosmid 8300.

0.066:273:58

40 U19028

F-PLACE1010081

Homo sapiens serine/threonine kinase RICK (RICK) mRNA, complete cds.

7.0e-150:733:97

45 AF027706

F-PLACE1010251

Sequence 1 from patent US 5665588.

0.0012:309:62

50 I64695

F-PLACE1010445

Herpes simplex virus type 2 (strain HG52), complete genome.

9.4e-07:511:58

55 Z86099

F-PLACE1010713

Mus musculus putative steroid dehydrogenase (KIK-I) mRNA, complete cds.

- 2.1e-89:612:83
AF064635
- 5 F-PLACE1010784
Sequence 1 from patent US 5686597.
2.5e-103:505:98
I73723
- 10 F-PLACE1010827
Cricetulus griseus COP-coated vesicle membrane protein CHOp24 mRNA, partial cds.
7.3e-13:327:66
U26264
- 15 F-PLACE1010968
O.cuniculus mRNA for titin.
0.44:165:64
X64696
- 20 F-PLACE1011045
Homo sapiens E1-like protein mRNA, complete cds.
1.8e-127:595:99
AF094516
- 25 F-PLACE1011116
HS_2033_A2_E05_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2033
Col=10 Row=1, genomic survey sequence.
8.3e-29:192:92
AQ229784
- 30 F-PLACE1011181
H.sapiens CpG island DNA genomic Mse1 fragment, clone 99f2, reverse read cpg99f2.rt1a.
4.8e-35:200:95
Z64239
- 35 F-PLACE1011236
Mus musculus mRNA for RST, complete cds.
4.5e-54:717:66
AB005451
- 40 F-PLACE1011364
Homo sapiens protein kinase/endoribonuclease (IRE1) mRNA, complete cds.
0.13:502:57
AF059198
- 45 F-PLACE1011407
M.domesticus (C57B1/6J) mRNA for zinc finger protein 30.
7.2e-15:313:68
Z30174
- 50 F-PLACE1011516
Drosophila melanogaster; Chromosome 3L; Region 79F1-80A2; BAC clone BACR48E05, WORKING DRAFT SE-
QUENCE, 4 unordered pieces.
1.8e-16:317:66
AC005720
- 55 F-PLACE1011708
Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds.
1.8e-143:722:96

AF034611

F-PLACE1011824

Human Ste20-like kinase (MST2) mRNA, complete cds.

5 5.0e-100:561:92

U26424

F-PLACE 10I 1978

10 Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.

9.6e-76:722:74

M27877

F-PLACE2000118

15 Homo sapiens DNA sequence from PAC 393P12 on chromosome Xp11.21. Contains a hypothetical protein KIAA0413 (KIAA0412, KIAA0065, KIAA0569) LIKE Zinc Finger protein pseudogene, a hypothetical Proline-rich protein KIAA0269 LIKE gene and a 60S Ribosomal Protein L7 LIKE pseudogene. Contains ESTs, an STS and a GSS (BAC end sequence), complete sequence.

5.2e-112:568:95

AL022578

20 F-PLACE2000219

Homo sapiens Down Syndrome critical region, partial sequence.

0.0059:144:71

AF015262

25 F-PLACE3000181

Sequence 102 from patent US 5643781.

4.1e-127:745:90

IS1041

30 F-PLACE3000213

F-PLACE4000354

35 HS_3071_A2_B06_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071 Col=12 Row=C, genomic survey sequence.

4.4e-12:335:64

AQ137396

40 F-PLACE4000455

Homo sapiens transcriptional enhancer factor (TEF1) DNA, complete CDS.

9.5e-118:563:98

M63896

45 F-SKNMC1000004

Homo sapiens clone RG031N19, WORKING DRAFT SEQUENCE, 1 unordered pieces.

2.9e-141:292:98

AC005632

50 F-SKNMC1000014

CIT-HSP-2359K11.TR CIT-HSP Homo sapiens genomic clone 2359K11, genomic survey sequence.

0.89:136:67

AQ075724

55 F-SKNMC1000082

H.sapiens CpG island DNA genomic Msel fragment, clone 26g3, reverse read cpg26g3.rt1b.

5.6e-06:60:98

265216

- 5 F-THYRO1000036
F-THYRO1000061
Homo sapiens chromosome 19, cosmid R28991, complete sequence.
2.4e-105:425:94
AC004623
- 10 F-THYRO1000099
Rattus norvegicus leukocyte common antigen receptor (LAR) gene, trans-spliced alternative untranslated exon.
0.35:609:57
U87960
- 15 F-THYRO1000196
Homo sapiens Ksp-cadherin (CDH16) mRNA, complete cds.
5.1e-125:475:98
AF016272
- 20 F-THYRO1000400
Mycobacterium tuberculosis sequence from clone y423.
1.0:264:59
AD000014
- 25 F-THYRO1000580
HS_3216_A1_H09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3216
Col=17 Row=O, genomic survey sequence.
2.8e-25:157:96
AQ184086
- 30 F-THYRO1000584
Boar mRNA for 135kDa protein, complete cds.
2.0e-104:787:80
D28521
- 35 F-THYRO1000678
M.musculus Cx30 gene.
6.9e-41:285:85
Z70023
- 40 F-THYRO1000776
Drosophila melanogaster DNA sequence (P1 DS08948 (D168)), complete sequence.
2.7e-10:389:59
AC004288
- 45 F-THYRO1000795
Rattus norvegicus mRNA for mitochondrial dicarboxylate carrier.
1.2e-107:736:83
AJ223355
- 50 F-THYRO1000846
CITBI-E1-2505H6.TR CITBI-E1 Homo sapiens genomic clone 2505H6, genomic survey sequence.
0.00025:351:61
AQ260270
- 55 F-THYRO1000866
Homo sapiens SKB1Hs mRNA, complete cds.
3.3e-91:529:89
AF015913

EP 1 130 094 A2

F-THYRO1000956

Human G protein-coupled receptor APJ gene, complete cds.

3.8e-148:724:97

U03642

5

F-THYRO1000964

Drosophila melanogaster Pelle associated protein Pellino (Pli) mRNA, complete cds.

5.0e-37:714:64

AF091624

10

F-THYRO1000999

CITBI-E1-2508B3.TF CITBI-E1 Homo sapiens genomic clone 2508B3, genomic survey sequence.

1.2e-06:280:62

AQ261426

15

F-THYRO1001063

H.sapiens (xs174) mRNA, 300bp.

1.6e-41:298:85

Z36825

20

F-THYRO1001071

Human mRNA for KIAA0154 gene, partial cds.

7.4e-16:197:73

D63876

25

F-THYRO1001102

Homo sapiens PAC clone DJ130H16 from 22q12.1-qter, complete sequence.

3.5e-10:128:83

AC004997

30

F-THYRO1001113

Homo sapiens mRNA for LGMD2B protein.

8.8e-52:684:68

AJ007670

35

F-THYRO1001128

Homo sapiens chromosome 9q34, clone 63G10, complete sequence.

1.2e-141:227:97

AC002096

40

F-THYRO1001205

F-THYRO1001237

Mus musculus interleukin-2 (IL-2) gene, 5'end.

45

0.77:78:74

L07576

50

F-THYRO1001242

Mouse mRNA for thymic epithelial cell surface antigen, complete cds.

5.1e-127:721:90

D67067

55

F-THYRO1001266

Human sodium iodide symporter mRNA, complete cds.

2.7e-41:806:62

U66088

F-THYRO1001327

EP 1 130 094 A2

Human DNA sequence from clone 453C12 on chromosome 20q12-13.12 Contains SDC4 (syndecan 4 (amphiglycan, ryudocan)) predicts a gene like the mouse transcription factor RBP-L, MATN4 (matrilin-4) STS, GSS, CpG island, complete sequence.

3.1e-117:374:96

5 AL021578

F-THYRO1001456

F-THYRO1001457

10 M.musculus (Balb/c) mRNA for serine/threonine protein kinase.

1.8e-57:491:69

Z34524

F-THYRO1001471

15 Sequence 52 from Patent WO9712992.

0.00019:546:58

A62364

F-THYRO1001478

20

F-THYRO1001495

Homo sapiens clone DJ1163L11, complete sequence.

4.4e-20:222:76

AC005230

25

F-THYRO1001523

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 407F17, WORKING DRAFT SEQUENCE.

8.8e-21:538:62

30 Z83845

F-THYRO1001529

M.musculus mRNA for serine palmitoyltransferase subunit B.

5.8e-32:448:66

35 X95642

F-THYRO1001593

Homo sapiens chromosome 19, cosmid R31237, complete sequence.

5.8e-91:213:98

40 AC005581

F-THYRO1001608

Homo sapiens T-cell receptor alpha delta locus from bases 1000498 to 1071650 (section 5 of 5) of the Complete Nucleotide Sequence.

45 0.0028:335:65

AE000662

F-THYRO1001641

Leishmania major chromosome 3 clone L6290 strain Friedlin, WORKING DRAFT SEQUENCE, 2 ordered pieces.

50 0.92:378:61

AC005928

F-THYRO1001700

HS_3220_A1_B08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3220 Col=15 Row=C, genomic survey sequence.

55 1.0e-49:265:96

AQ184388

EP 1 130 094 A2

5 F-THYRO1001702
Mus musculus mRNA for myeloid associated differentiation protein.
1.4e-70:502:82
AJ001616

10 F-THYRO1001725
F.rubripes GSS sequence, clone 133B16aE1, genomic survey sequence.
3.8e-06:249:65
AL004967

15 F-THYRO1001770
S.cerevisiae chromosome II reading frame ORF YBR059c.
1.5e-07:320:62
Z35928

20 F-THYRO1001803
Homo sapiens chromosome 10 clone CRI-JC2019 map 10q22.1-10q22.2, WORKING DRAFT SEQUENCE, 1 ordered pieces.
1.2e-38:234:94
AC006108

25 F-Y79AA1000030
Homo sapiens chromosome 5, BAC clone 319C17 (LBNL H159), complete sequence.
9.9e-92:389:98
AC005214

30 F-Y79AA1000127
Homo sapiens genomic DNA, chromosome 21q11.1, segment 5/28, WORKING DRAFT SEQUENCE.
9.2e-131:359:100
AP000034

35 F-Y79AA1000207
Homo sapiens chromosome 17, clone hRPK.271_K_11, complete sequence.
2.2e-151:302:98
AC005562

40 F-Y79AA1000226
Drosophila melanogaster, chromosome 2L, region 21C5-21D1, P1 clone DS07610, complete sequence.
1.1e-50:549:67
AC004573

45 F-Y79AA1000270
Bos taurus vacuolar H⁺ ATPase subunit Ac45 mRNA, complete cds.
6.4e-111:771:83
U10039

50 F-Y79AA1000426
Mus musculus activin beta E subunit mRNA, complete cds.
2.4e-87:703:76
U96386

55 F-Y79AA1000521
Homo sapiens LERK-6 (EPLG6) gene, exon 1.
0.0092:148:68
U92893

F-Y79AA1000750
Homo sapiens Chromosome 16 BAC clone CIT987SK-A-761H5, complete sequence.

9.0e-07:143:74
AC002544

F-Y79AA1000776

5 F-Y79AA1000777

Podospora anserina beta transducin-like protein (het-e1) gene, complete cds.

6.6e-17:760:59

L28125

10 F-Y79AA1000876

Homo sapiens long form transcription factor C-MAF (c-maf) mRNA, complete cds.

3.3e-10:323:66

AF055377

15 F-Y79AA1000888

Streptomyces coelicolor cosmid 8A6.

3.1e-06:665:59

AL031013

20 F-Y79AA1000959

Homo sapiens Hsp70 binding protein HspBP1 mRNA, complete cds.

1.6e-52:277:96

AF093420

25 F-Y79AA1000967

Rattus norvegicus vesicula-associate calmodulin-binding protein mRNA, complete cds.

2.9e-131:752:86

L22557

30 F-Y79AA1001013

F-Y79AA1001056

Mus musculus maternal transcript Maid (Maid) mRNA, complete cds.

35 1.2e-85:676:79

U50734

F-Y79AA1001062

Human Chromosome 11 Cosmid cSRL34e5, complete sequence.

40 8.6e-17:293:65

U73643

F-Y79AA1001090

Homo sapiens chromosome 17, clone hCIT.175_E_5, complete sequence.

45 1.9e-05:223:63

AC004596

F-Y79AA1001212

Homo sapiens SL15 protein mRNA, complete cds.

50 4.7e-162:763:98

AF038961

F-Y79AA1001264

Drosophila melanogaster DNA sequence (P1s DS00764 (D273) and DS00501 (D274)), complete sequence.

55 1.2e-32:599:63

AC005269

F-Y79AA1001272

EP 1 130 094 A2

Homo sapiens * SEQUENCING IN PROGRESS *** from cosmid 5L5, WORKING DRAFT SEQUENCE.**
1.2e-11:356:67
AJ009613

- 5 F-Y79AA1001328
Rattus norvegicus Delta 3 mRNA, complete cds.
2.1e-51:443:76
AF084576
- 10 F-Y79AA1001426
HS_3146_A1_A10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3146
Col=19 Row=A, genomic survey sequence.
9.0e-23:106:91
AQ141090
- 15 F-Y79AA1001427
Bovine cytochrome b5 reductase mRNA, partial cds.
1.4e-55:670:70
M83104
- 20 F-Y79AA1001430
Homo sapiens mRNA for KIAA0469 protein, complete cds.
8.6e-123:577:99
AB007938
- 25 F-Y79AA1001523
Homo sapiens transcription intermediary factor 1 (TIF1) mRNA, complete cds.
3.3e-91:496:93
AF009353
- 30 F-Y79AA1001530
Human DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubiuinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, Cl-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene similar to hypothetical proteins *S. pombe* C22F3.14C and *C. elegans* C16A3.8. Contains ESTs, an STS and GSSs, complete sequence.
1.8e-126:764:89
AL030996
- 35 F-Y79AA1001592
HS_3219_A2_E12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3219
Col=24 Row=1, genomic survey sequence.
5.2e-36:234:89
AQ180547
- 40 F-Y79AA1001727
- 45 F-Y79AA1001787
S.pombe chromosome III cosmid c1672.
8.8e-11:409:58
AL031324
- 50 F-Y79AA1001793
Fugu rubripes GSS sequence, clone 027L23aG3, genomic survey sequence.
0.12:131:70
AL025355
- 55 F-Y79AA1001795
Human DNA sequence from clone 1033B10 on chromosome 6p21.2-21.31. Contains the BINGS gene, exons 11

EP 1 130 094 A2

- to 15 of the BING4 gene, the gene for GalT3 (beta3-Galactosyltransferase), the RPS18 (40S ribosomal protein S18) gene, the SACM2L (suppressor of actin mutation 2, yeast, homolog) gene, a pseudogene similar to TAT-SF1, a Pseudogene similar to zinc finger genes, the RING1 gene, the gene for HKE6 (RING2), the gene for HKE4 (RINGS), the RXRB (Retinoid X receptor beta) gene, the COL11A2 (collagen, type XI, alpha 2) gene, the HLA-DPB2 pseudogene and part of the HLA-DPA3 pseudogene. Contains predicted CpG islands, ESTs, STSs, and GSSs, complete sequence.
5
1.2e-140:672:98
AL031228
- 10 F-Y79AA1001799
S.pombe chromosome I cosmid c8C9.
0.00031:300:60
Z99168
- 15 F-Y79AA1001803
Mus musculus secretogranin III (SgIII) mRNA, complete cds.
4.6e-101:516:82
U02982
- 20 F-Y79AA1001863
Homo sapiens DNA, anonymous heat-stable fragment RP5-6A.
5.2e-85:410:99
AB012170
- 25 F-Y79AA1002022
CIT-HSP-2053H1.TF CIT-HSP Homo sapiens genomic clone 2053H1, genomic survey sequence.
4.3e-20:130:95
B68526
- 30 F-Y79AA1002058
Homo sapiens clone 24733 mRNA sequence.
5.3e-153:740:98
AF052149
- 35 F-Y79AA1002121

F-Y79AA1002129
Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.
5.5e-12:565:61
40 L14320
- F-Y79AA1002213
Rattus norvegicus brain specific Na⁺-dependent inorganic phosphate cotransporter mRNA, complete cds.
4.0e-12:434:60
45 U07609
- F-Y79AA1002334
F.rubripes GSS sequence, clone 174E24aB10, genomic survey sequence.
3.0e-10:171:72
50 AL019366
- F-Y79AA1002373
Rattus norvegicus Smad8 mRNA, complete cds.
0.96:420:61
55 AF012347
- F-Y79AA1002376
Rattus norvegicus cytoplasmic dynein intermediate chain 2B mRNA, complete cds.

1.1e-132:805:88
U39045

5 F-Y79AA1002378
Mus musculus mRNA for zinc finger protein, complete cds, clone:CTfin51.
1.9e-64:521:78
D10630

10 F-Y79AA1002381
O.sativa mRNA for cdc2+/CDC28-related protein kinase.
3.3e-21:431:60
X58194

Homology search result 7

15 [0298] The result of the homology search in the GenBank(<http://www.ncbi.nlm.nih.gov/web/GenBank/>) using the clone sequences of the 3'-ends. except EST and STS sequences.

20 Indicated are from the top,
the name of the clone sequence,
definition of the top hit data,
the P-value: the length of the sequence used for comparison (nucleotide):similarity (%),
the Accession No. of the top hit data.

25 [0299] Blank indicates that the 3'-end sequence corresponding to the 5'-end was not determined in the clone. Data were not shown for the clones in which the P-value was higher than 1.

R-HEMBA1000006

30 R-HEMBA1000121
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 796F18, WORKING DRAFT SE-
QUENCE.
2.2e-43:355:80
AL031291

35 R-HEMBA1000128
Homo sapiens chromosome X, PAC 671D9, complete sequence.
0.99:389:60
AF031078

40 R-HEMBA1000275
Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.

45 3.4e-10:212:66
Z93023

R-HEMBA1000300
{Alu RNA transcript, clone NE461} [human, embryonal carcinoma cells, NTera2D1 pluripotential cells, Other RNA,
282 nt].
50 4.6e-42:246:89
S42653

R-nnnnnnnnnnnnn
Homo sapiens chromosome 17, clone hRPK.235_I_10, complete sequence.
55 1.0e-71:192:95
AC005922

R-HEMBA1000462

EP 1 130 094 A2

Homo sapiens clone 243 unknown mRNA, complete sequence.
8.3e-90:313:94
AF091094

5 R-HEMBA1000477
Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 8/11.
0.22:377:60
AB020865

10
R-HEMBA1000590
Homo sapiens mRNA for matrilin-4, partial.
8.0e-101:547:93
AJ007581

R-HEMBA1000634
*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0539L10; HTGS phase 1,
WORKING DRAFT SEQUENCE, 15 unordered pieces.

0.95:186:6
20 AC004480

R-HEMBA1000671
RPCI11-65E1.TJ RPCI11 Homo sapiens genomic clone R-65E1, genomic survey sequence.
2.1e-09:165:73
AQ237194

AQ207 194

R-HEMBA1000713
Homo sapiens 10kD protein (BC10) mRNA, complete cds.
1.2e-117:575:97
AF053470

NP_001603.2
Homo sapiens mRNA for latent transforming growth factor-beta binding protein-4.
1.e-108:581:93
Y13622

.....

40 Homo sapiens chromosome 17, clone hRPK.1090_M_7, complete sequence.
0.044:253:64
AC005274

R-HEMBA1000940
45 ***ALU WARNING: Human Alu-J subfamily consensus sequence.
1.9e-33:222:82
JU14567

B-HEMBA1000863

50 R-HEMBA1000952
R-HEMBA1001184
Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4
unordered pieces.
0.00044:466:58
55 AC004688

R-HEMBA1001221
Sequence 1 from patent US 5633147.

- 7.1e-11:232:65
I43819
- 5 R-HEMBA1001228
Human germline oligomeric matrix protein (COMP) mRNA, complete cds.
7.8e-89:358:96
L32137
- 10 R-HEMBA1001272
nxb0003bDO1r CUGI Rice BAC Library Oryza sativa genomic clone nxb0003G00r, genomic survey sequence.
0.00014:201:64
AQ050116
- 15 R-HEMBA1001296
Homo sapiens PAC clone DJ1168D11 from 7p21-p22, complete sequence.
0.13:440:58
AC004614
- 20 R-HEMBA1001297
Homo sapiens putative transcription factor CA150 mRNA, complete cds.
5.0e-92:466:96
AF017789
- 25 R-HEMBA1001390
CIT-HSP-2314K10.TR CIT-HSP Homo sapiens genomic clone 2314K10, genomic survey sequence.
3.4e-43:196:85
AQ027191
- 30 R-HEMBA1001563
H.sapiens villin gene, exon 1.
2.1e-43:342:81
X71058
- 35 R-HEMBA1001621
Human G protein-coupled receptor APJ gene, complete cds.
1.2e-41:288:87
U03642
- 40 R-HEMBA1001878
Homo sapiens U5 snRNP-specific 40 kDa protein mRNA, complete cds.
2.0e-79:434:93
AF090988
- 45 R-HEMBA1001886
Human zinc finger protein (ZNF141) mRNA, complete cds.
1.8e-59:530:80
L15309
- 50 R-HEMBA1002048
Homo sapiens chromosome 5, P1 clone 1307e8 (LBNL H60), complete sequence.
0.36:322:61
AC005355
- 55 R-HEMBA1002131
Human DNA sequence from clone 301K23 on chromosome 1p35.1-36.21. Contains the 5' part of a novel gene similar to predicted yeast and worm genes. Contains ESTs and GSSs, complete sequence.
0.22:233:61
AL031730

- 5 R-HEMBA1002163
Homo sapiens chromosome X, clone 592, WORKING DRAFT SEQUENCE, 8 unordered pieces.
1.1e-16:275:69
AC002489
- 10 R-HEMBA1002167
Rattus norvegicus neuroligin I mRNA, complete cds.
8.7e-23:193:84
U22952
- 15 R-HEMBA1002178
R-HEMBA1002195
Homo sapiens DHPS gene, exons 8 to 9.
1.4e-19:114:100
AJ001704
- 20 R-HEMBA1002227
Homo sapiens mRNA for 80K-L protein, complete cds.
6.1e-115:567:97
D10522
- 25 R-HEMBA1002316
Homo sapiens mRNA for putative GTP-binding protein.
1.5e-18:161:85
Y14391
- 30 R-HEMBA1002420
Caenorhabditis elegans cosmid C27A7, complete sequence.
0.88:214:62
Z81041
- 35 R-HEMBA1002421
Human heparan sulfate proteoglycan (HSPG) core protein, 3' end.
6.0e-90:443:97
J04621
- 40 R-HEMBA1002524
Human MHC Class I region proline rich protein mRNA, complete cds.
3.2e-110:551:96
U63336
- 45 R-HEMBA1002551
Mouse Bac 276o8, WORKING DRAFT SEQUENCE, 25 unordered pieces.
7.0e-06:397:61
AC003022
- 50 R-HEMBA1002767
Homo sapiens clone NH0486I22, WORKING DRAFT SEQUENCE, 5 unordered pieces.
4.2e-110:568:96
AC005038
- 55 R-HEMBA1002985
Homo sapiens chromosome 17, clone hRPK.15_K_2, complete sequence.
3.4e-23:184:86
AC005901
- R-HEMBA1003047

EP 1 130 094 A2

Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds.

5 5.0e-114:571:96

AF034611

5 R-HEMBA1003072

HS-1014-B1-F12-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 789
Col=23 Row=L, genomic survey sequence.

1.5e-62:340:94

B32084

10 R-HEMBA1003101

Homo sapiens tyrosylprotein sulfotransferase-2 mRNA, complete cds.

3.8e-116:575:97

AF049891

15 R-HEMBA1003120

HS_3220_A1_F04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3220
Col=7 Row=K, genomic survey sequence.

3.6e-61:354:92

20 AQ184345

R-HEMBA1003230

Homo sapiens UP50 mRNA, complete cds.

1.3e-42:258:93

25 AF093118

R-HEMBA1003294

HS_3220_A1_D03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3220
Col=5 Row=G, genomic survey sequence.

30 0.0095:204:63

AQ190655

R-HEMBA1003315

Sus scrofa DNA for LH beta, exons 1, 2, 3, complete cds.

35 6.6e-24:163:79

D00579

R-HEMBA1003392

Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds.

40 2.6e-115:557:98

AF074264

R-HEMBA1003399

Homo sapiens clone DJ1125K23, WORKING DRAFT SEQUENCE, 21 unordered pieces.

45 1.8e-63:166:100

AC004971

R-HEMBA1003487

50 R-HEMBA1003497

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 2705, WORKING DRAFT SEQUENCE.

1.4e-119:592:97

AL033529

55 R-HEMBA1003530

R-HEMBA1003602

Human Chromosome 16 BAC clone CIT987SK-A-17E1, complete sequence.

9.4e-79:468:91
AC002041

5 R-HEMBA1003732
Homo sapiens clone DJ0935K16, complete sequence.
2.0e-118:586:98
AC006011

10 R-HEMBA1003945
Human calcineurin B mRNA, complete cds.
8.9e-82:410:97
M30773

15 R-HEMBA1004007
Homo sapiens clone DJ0665P05, WORKING DRAFT SEQUENCE, 5 unordered pieces.
6.7e-56:404:75
AC004851

20 R-HEMBA1004085
G.gallus microsatellite DNA (LEI0311 (= EC12A05)).
0.66:144:65
Z95196

25 R-nnnnnnnnnnnnnn
Homo sapiens intersectin short form mRNA, complete cds.
2.1e-115:569:97
AF064243

30 R-HEMBA1004250
Homo sapiens chromosome 5, BAC clone 182a8 (LBNL H161), complete sequence.
3.8e-98:478:98
AC005752

35 R-HEMBA1004391
Plasmodium falciparum MAL3P8, complete sequence.
0.29:126:65
AL034560

40 R-HEMBA1004444
Homo sapiens clone DJ0971C03, WORKING DRAFT SEQUENCE, 18 unordered pieces.
8.4e-52:308:78
AC004938

45 R-HEMBA1004454
CIT-HSP-2337122.TF CIT-HSP Homo sapiens genomic clone 2337I22, genomic survey sequence.
0.78:59:77
AQ038475

50 R-HEMBA1004505
R-HEMBA1004785

R-HEMBA1004797
55 R-HEMBA1004952
Mus musculus diabetic embryopathy (Dep-1) mRNA.
3.4e-39:327:82
AF032130

R-HEMBA1004971

Homo sapiens BAC clone RG351J01 from 7q22-q31, complete sequence.

0.00040:251:66

AC005099

5

R-HEMBA1004982

Strongyloides fulleborni 18S ribosomal RNA and 5.8S ribosomal RNA genes, partial sequence, and internal transcribed spacer 1, complete sequence.

0.092:191:63

10

U43581

R-HEMBA1005070

Human mRNA for KIAA0310 gene, complete cds.

1.2e-94:381:91

15

AB002308

R-HEMBA1005084

20

R-HEMBA1005145

Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterranean Fever gene disease.

5.7e-58:283:84

AJ003147

25

R-HEMBA1005230

CIT-HSP-2333N15.TR CIT-HSP Homo sapiens genomic clone 2333N15, genomic survey sequence.

5.5e-31:363:73

AQ040189

30

R-HEMBA1005246

Homo sapiens full length insert cDNA clone YX52E07.

1.6e-11:173:72

AF086040

35

R-HEMBA1005267

Sequence 1 from patent US 5618695.

2.4e-73:536:81

I40055

40

R-HEMBA1005337

Caenorhabditis elegans cosmid K07D4.

0.16:157:63

AF077534

45

R-HEMBA1005430

R-HEMBA1005449

R-HEMBA1005489

50 Anopheles rangeli NADH dehydrogenase subunit 2 gene, mitochondrial gene encoding mitochondrial product, partial cds.

0.020:271:61

U35272

55

R-HEMBA1005522

R-HEMBA1005545

Human m3 muscarinic acetylcholine receptor (CHRM3) gene, complete cds.

EP 1 130 094 A2

- 1.8e-115:579:96
U29589
- 5 R-HEMBA1005698
0.0065:223:65
AG004952
- 10 R-HEMBA1005913
Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence.
3.7e-15:272:68
AC003037
- 15 R-HEMBA1005929
Homo sapiens chromosome 19, cosmid R31237, complete sequence.
9.4e-55:502:76
AC005581
- 20 R-HEMBA1005945
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 774G10, WORKING DRAFT SE-
QUENCE.
0.45:245:62
AL034410
- 25 R-HEMBA1006016
Homo sapiens chromosome 17, clone hRPK.271_K_11, complete sequence.
3.5e-25:415:66
AC005562
- 30 R-HEMBA1006171
Human DNA sequence from PAC 433M19 on chromosome Xq26.3-Xq27.1. Contains ESTs, STSs and polymorphic
CA repeat.
1.0:176:64
Z95703
- 35 R-HEMBA1006276
Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.
2.8e-118:592:96
AC005261
- 40 R-HEMBA1006299
- R-HEMBA1006311
- 45 R-HEMBA1006335
Human DNA sequence from clone 496H19 on chromosome 6q24 Contains ESTs, complete sequence.
6.1e-111:578:96
AL023582
- 50 R-HEMBA1006357
Homo sapiens chromosome Xp22-67-68, WORKING DRAFT SEQUENCE, 99 unordered pieces.
4.8e-11:174:74
AC004469
- 55 R-HEMBA1006430
Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered pieces.
8.7e-45:402:79
AC004086

R-HEMBA1006482

Homo sapiens h-sco1 (SCO1) mRNA, nuclear gene encoding mitochondrial protein, complete cds.

1.7e-105:537:96

AF026852

5

R-HEMBA1006517

345A19.TV CIT978SKA1 Homo sapiens genomic clone A-345A19, genomic survey sequence.

1.5e-44:176:88

B15409

10

R-HEMBA1006544

Homo sapiens PAC clone DJ130H16 from 22q12.1-qter, complete sequence.

2.5e-66:310:83

AC004997

15

R-HEMBA1006572

Homo sapiens reduced folate carrier (RFC1) gene, exons 1a, 1c and 1b.

0.028:255:64

U92868

20

R-HEMBA1006658

Homo sapiens mRNA for KIAA0687 protein, partial cds.

7.3e-1 11:570:94

AB014587

25

R-HEMBA1006707

Homo sapiens mRNA for matrilin-4, partial.

5.1e-78:389:97

AJ007581

30

R-HEMBA1006724

HS_2052_B1_C08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2052 Col=15 Row=F, genomic survey sequence.

2.6e-46:309:88

35 AQ305998

R-HEMBA1006749

Homo sapiens mRNA for matrilin-4, partial.

3.2e-88:472:94

40 AJ007581

R-HEMBA1006770

Homo sapiens CAGH4 mRNA, partial cds.

6.5e-25:145:82

45 U80746

R-HEMBA1006902

Homo sapiens mRNA for matrilin-4, partial.

9.3e-112:540:98

50 AJ007581

R-HEMBA1006912

***ALU WARNING: Human Alu-Sc subfamily consensus sequence.

6.6e-48:279:92

55 U14571

R-HEMBA1006916

Homo sapiens Grb14 mRNA, complete cds.

1.8e-114:346:99

L76687

R-HEMBA1006960

5 Homo sapiens chromosome 19, cosmid F16403, complete sequence.

0.78:203:62

AC005777

R-HEMBA1007013

10 Human mRNA for DNA-binding protein TAXREB302, complete cds.

6.3e-31:163:100

D28468

R-HEMBA1007057

15 CIT-HSP-517F5.TP CIT-HSP Homo sapiens genomic clone 517F5, genomic survey sequence.

1.0:128:67

B49904

R-HEMBA1007063

20 Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, EST, GSS, STS. CpG island, complete sequence.

5.0e-43:300:88

AL022069

R-HEMBA1007241

25 HIV-1 RNA V3 region (patient Y, sample Y1, clone 05).

0.74:148:66

Z47529

R-HEMBA1007291

30 Homo sapiens chromosome 19, fosmid 37502, complete sequence.

3.6e-36:300:80

AC004755

R-HEMBA1007332

35 Human HeLa mRNA isolated as a false positive in a two-hybrid-screen.

7.3e-15:148:80

U56430

R-HEMBB1000106

40 Plasmodium falciparum (strain FCR3) variant-specific surface protein (var-2, var-3) genes, complete cds's.

8.0e-05:313:60

L40609

R-HEMBB1000276

45 HS_3048_A2_C07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3048 Col=14 Row=E, genomic survey sequence.

0.91:234:58

AQ099411

50

R-HEMBB1000309

R-HEMBB1000407

55 Mus musculus clone OST5976, genomic survey sequence.

6.4e-28:226:81

AF046768

R-HEMBB1000447

EP 1 130 094 A2

- Homo sapiens JWA protein mRNA, complete cds.
1.7e-107:533:97
AF070523
- 5 R-HEMBB1000542
Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.
4.4e-72:547:80
AF084259
- 10 R-HEMBB1000567
Human insulin-like growth factor (IGF-II) gene, exon 1 of 4.
4.3e-60:368:88
M13970
- 15 R-HEMBB1000642
Human DNA sequence from PAC 46H23, BRCA2 gene region chromosome 13q12-13 contains Klotho, ESTs.
2.9e-42:431:75
Z84483
- 20 R-HEMBB1000668
CITBI-E1-2508D15.TR CITBI-E1 Homo sapiens genomic clone 2508D15, genomic survey sequence.
2.5e-40:249:91
AQ261535
- 25 R-HEMBB1000679
HS_3061_A1_C03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3061
Col=5 Row=E, genomic survey sequence.
1.8e-48:257:96
AQ127602
- 30 R-HEMBB1000881
CIT-HSP-2350020.TR CIT-HSP Homo sapiens genomic clone 2350O20, genomic survey sequence.
0.0072:248:61
AQ062620
- 35 R-HEMBB1000905
Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.
2.5e-104:547:94
AC005089
- 40 R-HEMBB1001026
- R-HEMBB1001048
- 45 R-HEMBB1001200
P.falciparum complete gene map of plastid-like DNA (IR-A).
1.5e-11:521:59
X95275
- 50 R-HEMBB1001407
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 2705, WORKING DRAFT SEQUENCE.
3.0e-29:308:77
AL033529
- 55 R-HEMBB1001530
Homo sapiens chromosome 19, cosmid R30538, complete sequence.
0.040:373:63
AC005943

R-HEMBB1001547

Rickettsia prowazekii strain Madrid E, complete genome; segment 1/4.

0.027:291:62

AJ235270

5

R-HEMBB1001573

CIT-HSP-2307C1.TR CIT-HSP Homo sapiens genomic clone 2307C1, genomic survey sequence.

1.3e-13:90:98

AQ020395

10

R-HEMBB1001847

Homo sapiens chromosome 21q22.3 PAC 21L13, complete sequence.

3.4e-27:147:80

AF064864

15

R-HEMBB1001959

Homo sapiens clone 24781 mRNA sequence.

4.4e-103:504:97

AF070640

20

R-HEMBB1001978

CIT-HSP-2328G6.TF CIT-HSP Homo sapiens genomic clone 2328G6, genomic survey sequence.

7.9e-29:220:86

AQ040310

25

R-HEMBB1002039

Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.

2.7e-37:550:68

AC005014

30

R-HEMBB1002041

Sequence 1 from patent US 5633147.

2.7e-23:322:70

I43819

35

R-HEMBB1002051

Homo sapiens clone DJ0292L20, WORKING DRAFT SEQUENCE, 2 unordered pieces.

9.2e-35:302:79

AC004825

40

R-HEMBB1002120

Homo sapiens Xp22 GS-524I1 (Genome Systems Human BAC library), complete sequence.

6.0e-05:479:59

AC003106

45

R-HEMBB1002162

Human DNA sequence from clone 739H11 on chromosome 1p33-34.2 Contains KIAA0237 gene, EST, STS, GSS, complete sequence.

3.7e-30:238:84

50

AL031289

R-HEMBB1002228

Homo sapiens BAC clone NH0436H22 from 2, complete sequence.

6.6e-57:274:86

55

AC005234

R-HEMBB1002245

Sequence 25 from patent US 5747660.

EP 1 130 094 A2

4.8e-30:361:73
AR005295

5 R-HEMBB1002302
Methanococcus jannaschii section 84 of 150 of the complete genome.
0.00019:362:59
U67542

10 R-HEMBB1002427
Genomic sequence from Human 9q34, complete sequence.
3.9e-105:533:96
AC001643

15 R-HEMBB1002465
Plasmodium falciparum chromosome 2, section 19 of 73 of the complete sequence.
2.9e-05:335:62
AE001382

20 R-HEMBB1002661

20 R-HEMBB1002663
***ALU WARNING: Human Alu-Sq subfamily consensus sequence.
8.3e-43:268:89
U14573

25 R-HEMBB1002693
Human BAC clone RG126M09 from 7q21-q22, complete sequence.
2.4e-24:220:76
AC002067

30 R-MAMMA1000046
Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8
unordered pieces.
0.032:402:57
AC005505

35 R-MAMMA1000102
Human DNA sequence from cosmid B33F2 on chromosome 22 Contains ESTs.
2.0e-84:428:96
Z79996

40 R-MAMMA1000106
Homo sapiens genomic DNA, chromosome 21q11.1, segment 2/28, WORKING DRAFT SEQUENCE.
0.095:138:66
AP000031

45 R-MAMMA1000118

50 R-MAMMA1000141
Homo sapiens 12q24.2 PAC RPCI1-128M12 (Roswell Park Cancer Institute Human PAC library) complete se-
quence.
9.0e-91:480:95
AC004024

55 R-MAMMA1000204
Homo sapiens mRNA for LGMD2B protein.
1.5e-107:544:96
AJ007670

R-MAMMA1000226
H.sapiens VASP gene, exons 4 to 13.
0.99:244:63
X98534

5

R-MAMMA1000403
CIT-HSP-2372A15.TF CIT-HSP Homo sapiens genomic clone 2372A15, genomic survey sequence.
8.0e-38:187:81
AQ112406

10

R-MAMMA1000449
Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.
1.2e-41:422:76
AC004491

15

R-MAMMA1000457
Homo sapiens clone 638 unknown mRNA, complete sequence.
7.4e-116:570:97
AF091084

20

R-MAMMA1000473
Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12, complete sequence.
9.6e-09:136:77
AC004131

25

R-MAMMA1000496
Homo sapiens PAC clone DJ130H16 from 22q12.1-qter, complete sequence.
2.6e-48:272:93
AC004997

30

R-MAMMA1000528
Human BAC clone RG114A06 from 7q31, complete sequence.
1.8e-13:109:80
AC002542

35

R-MAMMA1000591
Human cosmid g1572c264, complete sequence.
1.6e-22:329:71
AC000359

40

R-MAMMA1000614

R-MAMMA1000652
H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA28A10.

45

0.81:158:65
Z84499

R-MAMMA1000681
Homo sapiens full length insert cDNA clone YY85D04.

50

1.0e-107:560:94
AF088014

R-MAMMA1000706
Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds.

55

1.1e-46:232:100
AF067223

R-MAMMA1000788

- Bos taurus P14 (p14) mRNA, complete cds.
3.8e-72:493:84
AF037349
- 5 R-MAMMA1000810
Human DNA from overlapping chromosome 19-specific cosmids R29515 and R28253, genomic sequence, complete sequence.
5.0e-37:318:79
AC003002
- 10 R-MAMMA1000814
Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.
7.7e-15:140:85
AC003071
- 15 R-MAMMA1000881
Human DNA sequence from clone 105D16 on chromosome Xp11.3-11.4 Contains pseudogene similar to laminin-binding protein, CA repeat, STS, complete sequence.
8.8e-46:457:75
AL031311
- 20 R-MAMMA1000986
Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence.
7.7e-44:343:82
AF001550
- 25 R-MAMMA1000994
Homo sapiens mRNA for ISLR, complete cds.
3.6e-108:552:96
AB003184
- 30 R-MAMMA1001043
- 35 R-MAMMA1001066
Homo sapiens chromosome 17, clone hRPK.346_K_10, complete sequence.
1.3e-42:302:82
AC006120
- 40 R-MAMMA1001094
Homo sapiens clone 243 unknown mRNA, complete sequence.
5.4e-115:567:97
AF091094
- 45 R-MAMMA1001141
HS_3059_B1_H06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3059 Col=11 Row=P, genomic survey sequence.
1.3e-68:388:92
AQ214896
- 50 R-MAMMA1001150
H.sapiens mRNA for protein kinase C mu.
5.4e-20:340:66
X75756
- 55 R-MAMMA1001237
Mouse DNA fragment that hybridizes to HSV- 1 SmaI A fragment.
0.15:222:65
M11041

- 5 R-MAMMA1001284
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1185N5, WORKING DRAFT SEQUENCE.
1.2e-33:344:76
AL034423
- 10 R-MAMMA1001310
Human Bruton agammaglobulinemia (BTK) gene, exons 10-12.
1.8e-39:332:80
L31565
- 15 R-MAMMA1001418
Human proto-oncogene tyrosine-protein kinase (ABL) gene, exon 1a and exons 2-10, complete cds.
4.4e-42:411:76
U07563
- 20 R-MAMMA1001532
Homo sapiens PAC clone DJ0728D04, complete sequence.
2.3e-10:196:73
AC004865
- 25 R-MAMMA1001609
HS-1054-B2-H01-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 776 Col=2
Row=P, genomic survey sequence.
1.6e-34:170:79
B42016
- 30 R-MAMMA1001615
- 35 R-MAMMA1001623
Homo sapiens 12q24.2 BAC RPCI11-407A16 (Roswell Park Cancer Institute Human BAC Library) complete sequence.
8.8e-21:180:82
AC006065
- 40 R-MAMMA1001634
Homo sapiens chromosome 17, clone hRPK.85_B_7, complete sequence.
2.6e-40:283:86
AC005695
- 45 R-MAMMA1001893
Homo sapiens clone DJ0782K24, WORKING DRAFT SEQUENCE, 16 unordered pieces.
0.73:132:67
AC006003
- 50 R-MAMMA1001901
Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.
4.0e-43:288:77
Z93023
- 55 R-MAMMA1001957
Homo sapiens chromosome 16, P1 clone 96-4B (LANL), complete sequence.
1.2e-41:298:86
AC005212
- R-MAMMA1001978

EP 1 130 094 A2

- 5 R-MAMMA1002070
Homo sapiens clone DJ400N23, WORKING DRAFT SEQUENCE, 10 unordered pieces.
2.1e-104:530:97
AC005003
- 10 R-MAMMA1002080 rah=ras-related homolog [mice, HT4 neural cell line, mRNA, 993 nt].
5.9e-47:449:76
S72304
- 15 R-MAMMA1002087
Human Cosmid g1572c037 from 7q31.3, complete sequence.
1.7e-11:120:83
AC000125
- 20 R-MAMMA1002095
Rat alternatively spliced mRNA.
5.3e-30:289:74
M93018
- 25 R-MAMMA1002128
R-MAMMA1002142
- 30 R-MAMMA1002165
Homo sapiens chromosome 10 clone CIT987SK-1109P11, complete sequence.
1.1e-28:350:72
AC005871
- 35 R-MAMMA1002205
Human DNA sequence from PAC 368A4 on chromosome X. Contains ESTs, CELLULAR NUCLEIC ACID BINDING PROTEIN (CNBP) like gene and STSs.
1.2e-42:282:75
Z83843
- 40 R-MAMMA1002224
Arabidopsis thaliana DNA chromosome 4, BAC clone F1C12 (ESSAI project).
0.99:210:60
AL022224
- 45 R-MAMMA1002234
Canine mRNA for 68kDa subunit of signal recognition particle (SRP68).
1.7e-61:310:81
X53744
- 50 R-MAMMA1002586
Streptomyces collinus coenzyme B12-dependent mutase (meaA) gene, complete cds.
0.99:348:60
AF008569
- 55 R-MAMMA1002633
Homo sapiens, clone hRPK. 1_A_1, complete sequence.
2.6e-13:381:64
AC006196
- R-NT2RM4000100
Plasmodium falciparum MAL3P2, complete sequence.

0.00047:296:61
AL034558

R-NT2RM4000115

5 Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P3, WORKING DRAFT SEQUENCE.

0.079:270:64
AL031746

10 R-NT2RM4000198

Homo sapiens chromosome 10 clone LA10NC01_15_E_11 map 10q26.3, WORKING DRAFT SEQUENCE, 3 un-ordered pieces.

7.7e-24:244:78
AC006171

15 R-NT2RM4000284

Human IgG Fc receptor hFcRn mRNA, complete cds.

1.7e-93:440:100
U12255

20 R-NT2RM4000295

, complete sequence.

0.89:351:58
AC005663

25 R-NT2RM4000326

Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterranean Fever gene disease.

2.3e-112:602:94
AJ003147

30 R-NT2RM4000417

Human DNA sequence from PAC 326L13 containing brain-4 mRNA ESTs and polymorphic CA repeat.

0.78:229:62
Z82170

35 R-NT2RM4000444

40 R-NT2RM4000587

45 R-NT2RM4000593

R-NT2RM4000648

0.010:260:61
AG005508

50 R-NT2RM4000761

H.sapiens mitochondrial genome (consensus sequence).

3.2e-95:476:97
X62996

55 R-NT2RM4000965

R-NT2RM4000997

55 R-NT2RM4001321

Human DNA sequence from clone 1177E19 on chromosome 1p36.12-36.31. Contains the 3'part of the DNA-binding Zinc finger protein RIZ gene, ESTs, an STS, GSSs and a CpG island, complete sequence.

EP 1 130 094 A2

6.0e-19:282:73
AL031277

5 R-NT2RM4001325

R-NT2RM4001377
Homo sapiens mRNA for KIAA0638 protein, partial cds.
2.9e-111:553:96
AB014538

10 R-NT2RM4001735
Homo sapiens clone 23904 mRNA sequence.
4.6e-106:553:94
AF052129

15 R-NT2RM4001768
Human HepG2 3'region Mbol cDNA, clone hmd3c03m3.
4.1e-29:187:91
D17194

20 R-NT2RM4001843
Homo sapiens chromosome 17, clone hRPK.269_G_24, complete sequence.
0.95:366:58
AC005828

25 R-NT2RM4002352
Homo sapiens hLRp105 mRNA for LDL receptor related protein 105, complete cds.
5.5e-108:557:95
AB009462

30 R-NT2RP2000092
HS_3070_B1_B04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3070
Col=7 Row=D, genomic survey sequence.
1.1e-23:247:77

35 AQ120714

R-NT2RP2000178
E.amylovora lon gene.
1.1e-15:422:62

40 X77706

R-NT2RP2000240
*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0539L10; HTGS phase 1,
WORKING DRAFT SEQUENCE, 15 unordered pieces.

45 0.00010:260:62
AC004480

R-NT2RP2000394
HS_3211_B2_G06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3211
Col=12 Row=N, genomic survey sequence.
1.1e-61:316:97
AQ174850

50 R-NT2RP2000447
Homo sapiens clone DJ1129D05, complete sequence.
8.7e-67:357:94
AC005630

EP 1 130 094 A2

R-NT2RP2000479

Homo sapiens chromosome 17, clone 193h18, complete sequence.

5 5.7e-51:551:73

AC002546

5

R-NT2RP2000514

P.falciparum parasite antigen reactive with the parasite inhibitory mouse monoclonal antibody (mMAb) 43E5, clone #366, partial cds.

10 2.1e-08:192:68

M21323

10

R-NT2RP2000533

Mus musculus cornichon mRNA, complete cds.

15 3.5e-59:243:82

AF022811

15

R-NT2RP2000616

Human DNA sequence from clone 694E4 on chromosome 22 Contains exon similar to phosphatidylserine decarboxylase, EST, GSS, complete sequence.

20 0.0064:105:67

AL031255

20

R-NT2RP2000649

Homo sapiens mRNA for Hs Ste24p, complete cds.

25 1.4e-65:326:98

AB016068

25

R-NT2RP2000663

Human DNA sequence from cosmid U61B11, between markers DXS366 and DXS87 on chromosome X contains ESTs.

30 7.9e-110:555:96

Z73913

30

R-NT2RP2000712

Homo sapiens clone DJ0756H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.

35 9.8e-32:308:78

AC006001

35

R-NT2RP2000739

Bos taurus TATA box binding protein (TBP) gene, partial cds.

40 0.19:128:68

L47974

40

R-NT2RP2000818

Caenorhabditis elegans cosmid C48D5, complete sequence.

45 0.010:429:58

Z36237

45

R-NT2RP2000903

H.sapiens 5T4 gene for 5T4 Oncofetal antigen.

50 4.0e-99:505:96

Z29083

50

R-NT2RP2001200

Homo sapiens mRNA for KIAA0676 protein, partial cds.

55 2.0e-57:306:95

AB014576

R-NT2RP2001223

R-NT2RP2001276

Mouse regulatory protein (npdc-1) mRNA, complete cds.

5 5.8e-14:353:65

L03814

R-NT2RP2001388

Homo sapiens clone DJ1125K23, WORKING DRAFT SEQUENCE, 21 unordered pieces.

10 1.7e-31:291:77

AC004971

R-NT2RP2001469

M.musculus tex292 mRNA (3'region).

15 3.7e-26:188:89

X80433

R-NT2RP2001480

Homo sapiens thrombospondin 3 (THBS3) gene, complete cds.

20 6.6e-83:426:95

L38969

R-NT2RP2001495

transcript ch123.Rev [human, RF1,RF48 stomach cancer cell lines, mRNA, 252 nt].

25 6.3e-43:238:96

S77359

R-NT2RP2001514

Homo sapiens cyclin K (CPR4) mRNA, complete cds.

30 6.6e-06:57:100

AF060515

R-NT2RP2001538

Mus musculus transcriptional regulatory protein (mSin3) gene, complete cds.

35 6.9e-12:179:75

L36831

R-NT2RP2001562

Human PAC clone DJ0800B09 from 7q11.23-q21, complete sequence.

40 0.074:257:61

AC004028

R-NT2RP2001662

Homo sapiens clone 24615 mRNA sequence.

45 3.2e-94:485:95

AF055012

R-NT2RP2001755

Homo sapiens mRNA for KIAA0762 protein, partial cds.

50 1.3e-103:576:92

AB018305

R-NT2RP2001769

CIT-HSP-2376O23.TF CIT-HSP Homo sapiens genomic clone 2376023, genomic survey sequence.

55 1.5e-74:381:96

AQ111163

R-NT2RP2001817

EP 1 130 094 A2

HS_2037_B2_A09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2037
Col=18 Row=B, genomic survey sequence.

3.9e-60:430:84
AQ243047

- 5 R-NT2RP2001878
Human DNA sequence from PAC 296K21 on chromosome X contains cytokeratin exon, delta-aminolevulinate synthase (erythroid); 5-aminolevulinic acid synthase.(EC 2.3.1.37). 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (EC 2.7.1.105, EC 3.1.3.46), ESTs and STS.
10 0.018:148:67
Z83821
- R-NT2RP2001903
Human Not1 linking clone from chromosome 1q32.
15 0.99:160:63
U36769
- R-NT2RP2001915
- 20 R-NT2RP2001921
Homo sapiens clone NH0332L11, complete sequence.
6.5e-86:295:98
AC005538
- 25 R-NT2RP2001948
Homo sapiens chromosome 19, cosmid R33590, complete sequence.
2.3e-79:440:91
AC005620
- 30 R-NT2RP2001956
- R-NT2RP2002015
Human DNA sequence from clone 1177E19 on chromosome 1p36.12-36.31. Contains the 3'part of the DNA-binding Zinc finger protein RIZ gene, ESTs, an STS, GSSs and a CpG island, complete sequence.
35 1.1e-16:254:72
AL031277
- R-NT2RP2002063
Homo sapiens chromosome 4 clone B207D4 map 4q25, complete sequence.
40 5.8e-105:550:95
AC004050
- R-NT2RP2002188
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 134019, WORKING DRAFT SEQUENCE.
45 0.47:212:62
AL034555
- R-NT2RP2002232
50 R-nnnnnnnnnnnnn
Human mRNA for KIAA0383 gene, partial cds.
2.5e-100:511:96
AB002381
- 55 R-NT2RP2002409
S.pombe chromosome I cosmid c17H9.
1.0:241:63

Z98597

R-NT2RP2002510

Homo sapiens chromosome 19, cosmid F19847, complete sequence.

5
1.6e-38:307:81
AC005952

R-NT2RP2002527

Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete se-
quence.10
1.5e-18:165:83
AC004770

R-NT2RP2002533

Homo sapiens alpha 2 delta calcium channel subunit isoform II mRNA, complete cds.

15
9.7e-116:580:96
AF042793

R-NT2RP2002564

Homo sapiens clone DJ0800G07, complete sequence.

20
3.8e-110:580:94
AC004890

R-NT2RP2002674

Plasmodium falciparum chromosome 2, section 11 of 73 of the complete sequence.

25
1.0:244:60
AE001374

R-NT2RP2002721

Homo sapiens chromosome 17, clone HCIT217L10, complete sequence.

30
1.2e-10:221:73
AC003962

R-NT2RP2002824

Human HepG2 3' region MboI cDNA, clone hmd4f06m3.

35
3.0e-07:108:77
D17237

R-NT2RP2002942

Human DNA sequence from clone 88D7 on chromosome Xq25-26.3 Contains F9 (coagulation factor IX (plasma thromboplastic component, Christmas disease, haemophilia B)), dbl oncogene. EST, STS, GSS, complete se-
quence.40
2.0e-37:491:71
AL03340345
R-NT2RP2002974

H.sapiens DMAHP gene.

4.0e-118:585:97
X8481350
R-NT2RP2002976

CIT-HSP-2348J20.TF CIT-HSP Homo sapiens genomic clone 2348J20, genomic survey sequence.

8.4e-45:233:98
AQ05944455
R-NT2RP2003042

R-NT2RP2003179

- 5 R-NT2RP2003210
R-NT2RP2003302
Human DNA sequence from 4PTEL, Huntington's Disease Region, chromosome 4p16.3.
1.5e-24:255:78
Z95704
- 10 R-NT2RP2003369
Homo sapiens chromosome 7q22 sequence, complete sequence.
3.1e-95:514:92
AF053356
- 15 R-NT2RP2003383
Homo sapiens mRNA for KIAA0458 protein, complete cds.
3.9e-111:549:97
AB007927
- 20 R-NT2RP2003390
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 191J18, WORKING DRAFT SEQUENCE.
4.9e-102:413:99
AL024507
- 25 R-NT2RP2003469
Genomic sequence from Human 9q34, complete sequence.
1.4e-35:376:74
AC001644
- 30 R-NT2RP2003545
Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SE-
QUENCE.
1.5e-09:503:61
AL034557
- 35 R-NT2RP2003593
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 971N18, WORKING DRAFT SE-
QUENCE.
7.8e-81:433:93
AL021396
- 40 R-NT2RP2003599
HS_3240_A1_C04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3240
Col=7 Row=E, genomic survey sequence.
0.091:341:58
AQ206348
- 45 R-NT2RP2003655
Homo sapiens PAC clone DJ0015I23 from 22, complete sequence.
2.0e-08:249:69
AC004819
- 50 R-NT2RP2003664
Homo sapiens mRNA for leptin receptor gene-related protein.
1.7e-110:549:96
Y12670
- 55 R-NT2RP2003931
Human mRNA for KIAA0365 gene, partial cds.
5.4e-112:571:96

AB002363

R-NT2RP2003940

Human Chromosome 11 pac pDJ1173a5, complete sequence.

5 2.4e-20:353:70

AC000378

R-NT2RP2003950

Homo sapiens clone 24778 unknown mRNA.

10 1.5e-96:494:95

AF070572

R-NT2RP2004069

Human DNA sequence from clone 618F1 on chromosome Xq25 Contains part of gene similar to DOC4, CA repeat,
15 GSS, complete sequence.

2.6e-50:539:75

AL023878

R-NT2RP2004108

RPCII1-91F9.TV RPCI11 Homo sapiens genomic clone R-91F9, genomic survey sequence. 0.00013:281:63
20 AQ283338

R-NT2RP2004141

cSRL-115f11-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-115f11,
25 genomic survey sequence.

2.3e-05:239:64

B00539

R-NT2RP2004179

Genomic sequence from Human 9q34, complete sequence.

0.43:130:68

AC002322

R-NT2RP2004205

Homo sapiens chromosome 7q22 sequence, complete sequence.

1.4e-42:324:83

AF053356

R-NT2RP2004447

Homo sapiens Chromosome 11q13 BAC Clone 18h3, WORKING DRAFT SEQUENCE, 7 ordered pieces.

40 5.5e-35:285:84

AC000353

R-NT2RP2004495

transcript ch123.Rev [human, RF1,RF48 stomach cancer cell lines, mRNA, 252 nt].

45 3.4e-44:238:97

S77359

R-NT2RP2004524

Genomic sequence from Human 9q34, complete sequence.

50 7.4e-113:572:96

AC001644

R-NT2RP2004556

CIT-HSP-2306F6.TF CIT-HSP Homo sapiens genomic clone 2306F6, genomic survey sequence.

55 8.1e-99:514:95

AQ019229

EP 1 130 094 A2

R-NT2RP2004606 cDNA encoding NIC(Natural Inhibitor of Collagenase).

8.2e-116:576:96

E00985

5 R-NT2RP2004648

Homo sapiens chromosome 17, clone hRPK.269_G_24, complete sequence.

0.98:369:57

AC005828

10 R-NT2RP2004670

Rattus norvegicus vesicula-associate calmodulin-binding protein mRNA, complete cds.

4.5e-43:592:69

L22557

15 R-NT2RP2004794

R-NT2RP2004837

Human Chromosome 11 pac pDJ148f1, WORKING DRAFT SEQUENCE, 27 unordered pieces.

1.2e-60:366:90

20 AC001232

R-NT2RP2004847

Homo sapiens full length insert cDNA clone YY87C09.

1.0e-68:333:100

25 AF086055

R-NT2RP2005027

Human glucose transporter-like protein-III (GLUT3), complete cds.

7.8e-103:508:97

30 M20681

R-NT2RP2005069

Rat vacuolar protein sorting homolog r-vps33b mRNA, complete cds.

3.8e-42:463:73

35 U35245

R-NT2RP2005163

CIT-HSP-2348J20.TF CIT-HSP Homo sapiens genomic clone 2348J20, genomic survey sequence.

7.4e-44:233:96

40 AQ059444

R-NT2RP2005181

Rattus norvegicus mRNA for cationic amino acid transporter 3, complete cds.

7.6e-53:567:73

45 AB000113

R-NT2RP2005247

Homo sapiens Xp22 Cosmid U151G1 (from Lawrence Livermore X library) and PAC RPCI1-93D11 (from Roswell Park Cancer Center) complete sequence.

50 5.8e-38:341:76

AC002357

R-NT2RP2005378

Homo sapiens full length insert cDNA clone YW25A12.

0.13:152:66

55 AF086029

R-NT2RP2005391

EP 1 130 094 A2

HS_3056_A1_C03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone
Plate=3056 Col=5 Row=E, genomic survey sequence.

1.1e-14:140:84
AQ134064

5

R-NT2RP2005425
Homo sapiens mRNA for KIAA0803 protein, partial cds.
8.2e-100:526:94

AB018346

10

R-NT2RP2005463

R-NT2RP2005514

15

R-NT2RP2005535
Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.
1.9e-11:488:62
AC003973

20

R-NT2RP2005541
CIT-HSP-2034G23.TF CIT-HSP Homo sapiens genomic clone 2034G23, genomic survey sequence.
2.7e-61:311:98
B74709

25

R-NT2RP2005597

R-nnnnnnnnnnnnn
{FRA16A, folate-sensitive fragile site} [human, Genomic, 160 nt].
0.92:104:65

30

S70397

R-NT2RP2005666

35

R-NT2RP2005774
Homo sapiens apoptosis-related mRNA, 3'UTR, partial sequence.
2.2e-94:440:96
AF035364

40

R-NT2RP2005878
Homo sapiens chromosome 19, cosmid F17987, complete sequence.
1.3e-32:340:76
AC004790

45

R-NT2RP2005883
Human DNA sequence from clone 248E1 on chromosome 6q23.1-23.3 Contains DOPAMINE-BETA-MONOXY-
GENASE PRECURSOR, EF-1-ALPHA-2 pseudogene EST GSS and CA repeat, complete sequence.
1.3e-117:581:97
AL023578

50

R-NT2RP2005887
Human Chromosome 11 pac pDJ148f1, WORKING DRAFT SEQUENCE, 27 unordered pieces
2.5e-61:367:90
AC001232

55

R-nnnnnnnnnnnnn
Human paired box gene (PAX6) homologue, complete cds.
5.0e-115:578:96
M93650

EP 1 130 094 A2

- 5 R-NT2RP2005994
Homo sapiens chromosome 4 clone B207D4 map 4q25, complete sequence.
2.4e-116:594:96
AC004050
- 10 R-NT2RP2006004
Rattus norvegicus Shal-related potassium channel Kv4.3 mRNA, complete cds.
1.8e-45:264:93
U42975
- 15 R-NT2RP2006042
T31H24TF TAMU Arabidopsis thaliana genomic clone T31H24, genomic survey sequence.
0.42:111:70
B78148
- 20 R-NT2RP2006092
Homo sapiens chromosome 5, BAC clone 319C17 (LBNL H159), complete sequence.
1.7e-73:385:95
AC005214
- 25 R-NT2RP2006099
Homo sapiens PAC clone DJ0903G02, complete sequence.
1.3e-27:335:74
AC004924
- 30 R-NT2RP2006134
Homo sapiens chromosome 4 clone B139M23 map 4q25, complete sequence.
1.0:143:63
AC004045
- 35 R-NT2RP2006269
Phreatamoeba balamuthi UBI3 sequence, putative polyubiquitin gene.
0.82:153:63
AJ000657
- 40 R-NT2RP2006512
Homo sapiens clone 23904 mRNA sequence.
4.6e-106:531:96
AF052129
- 45 R-NT2RP3000011
HS_2196_A2_E08_MRCIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2196
Col=16 Row=1, genomic survey sequence.
1.3e-36:292:83
AQ210450
- 50 R-NT2RP3000022
Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-15, complete sequence.
0.28:248:60
Z98550
- 55 R-NT2RP3000059
Homo sapiens chick ovalbumin upstream promoter transcription factor II (COUP-TFII) mRNA, partial cds.
0.047:393:61
M62760
- R-NT2RP3000063
HS_3190_B2_D10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone

EP 1 130 094 A2

Plate=3190 Col=20 Row=H, genomic survey sequence.
0.88:232:63
AQ172428

- 5 R-nnnnnnnnnnnnnn
RPCI11-35A1.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-35A1, genomic survey sequence.
3.8e-29:159:99
AQ045699
- 10 R-NT2RP3000148
Homo sapiens full length insert cDNA clone ZE03A07.
2.8e-112:574:95
AF086510
- 15 R-NT2RP3000169
Homo sapiens MRS1 mRNA, complete cds.
4.4e-110:551:96
AF093239
- 20 R-NT2RP3000171

R-NT2RP3000172
Rattus norvegicus vesicula-associate calmodulin-binding protein mRNA, complete cds.
1.3e-40:554:70
- 25 L22557

R-NT2RP3000201
Homo sapiens BAC clone NH0353P23 from 2, complete sequence.
6.4e-96:478:97
- 30 AC005035

R-NT2RP3000232
Plasmodium falciparum MAL3P2, complete sequence.
0.93:262:61
- 35 AL034558

R-NT2RP3000304
Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds.
2.4e-109:546:97
- 40 AF074264

R-NT2RP3000378
Mus musculus mSin3A (sin3A) mRNA, complete cds.
3.0e-27:411:72
- 45 U22394

R-NT2RP3000436
Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.
1.1e-06:440:57
- 50 AE001398

R-NT2RP3000444
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 889J22, WORKING DRAFT SEQUENCE.
5.9e-105:543:95
- 55 AL031406

R-NT2RP3000460
Canis familiaris sec61 homologue mRNA, complete cds.

- 2.8e-12:292:68
M96629
- 5 R-NT2RP3000481
WORKING DRAFT SEQUENCE, 8 unordered pieces.
0.99:160:65
AC005992
- 10 R-NT2RP3000616
Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5
unordered pieces.
0.00087:412:57
AC005308
- 15 R-NT2RP3000645
- R-NT2RP3000652
Homo sapiens DNA from chromosome 19, cosmid R32532, complete sequence.
1.9e-44:539:74
20 AC004004
- R-NT2RP3000676
Homo sapiens mRNA for KIAA0446 protein, complete cds.
3.1e-103:542:94
25 AB007915
- R-NT2RP3000677
Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 4/10.
0.067:235:61
30 AB020872
- R-NT2RP3000721
CIT-HSP-2348J20.TF CIT-HSP Homo sapiens genomic clone 2348J20, genomic survey sequence.
4.0e-45:233:98
35 AQ059444
- R-NT2RP3000789
- R-NT2RP3000818
40 Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 94M16, WORKING DRAFT SEQUENCE.
5.7e-95:510:93
Z97201
- R-NT2RP3000820
45 RPCI11-77B13.TJ RPCI11 Homo sapiens genomic clone R-77B13, genomic survey sequence.
2.1e-50:266:96
AQ283547
- R-NT2RP3000838
50 Homo sapiens mRNA for KIAA0638 protein, partial cds.
4.6e-99:522:94
AB014538
- R-NT2RP3000871
55 Homo sapiens clone DJ0703P08, WORKING DRAFT SEQUENCE, 23 unordered pieces.
0.68:249:61
AC005481

EP 1 130 094 A2

- 5 R-NT2RP3000907
X.laevis oocyte repetitive sequence (XLOREP) mRNA.
2.9e-30:386:69
X65290
- 10 R-NT2RP3000921
HS_2026_A1_B06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2026
Col=11 Row=C, genomic survey sequence.
2.2e-54:311:92
AQ232644
- 15 R-NT2RP3001012
Rattus norvegicus mRNA for TIP120, complete cds.
9.2e-63:456:83
D87671
- 20 R-NT2RP3001044
Human Chromosome 11 pac pDJ148f1, WORKING DRAFT SEQUENCE, 27 unordered pieces.
1.2e-60:366:90
AC001232
- 25 R-NT2RP3001061
Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7
unordered pieces.
0.17:357:61
AC005506
- 30 R-NT2RP3001159
Homo sapiens Chromosome 11q12.2 PAC clone pDJ519o13 containing human gene for ferritin heavy chain (FTH),
complete sequence.
8.8e-111:561:96
AC004228
- 35 R-NT2RP3001170
Homo sapiens mRNA for KIAA0784 protein, partial cds.
8.8e-117:561:98
AB018327
- 40 R-NT2RP3001195
Genomic sequence from Human 9q34, complete sequence.
1.4e-35:376:74
AC001644
- 45 R-NT2RP3001240
Canis familiaris sec61 homologue mRNA, complete cds.
2.8e-12:292:68
M96629
- 50 R-NT2RP3001271
Homo sapiens chromosome 19, BAC CIT-B-470f8 (BC330812), complete sequence.
7.9e-17:260:71
AC006115
- 55 R-NT2RP3001322
Human DNA sequence from PAC 128N22 on chromosome Xq25-Xq26.3. contains STS.
0.035:451:60
Z97629

EP 1 130 094 A2

- 5 R-NT2RP3001542
Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8
unordered pieces.
4.1e-08:500:61
AC004153
- 10 R-NT2RP3001560
Mouse mRNA for thymic epithelial cell surface antigen, complete cds.
1.0e-30:523:65
D67067
- R-NT2RP3001592
- 15 R-NT2RP3001685
Human DNA sequence from clone 91J24 on chromosome 6q24 Contains part of utrophin Gene, part of cytochrome
C oxidase gene, EST, CpG island, complete sequence.
2.4e-30:147:85
AL024474
- 20 R-NT2RP3001738
Homo sapiens Chromosome 11q12.2 PAC clone pDJ519o13 containing human gene for ferritin heavy chain (FTH),
complete sequence.
9.2e-107:553:95
AC004228
- 25 R-NT2RP3001754
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 50024, WORKING DRAFT SEQUENCE.
2.0e-67:345:97
AL034380
- 30 R-NT2RP3001858
- 35 R-NT2RP3001976
Homo sapiens chromosome 9, clone hRPK.467_F_21, complete sequence.
4.4e-14:302:62
AC006239
- 40 R-NT2RP3002015
Homo sapiens clone DJ0539M06, WORKING DRAFT SEQUENCE, 10 unordered pieces.
6.2e-65:492:82
AC004832
- 45 R-NT2RP3002160
Genomic sequence from Human 9q34, complete sequence.
2.1e-82:431:95
AC001643
- 50 R-NT2RP3002281
Homo sapiens mRNA for KIAA0765 protein, partial cds.
1.1e-81:446:93
AB018308
- 55 R-NT2RP3002286
Mus musculus EGF repeat transmembrane protein mRNA, complete cds.
1.0e-80:378:90
U57368
- R-NT2RP3002311

EP 1 130 094 A2

Homo sapiens chromosome 17, clone hRPK.269_G_24, complete sequence.
0.57:366:58
AC005828

5 R-NT2RP3002324
H.sapiens gene for nitric oxide synthase (promoter region).
1.6e-30:337:72
Z49251

10 R-NT2RP3002342
transcript ch123.Rev [human, RF1,RF48 stomach cancer cell lines, mRNA, 252 nt].
6.5e-45:238:98
S77359

15 R-NT2RP3002353
Human Chromosome 16 BAC clone CIT987SK-A-418G10, complete sequence. 0.00015:164:70
AC002044

20 NNNNNNNNNNNNNNN
Homo sapiens mRNA for KIAA0788 protein, partial cds.
4.5e-98:493:96
AB018331

25 NNNNNNNNNNNNNNN
R-NT2RP3002448
S.cerevisiae DNA for ori 2.
0.52:91:71
X59535

30 /
R-NT2RP3002571

35 R-NT2RP3002664
Homo sapiens full length insert cDNA clone ZC48G09.
9.9e-103:522:96
AF086209

R-NT2RP3002721

40 R-NT2RP3002737

R-NT2RP3002738
Sequence 4 from patent US 5541109.
2.9e-22:171:74
I24014

R-NT2RP3002790

50 R-NT2RP3002836
Bos taurus retina specific RGS protein (RET-RGS1) mRNA, complete cds.
2.3e-34:384:75
U89254

55 R-NT2RP3002887
Mus musculus cathepsin S (CatS) gene, promoter region and exons 1 and 2.
1.6e-05:435:62
AF051726

EP 1 130 094 A2

- 5 R-NT2RP3002900
Homo sapiens mRNA from chromosome 5q21-22, clone:A3-B.
1.3e-116:569:97
AB002451
- 10 R-NT2RP3002958
Homo sapiens clone 23851 mRNA sequence.
2.0e-117:575:98
AF035313
- 15 R-NT2RP3002983
Homo sapiens genomic DNA, chromosome 21q11.1, segment 17/28, WORKING DRAFT SEQUENCE.
5.1e-59:295:99
AP000046
- 20 R-NT2RP3003000
Homo sapiens clone 24597 mRNA sequence.
6. 1e-109:562:95
AF070604
- 25 R-NT2RP3003076
R-NT2RP3003354
Human protocadherin 42 mRNA, complete cds for abbreviated PC42.
0.87:208:61
L11370
- 30 R-NT2RP3003448
High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces.
1.3e-41:287:80
AC005840
- 35 R-NT2RP3003469
Human DNA sequence from clone 1177E19 on chromosome 1p36.12-36.31. Contains the 3'part of the DNA-binding Zinc finger protein RIZ gene, ESTs, an STS, GSSs and a CpG island, complete sequence.
2.1e-18:223:77
AL031277
- 40 R-NT2RP3003473
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 250D10, WORKING DRAFT SEQUENCE.
1.5e-54:294:96
Z99716
- 45 R-NT2RP3003527
Homo sapiens mRNA for protein kinase Dyrk1B.
5.1e-91:445:97
Y17999
- 50 R-NT2RP3003532
Mus musculus cell surface molecule OX-2 mRNA, complete cds.
1.2e-30:529:67
AF004023
- 55 R-nnnnnnnnnnnnn
Homo sapiens PAC clone DJ0531G15 from 7p21, complete sequence.
0.13:294:61
AC004739

EP 1 130 094 A2

- 5 R-NT2RP3003559
CIT-HSP-2307F17.TR CIT-HSP Homo sapiens genomic clone 2307F17, genomic survey sequence.
1.4e-15:342:68
AQ016972
- 10 R-NT2RP3003614
Homo sapiens chromosome 19, cosmid F21967, complete sequence.
0.013:174:64
AC005256
- 15 R-NT2RP3003729
- R-NT2RP3003849
Genomic sequence from Human 9q34, WORKING DRAFT SEQUENCE, 6 unordered pieces.
8.9e-106:557:94
AC002320
- 20 R-NT2RP3003874
Homo sapiens incomplete cDNA for a mutated allele of a myosin class I, myh-1c.
1.6e-55:302:94
AJ001381
- 25 R-NT2RP3003963
cSRL-66f9-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-66f9, genomic
survey sequence.
0.028:78:76
B05608
- 30 R-NT2RP3004000
Tapa-1= integral membrane protein TAPA-1 [mice, B cell lymphoma line 38C13, Genomic, 861 nt, segment 7 of 7].
0.87:212:62
S45012
- 35 R-NT2RP3004025
Homo sapiens chromosome 19, cosmid F17987, complete sequence.
0.71:197:62
AC004790
- 40 R-NT2RP3004075
- R-NT2RP3004083
Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 5.
0.27:375:59
Z97340
- 45 R-NT2RP3004090
CIT-HSP-2172H20.TR CIT-HSP Homo sapiens genomic clone 2172H20, genomic survey sequence.
2.2e-40:243:91
B99962
- 50 R-NT2RP3004119
Homo sapiens PAC clone DJ1059M17 from 7q21-q31.1, complete sequence.
8.3e-42:475:73
AC004953
- 55 R-NT2RP3004130
- R-NT2RP3004133

EP 1 130 094 A2

CIT-HSP-2306G15.TR CIT-HSP Homo sapiens genomic clone 2306G15, genomic survey sequence.
0.00037:194:64
AQ022229

- 5 R-NT2RP3004202
Homo sapiens BAC clone GS285F21 from 7q21-q22, complete sequence.
0.65:209:62
AC004012
- 10 R-NT2RP3004294

R-NT2RP3004309
Homo sapiens Chromosome 11q12.2 PAC clone pDJ519o13 containing human gene for ferritin heavy chain (FTH),
complete sequence.
15 7.4e-99:500:96
AC004228
- 20 R-NT2RP3004321
Human chromosome 11 168h3 cosmid, complete sequence.
20 1.7e-105:540:96
U73637
- 25 R-NT2RP3004345
Human BAC clone RG016J04 from 7q21, complete sequence.
25 0.00033:348:61
AC002064
- 30 R-NT2RP3004355
Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE,
30 3 unordered pieces.
0.0029:180:66
AC004709
- 35 R-NT2RP3004374
Human DNA sequence from clone 1177E19 on chromosome 1p36.12-36.31. Contains the 3' part of the DNA-
binding Zinc finger protein RIZ gene, ESTs, an STS, GSSs and a CpG island, complete sequence.
4.3e-18:223:77
AL031277
- 40 R-NT2RP3004406
Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-70, complete sequence.
1.0:201:62
AL010239
- 45 R-NT2RP3004481

R-NT2RP3004552
Human germline immunoglobulin lambda light chain pseudogene (VII.1).
1.0:165:63
50 X57825
- R-NT2RP3004625
Homo sapiens I-1 receptor candidate protein mRNA, complete cds.
8.2e-49:352:84
55 AF082516
- R-NT2RP3004640
Homo sapiens full length insert cDNA clone ZC45E05.

- 1.2e-96:471:98
AF086205
- 5 R-NT2RP3004647
Homo sapiens mRNA for KIAA0446 protein, complete cds.
1.5e-109:555:96
AB007915
- 10 R-NT2RP4000108
Mouse neurofilament protein (NF-L) gene, 3' flank.
1.0e-09:344:63
M55424
- 15 R-NT2RP4000634
Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence.
1.6e-16:267:71
AC003037
- 20 R-NT2RP4000962
Human DNA sequence from PAC 970D1 on chromosome 1q24. Contains ESTs, STSs and a BAC end-sequence (GSS).
0.026:176:67
AL021069
- 25 R-NT2RP4001001
Drosophila melanogaster Oregon-R mitochondrial A+T region.
0.00026:354:61
U11584
- 30 R-NT2RP4001009
Homo sapiens mRNA for Hs Ste24p, complete cds.
1.6e-82:408:98
AB016068
- 35 R-NT2RP4001467
Human placental cDNA coding for 5'nucleotidase (EC 3.1.3.5).
1.8e-111:545:97
X55740
- 40 R-NT2RP4001877
Yeast (*S.cerevisiae*) mitochondrial cob gene, intron 4.
0.19:384:59
J01469
- 45 R-NT2RP4001879
Homo sapiens full length insert cDNA clone ZD76G10.
4.4e-107:548:94
AF086408
- 50 R-NT2RP4002187
RPCI11-69F22.TK RPCI11 Homo sapiens genomic clone R-69F22, genomic survey sequence.
7.1e-37:240:89
AQ238297
- 55 R-NT2RP4002451
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 111B22, WORKING DRAFT SEQUENCE.
5.8e-111:575:96
Z98200

R-NT2RP4002715

Human Chromosome 11 pac pDJ148f1, WORKING DRAFT SEQUENCE, 27 unordered pieces.

2.5e-61:367:90

AC001232

5

R-NT2RP4002750

Rattus norvegicus mRNA for cationic amino acid transporter 3, complete cds.

1.2e-52:527:74

AB000113

10

R-OVARC1000003

Homo sapiens clone DJ0856O24, WORKING DRAFT SEQUENCE, 4 unordered pieces.

2.3e-10:140:77

AC004909

15

R-OVARC1000090

Homo sapiens genomic DNA, 237 kb segment from 6p21.3 region including HLA genes, WORKING DRAFT SEQUENCE.

2.8e-59:323:78

20

D84394

R-OVARC1000105

H.sapiens gene for ribosomal protein L38.

2.7e-12:83:100

25

Z26876

R-OVARC1000137

R-OVARC1000208

Homo sapiens PAC clone DJ0817I18 from 7p11.2p13, complete sequence.

2.7e-52:464:79

AC004901

30

R-OVARC1000255

H.sapiens syk mRNA for protein-tyrosine kinase.

1.9e-105:511:98

Z29630

35

R-OVARC1000275

40

R-OVARC1000298

Plasmodium falciparum carbamoyl phosphate synthetase II gene, complete cds.

0.66:364:59

L32150

45

R-OVARC1000307

R-OVARC1000313

Homo sapiens mRNA for KIAA0573 protein, partial cds.

50

1.6e-96:534:93

AB011145

R-OVARC1000331

Sequence 2 from patent US 5763589.

55

8.1e-66:335:97

AR012692

R-OVARC1000410

EP 1 130 094 A2

Homo sapiens clone 23767 and 23782 mRNA sequences.
1.0e-88:462:94
AF007150

5 R-OVARC1000439
E.coli fang and fanH genes.
0.99:424:58
Y00531

10 R-OVARC1000467
HS_3235_A2_A12_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3235
Col=24 Row=A, genomic survey sequence.
9.2e-09:125:76
AQ206826

15 R-OVARC1000529

R-OVARC1000553
Homo sapiens chromosome 19, cosmid R26894, complete sequence.
2.0e-84:437:96
AC005594

20 R-OVARC1000775
CIT-HSP-2060P5.TF CIT-HSP Homo sapiens genomic clone 2060P5, genomic survey sequence. 0.29:223:63
B70025

25 R-OVARC1000811
Homo sapiens chromosome 16, cosmid clone 432A1 (LANL), complete sequence.
2.8e-89:438:98
AC004235

30 R-OVARC1000853
RPCI11-16C11.TV RPCI-11 Homo sapiens genomic clone RPCI-11-16C11, genomic survey sequence.
5.3e-53:317:92
B76661

35 R-OVARC1000873
Human DNA sequence from clone 1049G16 on chromosome 20q12-13.2 Contains gene similar to GLU-COSAMINE-6-SULFATASE, a nuclear receptor coactivator gene, ESTs, STSs, GSSs, complete sequence.
1.2e-102:511:97
AL034418

40 R-OVARC1000916
H.sapiens PISSLRE mRNA.
5.8e-111:588:94
X78342

45 R-OVARC1000956
Human DNA sequence from cosmid L241B9, Huntington's Disease Region, chromosome 4p16.3 contains polymorphic VNTR pYNZ32.
2.7e-89:478:94
Z69708

50 R-OVARC1000995
Human DNA sequence from clone 885E17 on chromosome 1p33-34.1. Contains STSs and GSSs and genomic marker D1S1302, complete sequence.
9.5e-46:325:84
AL031294

- 5 R-OVARC1001030
 Homo sapiens neuroendocrine-specific protein C (NSP) mRNA, complete cds.
 1.2e-05:197:63
 L10335
- 10 R-OVARC1001049
- R-OVARC1001086
 Homo sapiens cyclin T2a mRNA, complete cds.
 4.3e-105:569:94
 AF048731
- 15 R-OVARC1001132
 Homo sapiens genomic DNA, chromosome 21q11.1, segment 9/28, WORKING DRAFT SEQUENCE.
 2.2e- 111:569:96
 AP000038
- 20 R-OVARC1001163
 Sus scrofa MHC SLA class III steroid 21-hydroxylase (CYP21) gene, complete cds, ORF human-like gene, last 5 exons.
 0.010:349:60
 M83939
- 25 R-OVARC1001222
 Spiroplasma citri orfa and orff genes, partial cds, orfb, orfc, and orfe genes and Spiroplasma virus SpV1-derived ORF1 and ORF3 genes, complete cds, and SpV1-derived ORF14 gene, partial cds.
 0.58:184:60
 U28972
- 30 R-OVARC1001260
 Homo sapiens clone DJ0856O24, WORKING DRAFT SEQUENCE, 4 unordered pieces.
 1.1e-10:140:78
 AC004909
- 35 R-OVARC1001336
 Homo sapiens clone DJ0856O24, WORKING DRAFT SEQUENCE, 4 unordered pieces.
 2.3e-10:140:77
 AC004909
- 40 R-OVARC1001338
- R-OVARC1001569
- R-OVARC1001570
- 45 R-OVARC1001596
 Homo sapiens chromosome 17, clone hRPK.372_K_20, complete sequence.
 5.9e-47:361:83
 AC005951
- 50 R-OVARC1001607
 Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds.
 3.3e-112:559:96
 U15128
- 55 R-OVARC1001725
 Homo sapiens patched related protein TRC8 (TRC8) gene, exon 1 and partial cds.
 3.9e-56:318:95

EP 1 130 094 A2

AF064800

R-OVARC1001727

5 Human DNA sequence from clone 48A11 on chromosome 20p12 Contains EST, STS, GSS, complete sequence.
6.1e-101:533:94
AL031132

R-OVARC1001807

10 Human TR3 orphan receptor mRNA, complete cds.
2.8e-87:426:97
L13740

R-OVARC1001833

15 Mouse fork head related protein (HNF-3beta) mRNA, complete cds.
1.1e-21:263:76
L10409

R-OVARC1001991

20 H.sapiens chromosome 22 CpG island DNA genomic Mse1 fragment, clone 301e3, reverse read 301e3.r.
0.90:151:59
Z79826

R-OVARC1002058

25 Homo sapiens full length insert cDNA clone ZD58C02.
1.9e-105:547:95
AF088043

R-OVARC1002178

30 Human DNA sequence from clone 267M20 on chromosome Xq22.2-22.3. Contains part of the DIAPH2 gene and
a pseudogene, ESTs, STSs and GSSs, complete sequence.
0.26:429:58
AL031053

R-PLACE1000033

35 Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4
unordered pieces.
0.098:467:59
AC004688

R-PLACE1000231

40 Homo sapiens BAC clone RG060N22 from 7q21, complete sequence.
0.91:141:64
AC003083

R-PLACE1000258

45 Human DNA sequence from clone 710L4 on chromosome Xq11.2-12 Contains part of a gene similar to myotubu-
larin-related protein, EST, STS and GSS, complete sequence.
3.8e-53:524:75
AL034408

R-PLACE1000442

50 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K22F20, complete sequence.
3.0e-07:413:62
AB016873

R-PLACE1000560

55 Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158), complete sequence.
6.3e-59:323:94

AC005368

R-PLACE1000740

H.sapiens PEX gene.

5 0.0065:202:63

Y10196

R-PLACE1000912

10 R-PLACE1000914

Homo sapiens chromosome 17, clone HCIT145P4, WORKING DRAFT SEQUENCE, 8 unordered pieces.

3.4e-68:452:86

AC002093

15 R-PLACE1000927

Cowpox virus strain GRI-90 DNA (49 kb fragment).

1.8e-46:432:76

Y15035

20 R-PLACE1000986

HS_2037_A2_B06_MRC CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2037

Col=12 Row=C, genomic survey sequence.

0.087:48:89

AQ232754

25 R-PLACE1001016

M.fascicularis gene for apolipoprotein A-IV.

0.016:226:61

X68361

30 R-PLACE1001100

Human DNA sequence from PAC 426I6 on chromosome 1p34.1-1p35. Contains NIPP-1-like gene a nuclear inhibitor of protein phosphatase-1, ESTs, and a CA repeat.

3.4e-37:320:80

35 AL020997

R-PLACE1001114

RPCI11-5C23.TV RPCI-11 Homo sapiens genomic clone RPCI-11-5C23, genomic survey sequence.

9.2e-44:173:85

40 B49180

R-PLACE1001123

R-PLACE1001183

45 Plasmodium falciparum MAL3P8, complete sequence.

0.47:217:63

AL034560

R-PLACE1001229

50 Mitochondrion Culex torrentium A+T rich mitochondrial control region.

3.3e-09:356:63

U69573

R-PLACE1001231

55 Rattus norvegicus sodium-dependent multi-vitamin transporter (SMVT) mRNA, complete cds.

1.2e-09:186:72

AF026554

R-PLACE1001340

Homo sapiens mRNA for KIAA0719 protein, complete cds.

2.0e-51:265:98

AB018262

5

R-PLACE1001401

Bactrocera dorsalis strain Tahiti mitochondrial D-loop region, complete sequence.

0.0073:203:60

AF033929

10

R-PLACE1001407

Human DNA sequence from clone 496H19 on chromosome 6q24 Contains ESTs, complete sequence.

5.8e-70:360:96

AL023582

15

R-PLACE1001464

Human placental cDNA coding for 5'nucleotidase (EC 3.1.3.5).

3.1e-90:457:96

X55740

20

R-PLACE1001500

Homo sapiens clone DJ0917G04, WORKING DRAFT SEQUENCE, 35 unordered pieces.

1.0:232:62

AC004929

25

R-PLACE1001516

Homo sapiens Chromosome 16 BAC clone CIT987SK-A-575C2, complete sequence.

1.9e-26:168:88

AC002425

30

R-PLACE1001536

Human Chromosome X clone bWXD187, complete sequence.

6.5e-61:310:98

AC004383

35

R-PLACE1001564

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 287G14, WORKING DRAFT SEQUENCE.

2.9e-100:504:97

40

AL033377

R-PLACE1001655

Homo sapiens Shab-related delayed-rectifier K+ channel alpha subunit (KCNS3) mRNA, complete cds.

3.8e-1 17:578:97

45

AF043472

R-PLACE1001788

Sequence 9 from Patent WO9722695.

1.9e-05:91:82

50

A63556

R-PLACE1001795

R-PLACE1001836

, complete sequence.

4.1e-14:269:69

AC005406

- 5 R-PLACE1001918
Human HepG2 3' region Mbol cDNA, clone hmd4f06m3.
7.3e-25:151:95
D17237
- 10 R-PLACE1001949
Human DNA sequence from PAC 436M11 on chromosome Xp22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the RS1 gene for retinoschisis (X-linked, juvenile) 1 (XLRS1). Contains ESTs, an STS and GSSs, complete sequence.
0.54:165:63
Z94056
- 15 R-PLACE1002080
Homo sapiens chromosome 17, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.
3.7e-60:289:95
AC004150
- 20 R-PLACE1002095
Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-52, complete sequence.
0.00052:422:59
AL008982
- 25 R-PLACE1002153
Homo sapiens TACC2 protein (TACC2) mRNA, partial cds.
4.6e-100:514:95
AF095791
- 30 R-PLACE1002329
Homo sapiens chromosome 19, cosmid R31855, complete sequence.
1.3e-46:257:95
AC005782
- 35 R-PLACE1002355
HS_2057_B1_D01_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2057
Col=1 Row=H, genomic survey sequence.
0.089:132:65
AQ245227
- 40 R-PLACE1002374
Human mRNA for pro-cathepsin L (major excreted protein MEP).
2.6e-101:501:97
X12451
- 45 R-PLACE1002518
HS_2176_A2_D04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone
Plate=2176 Col=8 Row=G, genomic survey sequence.
1.7e-43:221:100
AQ014851
- 50 R-PLACE1002547
Homo sapiens mRNA for KIAA0719 protein, complete cds.
2.0e-53:276:97
AB018262
- 55 R-PLACE1002726
Human DNA-binding protein ABP/ZF mRNA, complete cds.
1.1e-37:212:94
U82613

- 5 R-PLACE1002905
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 215D11, WORKING DRAFT SE-
QUENCE.
1.2e-42:302:86
AL034417
- 10 R-PLACE1002911
- 10 R-PLACE1002967
Homo sapiens chromosome 16, BAC clone 461A8, complete sequence.
2.3e-39:310:82
AC006111
- 15 R-PLACE1003135
Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SE-
QUENCE.
2.2e-07:418:60
AL034557
- 20 R-PLACE1003163
Homo sapiens DBI-related protein mRNA, complete cds.
4.7e-110:547:96
AF069301
- 25 R-PLACE1003407
Homo sapiens putative transmembrane protein (CLN5) mRNA, complete cds.
1.7e-47:287:91
AF068227
- 30 R-PLACE1003428
Human DNA sequence from clone 55C23 on chromosome 6q22.3-23.3 contains vanin-like genes VNN1 and VNN2,
ESTs, GSs, complete sequence.
1.1e-75:268:98
AL032821
- 35 R-PLACE1003438
- 40 R-PLACE1003460
HS_3026_B1_A08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3026
Col=15 Row=B, genomic survey sequence.
0.30:100:69
AQ093523
- 45 R-nnnnnnnnnnnnn
45 Homo sapiens clone DJ0981007, complete sequence.
3.3e-46:135:98
AC006017
- 50 R-PLACE1003573
HS_3079_B2_A02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3079
Col=4 Row=B, genomic survey sequence.
1.1e-49:261:96
AQ121751
- 55 R-PLACE1003598
- R-PLACE1003644
Caenorhabditis elegans cosmid F52H3, complete sequence.

- 0.38:345:62
Z66512
- 5 R-PLACE1003737
Homo sapiens Xp22-83 BAC GS HB-324M7 (Genome Systems Human BAC Library) complete sequence.
1.9e-77:406:96
AC005859
- 10 R-PLACE1003772
Human DNA sequence from PAC 426I6 on chromosome 1p34.1-1p35. Contains NIPP-1-like gene a nuclear inhibitor of protein phosphatase-1, ESTs, and a CA repeat.
2.2e-29:454:70
AL020997
- 15 R-PLACE1003839
Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12, complete sequence.
3.0e-52:272:97
AC004131
- 20 R-PLACE1003845
HS_3219_A1_A10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3219 Col=19 Row=A, genomic survey sequence.
1.5e-13:231:70
AQ181482
- 25 R-PLACE1003852
Homo sapiens mRNA for KIAA0758 protein, partial cds.
6.8e-86:439:96
AB018301
- 30 R-PLACE1004028
- 35 R-PLACE1004078
Homo sapiens 12p13.3 PAC RPCI5-940J5 (Roswell Park Cancer Institute Human PAC Library) complete sequence.
5.0e-36:310:80
AC006064
- 40 R-PLACE1004166
Petromyzon marinus neurofilament subunit NF-180 mRNA, complete cds.
0.95:224:62
U19361
- 45 R-nnnnnnnnnnnnnn
Fugu rubripes GSS sequence, clone 076D01bH10, genomic survey sequence.
3.0e-08:107:77
AL026605
- 50 R-PLACE1004199
Human prostaglandin D2 synthase gene, exons 2 through 6 and complete cds.
0.0028:157:67
M98538
- 55 R-PLACE1004279
Human DNA sequence from PAC 193B12 on chromosome 6p21.3-22.3. Contains histone H2A/d, H2B/d, H2A.i, H1.5, H3.F, H4.k, H3/j genes, histone pH2b.i and hypothetical protein A4 pseudogenes, histone H2A.1 and H2B.2 duplicate genes, Glycine (GGC) tRNA gene, olfactory receptor OL1 like gene, ESTs STSs and predicted CpG islands.

0.00065:228:58

Z98744

R-PLACE1004282

5

R-PLACE1004305

Homo sapiens mRNA for KIAA0740 protein, complete cds.

2.0e-77:377:99

AB018283

10

R-PLACE1004441

RPCI11-76P13.TV RPCI11 Homo sapiens genomic clone R-76P13, genomic survey sequence.

1.8e-73:370:97

AQ281810

15

R-PLACE1004450

Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K24G6, complete sequence.

0.87:269:59

AB012242

20

R-PLACE1004482

Mus musculus hematopoietic lineage switch 2 (HLS2) mRNA, complete cds.

5.2e-33:356:75

AF009513

25

R-PLACE1004492

Mus musculus mRNA for Doc2, partial cds.

4.1e-28:268:77

D50000

30

R-PLACE1004519

Human DNA sequence from clone 24o18 on chromosome 6p21.31-22.2 Contains zinc finger protein pseudogene, VNO-type olfactory receptor pseudogene, nuclear envelope pore membrane protein, EST, STS, GSS, complete sequence.

35

1.8e-14:330:67

AL021808

40

R-PLACE1004520

Human pregnancy specific beta-1-glycoprotein 1 (PSG1) gene.

1.4e-73:397:93

M93705

R-PLACE1004630

45

R-PLACE1004637

Human Chromosome 11 Cosmid cSRL16b6, complete sequence.

5.5e-108:625:91

U73638

50

R-PLACE1004648

R-PLACE1004816

Homo sapiens mRNA for Hakata antigen, complete cds.

5.6e-103:586:90

55

D88587

R-PLACE1004887

CIT-HSP-2172H20.TR CIT-HSP Homo sapiens genomic clone 2172H20, genomic survey sequence.

1.2e-31:177:97

B99962

R-PLACE1005003

5 Mus musculus clone OST13719, genomic survey sequence.

0.0043:159:64

AF046703

R-PLACE1005005

10 Homo sapiens ubiquitin conjugating enzyme G2 (UBE2G2) mRNA, complete cds.

2.1e-56:299:95

AF032456

R-PLACE1005031

15 Homo sapiens chromosome 17, clone hRPK.156_L_14, complete sequence.

1.0:155:65

AC005821

R-PLACE1005239

20 Homo sapiens mRNA for HIRIP3 protein (clone pH4-31, pH4-17).

4.4e-85:450:93

AJ223351

R-PLACE1005250

25 Mus musculus maternal transcript Maid (Maid) mRNA, complete cds.

7.7e-19:232:73

U50734

R-PLACE1005383

30 Homo sapiens UP50 mRNA, complete cds.

2.0e-77:471:88

AF093118

R-PLACE1005410

35 Canis familiaris sec61 homologue mRNA, complete cds.

6.4e-12:132:82

M96629

R-PLACE1005426

40 Human pregnancy specific beta-1-glycoprotein 4 (PSG4) mRNA, complete cds.

2.3e-109:574:94

M94891

R-PLACE1005519

45 Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SEQUENCE.

4.1e-08:426:61

AL034557

50 R-PLACE1005539

R-PLACE1005544

Homo sapiens chromosome 19, cosmid F20887, complete sequence.

1.0e-17:202:73

55 AC005578

R-PLACE1005569

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 159A1, WORKING DRAFT SEQUENCE.

3.8e-89:470:95
AL034397

5 R-PLACE 1005601
Homo Sapiens angiotensin II receptor gene, complete cds.
8.0e-52:301:90
L48211

10 R-PLACE1005660

R-PLACE1005669
Mitochondrion Culex torrentium A+T rich mitochondrial control region.
9.5e-09:338:63
U69573

15 R-PLACE1005682
Caenorhabditis elegans cosmid M70.
0.012:226:62
AF047661

20 R-PLACE1005725
Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y48E1, WORKING DRAFT SE-
QUENCE.
0.42:435:59

25 Z92856

R-PLACE1005736
Rattus norvegicus DD6A4-1 mRNA, partial sequence.
9.0e-21:282:73

30 AF034237

R-PLACE1005745
RPCI11-88L20.TJ RPCI11 Homo sapiens genomic clone R-88L20, genomic survey sequence.
2.4e-62:310:99

35 AQ281511

R-PLACE1005768
Human DNA sequence from Fosmid 24E5 on chromosome 22q11.2-qter contains parvalbumin, ESTs, STS.
5.6e-94:511:93

40 Z82185

R-PLACE1005815
Human Chromosome 16 BAC clone CIT987SK-A-635H12, complete sequence.
9.0e-55:586:73

45 AC002310

R-PLACE1005878

R-PLACE1005927

50 R-PLACE1006071
CIT-HSP-2308A18.TR CIT-HSP Homo sapiens genomic clone 2308A18, genomic survey sequence.
1.6e-76:410:95

55 AQ022149

R-PLACE1006073
Homo sapiens mRNA for glucuronyltransferase I, complete cds.
2.2e-97:513:93

AB009598

R-PLACE1006079

Homo sapiens distal-less homeobox protein (DLX3) gene, complete cds.

5
5.4e-57:333:91
AF028233

R-PLACE1006093

10
R-nnnnnnnnnnnnn
Caenorhabditis elegans mRNA for GAP-2-7, partial cds.
1.9e-08:251:60
AB01128315
R-PLACE1006219
HS_3219_A1_A10_MRCIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3219
Col=19 Row=A, genomic survey sequence.
3.1e-12:228:69
AQ18148220
R-PLACE1006277
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 159A1, WORKING DRAFT SEQUENCE.
7.8e-96:557:91
AL03439725
R-PLACE1006290
Bacillus whitei clone pWH/Cugl satellite DNA.
0.37:209:62
U9015930
R-PLACE1006443
Homo sapiens chromosome 17, clone HCIT145P4, WORKING DRAFT SEQUENCE, 8 unordered pieces.
8.9e-76:451:91
AC00209335
R-PLACE1006515
Homo sapiens mRNA for KIAA0576 protein, partial cds.
2.1e-76:413:94
AB01114840
R-PLACE1006716
M.musculus gene encoding prostaglandin D synthase, putative.
1.0:199:59
Y1013845
R-PLACE1006786
HS_2037_A2_B06_MRCIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2037
Col=12 Row=C, genomic survey sequence.
0.33:47:91
AQ23275450
R-PLACE1006809
Homo sapiens Xq28 genomic DNA in the region of the L1CAM locus containing the genes for neural cell adhesion molecule L1 (L1CAM), arginine-vasopressin receptor (AVPR2), C1 p115 (C1), ARD1 N-acetyltransferase related protein (TE2), renin-binding protein (RbP), host cell factor 1 (HCF1), and interleukin-1 receptor-associated kinase (IRAK) genes, complete cds, and Xq28lu2 gene.
0.67:241:59
U52112

EP 1 130 094 A2

- R-PLACE1006959
- R-PLACE1007028
- 5 R-PLACE1007040
Rabbit angiotensin-converting enzyrne (ACE-P) gene, 5' end.
0.0037:208:65
M58579
- 10 R-PLACE1007077
CIT-HSP-2308A18.TR CIT-HSP Homo sapiens genomic clone 2308A18, genomic survey sequence.
3.0e-76:411:94
AQ022149
- 15 R-PLACE1007081
RPCI11-31D7.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-31D7, genomic survey sequence.
1.9e-06:88:84
AQ016433
- 20 R-PLACE1007096
H.sapiens DMD gene microsatellite (147-200bp).
1.0:142:59
X77677
- 25 R-PLACE1007296
- R-PLACE1007591
Human DNA sequence from clone 113J7 on chromosome Xp11.22-11.4. Contains part of a putative Homeobox
(pseudo?) gene, ESTs and an STS, complete sequence.
- 30 1.6e-11:203:66
AL023574
- R-PLACE1007626
Homo sapiens unknown mRNA, complete cds.
- 35 4.9e-29:183:91
AF047439
- R-PLACE1007702
Homo sapiens chromosome 17, clone 363G12, WORKING DRAFT SEQUENCE, 11 unordered pieces.
- 40 2.3e-75:445:90
AC002348
- R-PLACE1007845
CIT-HSP-2306G15.TR CIT-HSP Homo sapiens genomic clone 2306G15, genomic survey sequence.
- 45 0.00045:194:64
AQ022229
- R-PLACE1007881
CITBI-E1-2503C21.TF CITBI-E1 Homo sapiens genomic clone 2503C21, genomic survey sequence.
- 50 0.43:104:69
AQ263355
- R-PLACE1007971
- 55 R-PLACE1008282
Homo sapiens clone DJ0042M02, WORKING DRAFT SEQUENCE, 20 unordered pieces.
7.7e-73:396:94
AC005995

- 5 R-PLACE1008297
N.frontalis enolase gene, promotor region.
1.2e-08:457:57
X81451
- 10 R-PLACE1008359
Plasmodium falciparum MAL3P1, complete sequence.
0.00044:443:56
Z97348
- 15 R-PLACE1008469
Homo sapiens chromosome 17, clone HCIT145P4, WORKING DRAFT SEQUENCE, 8 unordered pieces.
4.4e-78:536:84
AC002093
- 20 R-PLACE1008549
Mus musculus E74-like factor 5 (Elf5) mRNA, complete cds.
3.4e-30:256:75
AF049702
- 25 R-PLACE1008657
Homo sapiens BAC clone GS067A24 from 7q21.q21.2, complete sequence.
1.9e-40:320:82
AC005009
- 30 R-PLACE1008716
Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds.
8.2e-118:591:96
U15128
- 35 R-PLACE1008744
Sequence 1 from patent US 5691147.
3.1e-108:559:94
I76197
- 40 R-PLACE1008984
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 167A19, WORKING DRAFT SE-
QUENCE.
1.6e-102:503:96
AL031427
- 45 R-PLACE1008985
Mus musculus synaptotagmin VIII mRNA, partial cds.
9.7e-29:255:77
U20107
- R-PLACE1009067
- 50 R-PLACE1009196
Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y48A6, WORKING DRAFT SE-
QUENCE.
0.0094:206:65
Z92854
- 55 R-PLACE1009279
Homo sapiens serine protease (PRSS11) mRNA, partial cds.
2.4e-26:553:62
AF097709

- 5 R-PLACE1009527
Human DNA-binding protein ABP/ZF mRNA, complete cds.
7.9e-91:497:91
U82613
- 10 R-PLACE1009546
Human PAC clone DJ218B13 from Xq23, complete sequence.
0.29:147:64
AC002072
- 15 R-PLACE1009600
Mouse mRNA for tetracycline transporter-like protein, complete cds.
6.1e-81:466:90
D88315
- 20 R-PLACE1009735
Homo sapiens clone NH0523H20, complete sequence.
2.0e-74:268:99
AC005041
- 25 R-nnnnnnnnnnnnnn
Homo sapiens DNA sequence from PAC 833B2 on chromosome Xq26.1-27.2. Contains an EST, complete sequence.
1.9e-05:255:65
AL023800
- 30 R-PLACE1010011
, complete sequence.
2.9e-77:174:100
AC005409
- 35 R-PLACE1010078
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 209H1, WORKING DRAFT SEQUENCE.
1.0:108:65
Z84465
- 40 R-PLACE1010081
Homo sapiens serine/threonine kinase RICK (RICK) mRNA, complete cds.
9.2e-105:560:93
AF027706
- 45 R-PLACE1010251
Plasmodium falciparum MAL3P4, complete sequence.
5.0e-07:468:58
AL008970
- 50 R-PLACE1010445
Pan troglodytes HS19.8-similar locus and Y Alu element, genomic survey sequence.
1.2e-49:303:90
AF077058
- 55 R-PLACE1010713
RPCI11-69F22.TK RPCI11 Homo sapiens genomic clone R-69F22, genomic survey sequence.
7.4e-11:114:80
AQ238297
- R-PLACE1010784
Capra hircus strain Saanen, genomic survey sequence.

- 7.4e-24:182:87
AF083406
- 5 R-PLACE1010827
nbxb0026K23f CUGI Rice BAC Library Oryza sativa genomic clone nbxb0026K23f, genomic survey sequence.
1.0:252:61
AQ271546
- 10 R-PLACE1010968
Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5
unordered pieces.
0.0038:295:57
AC005308
- 15 R-PLACE1011045
Homo sapiens E1-like protein mRNA, complete cds.
1.6e-90:453:96
AF094516
- 20 R-PLACE1011116
Homo sapiens embryonic lung protein (HUEL) mRNA, complete cds.
4.6e-72:385:94
AF006621
- 25 R-PLACE1011236
*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0289H06; HTGS phase 1,
WORKING DRAFT SEQUENCE, 4 unordered pieces.
0.98:142:65
AC004580
- 30 R-PLACE1011364
- R-PLACE1011407
Human DNA sequence from clone 127F18 on chromosome Xp11.4-21.3. Contains part of a novel gene with some
similarity to parts of chicken Myosin Light Chain and various species' Interleukin-1 Receptor Type 1 (IL1-R-1).
Contains GSSs, complete sequence.
9.1e-27:293:74
AL031575
- 40 R-PLACE1011516
Fugu rubripes GSS sequence, clone 190N14aC12, genomic survey sequence.
1.0:96:68
AL030602
- 45 R-PLACE1011708
Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds.
2.4e-91:521:91
AF034611
- 50 R-PLACE1011824
Figure 6. DNA sequence of three 3'apoB VNTR alleles.
2.2e-06:264:65
M23046
- 55 R-PLACE1011978
Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.
4.8e-50:553:69
M27877

- 5 R-PLACE2000118
Homo sapiens DNA sequence from PAC 393P12 on chromosome Xp11.21. Contains a hypothetical protein KIAA0413 (KIAA0412, KIAA0065, KIAA0569) LIKE Zinc Finger protein pseudogene, a hypothetical Proline-rich protein KIAA0269 LIKE gene and a 60S Ribosomal Protein L7 LIKE pseudogene. Contains ESTs, an STS and a GSS (BAC end sequence), complete sequence.
3.9e-107:567:94
AL022578
- 10 R-PLACE2000219
Homo sapiens clone RG132J19, complete sequence.
4.7e-39:317:82
AC005163
- 15 R-PLACE3000181
Human protocadherin 42 mRNA, 3' end of cds for alternative splicing PC42-8.
3.9e-81:441:94
L11369
- 20 R-PLACE3000213
Sequence 1 from patent US 5691147.
1.5e-109:559:95
I76197
- 25 R-PLACE4000354
Sequence 1 from patent US 5691147.
2.7e-106:548:95
I76197
- 30 R-PLACE4000455
Arabidopsis thaliana genomic DNA chromosome 3, P1 clone: MEBS, complete sequence.
9.3e-07:357:60
AB019230
- 35 R-THYRO1000036
Sequence 11 from patent US 5773248.
4.0e-99:527:93
AR014074
- 40 R-THYRO1000061
Homo sapiens chromosome 19, cosmid R34382, complete sequence.
7.3e-90:460:96
AC005329
- 45 R-THYRO1000099
R-THYRO1000196
Homo sapiens Ksp-cadherin (CDH16) mRNA, complete cds.
1.1e-104:530:96
AF016272
- 50 R-THYRO1000400
Homo sapiens Chromosome 16 BAC clone CIT987SK-A-233A8, complete sequence.
1.0:308:61
AC004685
- 55 R-THYRO1000580
Human Kox26 mRNA for zinc finger protein, partial.
0.11:105:67

X52357

R-THYRO1000584

*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0539L10; HTGS phase 1,
WORKING DRAFT SEQUENCE, 15 unordered pieces.

5 1.4e-14:241:68

AC004480

R-THYRO1000678

10 Belonogaster petiolata 16S ribosomal RNA gene, mitochondrial gene for mitochondrial rRNA, partial sequence.

0.049:150:64

AF066910

R-THYRO1000776

15 CITBI-E1-2505N5.TF.1 CITBI-E1 Homo sapiens genomic clone 2505N5, genomic survey sequence.

0.38:179:63

AQ241670

R-THYRO1000795

20

R-THYRO1000846

Homo sapiens hJAG2.del-E6 (JAG2) mRNA, alternatively spliced isoform of Jagged2, complete cds.

3.6e-06:425:61

AF029779

25

R-THYRO1000866

Homo sapiens SKB1Hs mRNA, complete cds.

4.0e-42:251:92

AF015913

30

R-THYRO1000956

R-THYRO1000964

35 Human Chromosome 11 Cosmid cSRL186g7, complete sequence.

0.18:292:61

U73627

R-THYRO1000999

40 CIT-HSP-2288E24.TR CIT-HSP Homo sapiens genomic clone 2288E24, genomic survey sequence.

3.6e-18:292:71

AQ002356

R-THYRO1001063

45 Homo sapiens chromosome 16 BAC clone CIT987SK-381E11 complete sequence.

1.5e-27:292:76

AF001552

R-THYRO1001071

50 Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 37E16, WORKING DRAFT SEQUENCE.

1.7e-105:513:98

Z83844

R-THYRO1001102

55 Homo sapiens clone DJ0539M06, WORKING DRAFT SEQUENCE, 10 unordered pieces.

3.2e-62:429:86

AC004832

R-THYRO1001113

EP 1 130 094 A2

- Caenorhabditis elegans cosmid C25F9, complete sequence.
0.026:338:58
Z81476
- 5 R-THYRO1001128
Homo sapiens chromosome 9q34, clone 63G10, complete sequence.
5.3e-12:132:79
AC002096
- 10 R-THYRO1001205
Homo sapiens clone DJ1173I20, WORKING DRAFT SEQUENCE, 5 unordered pieces.
1.9e-60:251:85
AC004987
- 15 R-THYRO1001237
- R-THYRO1001242
Mouse mRNA for thymic epithelial cell surface antigen, complete cds.
1.5e-45:525:75
- 20 D67067
- R-THYRO1001266
H.sapiens DNA containing a polymorphic (CA)n repeat (436bp).
6.0e-05:258:67
- 25 X65457
- R-THYRO1001327
Human DNA sequence from clone 453C12 on chromosome 20q12-13.12 Contains SDC4 (syndecan 4 (amphiglycan, ryudocan)) predicts a gene like the mouse transcription factor RBP-L, MATN4 (matrilin-4) STS, GSS, CpG island, complete sequence.
2.8e-104:541:95
AL021578
- 30
- 35 R-THYRO1001456
- R-THYRO1001457
H.sapiens mRNA for protein kinase C mu.
2.9e-23:391:66
X75756
- 40 R-THYRO1001471
Homo sapiens Chromosome 16 BAC clone CIT987SK-A-952F10, complete sequence.
0.39:271:61
AC004787
- 45 R-THYRO1001478
- R-THYRO1001495
Homo sapiens clone DJ0813F11, WORKING DRAFT SEQUENCE, 5 unordered pieces.
2.8e-88:446:88
AC006006
- 50
- 55 R-THYRO1001523
CIT-HSP-2333F9.TF CIT-HSP Homo sapiens genomic clone 2333F9, genomic survey sequence.
1.4e-05:126:71
AQ039390
- R-THYR01001529

EP 1 130 094 A2

R-THYRO1001593

Homo sapiens chromosome 19, cosmid R33632, complete sequence.

3.7e-100:514:96

AC005781

5

R-THYRO1001608

Homo sapiens clone DJ0635O05, WORKING DRAFT SEQUENCE, 7 unordered pieces.

2.3e-40:369:79

AC004845

10

R-THYRO1001641

Homo sapiens clone 24448 unknown mRNA, partial cds.

3.4e-110:562:96

AF070638

15

R-THYRO1001700

R-THYRO1001702

Mus musculus mRNA for myeloid associated differentiation protein.

20

1.1e-11:367:66

AJ001616

25

R-THYRO1001725

Homo sapiens, clone hRPK.1_A_1, complete sequence.

30

9.1e-12:329:65

AC006196

35

R-THYRO1001770

Homo sapiens PAC clone DJ0755G17 from 7p21-p22, complete sequence.

40

0.12:339:59

AC004879

45

R-THYRO1001803

50

R-Y79AA1000030

Homo sapiens chromosome 5, BAC clone 319C17 (LBNL H159), complete sequence.

2.0e-98:515:95

AC005214

55

R-Y79AA1000127

Homo sapiens genomic DNA, chromosome 21q11.1, segment 5/28, WORKING DRAFT SEQUENCE.

3.2e-115:551:99

AP000034

60

R-Y79AA1000207

Homo sapiens chromosome 17, clone hRPK.271_K_11, complete sequence.

1.8e-38:282:85

AC005562

65

R-Y79AA1000226

Homo sapiens full length insert cDNA YN52F10.

4.8e-09:104:85

AF075033

70

R-Y79AA1000270

Human mRNA for ORF, Xq terminal portion.

1.0e-105:564:93

D16469

EP 1 130 094 A2

- 5 R-Y79AA1000426
Rattus norvegicus activin beta E mRNA, complete cds.
6.1e-50:562:72
AF089825
- 10 R-Y79AA1000521
Rattus norvegicus steroid sulfatase (Sts) mRNA, complete cds.
0.48:233:62
U37138
- 15 R-Y79AA1000750
Human DNA from cosmid f23280 from chromosome 19q13.2, genomic sequence.
6.8e-07:320:60
L47334
- 20 R-Y79AA1000777
Homo sapiens full length insert cDNA clone ZD93D10.
2.9e-110:574:95
AF088072
- 25 R-Y79AA1000876
Mus musculus bone morphogenetic protein-6 (BMP-6) gene, exons 6 and 7 and complete cds.
0.0096:105:71
U73520
- 30 R-Y79AA1000959
Homo sapiens Hsp70 binding protein HspBP1 mRNA, complete cds.
1.0e-78:453:92
AF093420
- 35 R-Y79AA1000967
Rattus norvegicus vesicula-associate calmodulin-binding protein mRNA, complete cds.
2.3e-43:263:84
L22557
- 40 R-Y79AA1001013
- 45 R-Y79AA1001056
Mus musculus maternal transcript Maid (Maid) mRNA, complete cds.
1.5e-22:269:73
U50734
- 50 R-Y79AA1001062
D.teissieri mitochondrial DNA for tRNA-fmet, tRNA-Ile, tRNA-Gln & tRNA-Val.
1.1e-07:494:57
X54011
- 55 R-Y79AA1001090
Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.
1.2e-26:269:77
AC002300
- R-Y79AA1001212
Homo sapiens SL15 protein mRNA, complete cds.
5.7e-82:407:97
AF038961

EP 1 130 094 A2

5 R-Y79AA1001264
HS_2195_A2_A07_MRCIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2195
Col=14 Row=A, genomic survey sequence.
3.4e-07:101:82
AQ191092

10 R-Y79AA1001272
Hansenula wingei mitochondrial DNA, complete sequence.
2.1e-05:435:60
D31785

15 R-Y79AA1001328
Rattus norvegicus Delta 3 mRNA, complete cds.
1.0e-29:356:72
AF084576

20 R-Y79AA1001426

25 R-Y79AA1001430
Homo sapiens mRNA for KIAA0469 protein, complete cds.
6.2e-111:555:96
AB007938

30 R-Y79AA1001523
Homo sapiens DNA sequence from PAC 418A9 on chromosome 6q21. Contains the first (5') two exons of a CDK8 (Cell Division Protein Kinase 8) LIKE gene, a Neutral Calponin LIKE pseudogene, ESTs and STSs, complete sequence.
3.7e-71:259:90
Z84480

35 R-Y79AA1001530
Human beta-tubulin gene (5-beta) with ten Alu family members.
2.6e-56:301:96
X00734

40 R-Y79AA1001592
HS_2175_A2_B11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2175
Col=22 Row=C, genomic survey sequence.
1.0:237:59
AQ307634

45 R-Y79AA1001727

50 R-Y79AA1001787
Homo sapiens mRNA for putative ATPase, partial.
7.2e-80:405:97
AJ009947

55 R-Y79AA1001795
Human DNA sequence from clone 1033B10 on chromosome 6p21.2-21.31. Contains the BING5 gene, exons 11 to 15 of the BING4 gene, the gene for GalT3 (beta3-Galactosyltransferase), the RPS18 (40S ribosomal protein S18) gene, the SACM2L (suppressor of actin mutation 2, yeast, homolog) gene, a pseudogene similar to TAT-SF1, a Pseudogene similar to zinc finger genes, the RING1 gene, the gene for HKE6 (RING2), the gene for HKE4 (RING5), the RXRB (Retinoid X receptor beta) gene, the COL11A2 (collagen, type XI, alpha 2) gene, the HLA-DPB2 pseudogene and part of the HLA-DPA3 pseudogene. Contains predicted CpG islands, ESTs, STSs, and GSSs, complete sequence.
4.2e-110:555:97
AL031228

- R-Y79AA1001799
- 5 R-Y79AA1001803
Rattus norvegicus secretogranin III (SgIII) mRNA, complete cds.
6.2e-60:499:77
U02983
- 10 R-Y79AA1001863
Human DNA sequence from PAC 365E2 on chromosome 6p22.3-24.1. Contains EST and STS.
1.4e-45:261:75
AL009177
- 15 R-Y79AA1002022
H.sapiens mRNA for basement membrane heparan sulfate proteoglycan.
1.0:311:61
X62515
- 20 R-nnnnnnnnnnnnn
Plasmodium falciparum chromosome 2, section 18 of 73 of the complete sequence.
1.0:208:62
AE001381
- 25 R-nnnnnnnnnnnnn
Homo sapiens DNA, trinucleotide repeats region, clone CAG83.
0.17:132:67
AB018494
- 30 R-Y79AA1002213
Human DNA sequence from PAC 340G1 on chromosome 6 contains STS.
5.6e-46:490:73
Z84719
- 35 R-Y79AA1002334
Japanese Quail (*C. coturnix*) troponin T isoform mRNA, clone cC501.
0.96:210:63
M26599
- 40 R-Y79AA1002373
Human BAC clone RG126M09 from 7q21-q22, complete sequence.
9.7e-82:544:85
AC002067
- 45 R-Y79AA1002376
Human mitochondrial DNA, fragment M1, encoding transfer RNAs, cytochrome oxidase I, and 2 URFs.
1.9e-111:546:97
M10546
- 50 R-Y79AA1002378
Mus musculus mRNA for zinc finger protein, complete cds, clone:CTfin51.
1.5e-33:244:74
D10630
- 55 R-Y79AA1002381
Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains the SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete sequence.
0.0046:177:68
Z95152

Homology search result 8.

[0300] The result of the homology search in the Human Unigene(<http://www.ncbi.nlm.nih.gov/UniGene>) using the clone sequences of the 5'-ends.

5 Indicated are from the top,
the name of the clone sequence,
title of the top hit data,
the P-value: the length of the sequence used for comparison (nucleotide):similarity (%),
10 the Accession No. of the top hit data.

[0301] Data were not shown for the clones in which the P-value was higher than 1.

15 F-BNGH41000020
ESTs
6.6e-72:412:92
Hs.153375:AI287812

20 F-BNGH41000087
Homo sapiens mRNA for MIFR-1, complete cds
0.027:499:57
Hs.58269:AB010962

25 F-BNGH41000091
Homo sapiens voltage-gated potassium channel eag (EAG) mRNA, complete cds
5.2e-81:687:76
Hs.158305:AJ001366

30 F-HEMBA1000006
ESTs, Weakly similar to HYPOTHETICAL 51.2 KD PROTEIN IN LAG1-RPL14B INTERGENIC REGION [S.cerevisiae]
2.0e-25:167:91
Hs.9252:R53360

35 F-HEMBA1000121
ESTs, Moderately similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III [Caenorhabditis elegans]
3.0e-34:180:98
Hs.149509:N24022

40 F-HEMBA1000128
EST
0.00069:177:62
Hs.158854:AI377837

45 F-HEMBA1000275
Human modulator recognition factor I (MRF-1) mRNA, 3'end
0.012:508:58
Hs.920:M62324

50 F-HEMBA1000300
Human mRNA for KIAA0355 gene, complete cds
1.6e-46:402:78
Hs.153014:AB002353

55 F-HEMBA1000349
EST
6.7e-08:65:95

Hs.54372:N80032

- 5 F-HEMBA1000443
ESTs
6.1e-23:278:76
Hs.69492:AA116026
- 10 F-HEMBA1000462
- 15 F-HEMBA1000477
ESTs
6.9e-78:414:94
Hs.152861:AA287444
- 20 F-HEMBA1000590
Homo sapiens mRNA for matrilin-4, partial
7.3e-95:482:96
Hs.129361:AJ007581
- 25 F-HEMBA1000634
ESTs
1.3e-38:246:86
Hs.6145:W26640
- 30 F-HEMBA1000671
Zinc finger protein 140 (clone pHZ-39)
2.4e-53:469:68
Hs.154205:U09368
- 35 F-HEMBA1000713
Homo sapiens 10kD protein (BC10) mRNA, complete cds
2.1e-127:442:97
Hs.5300:AF053470
- 40 F-HEMBA1000732
Homo sapiens latent transforming growth factor-beta binding protein 4S mRNA, complete cds
1.0e-45:258:94
Hs.85087:AF051344
- 45 F-HEMBA1000745
Human cardiotrophin-1 (CTF1) mRNA, complete cds
1.1e-07:316:61
Hs.25537:U43030
- 50 F-HEMBA1000835
ESTs
4.2e-11:188:72
Hs.116265:AI184988
- 55 F-HEMBA1000875
Zinc finger protein 133 (clone pHZ-13)
1.5e-27:169:93
Hs.78434:U09366
- F-HEMBA1000907
Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds
1.3e-06:545:60
Hs.143551:AF048693

- 5 F-HEMBA1000940
 Homo sapiens connexin46.6 (Cx46.6) gene, complete cds
 4.1e-18:307:66
 Hs.100072:AF014643
- 10 F-HEMBA1000962
 Homo sapiens mRNA for MEGF8, partial cds
 0.0018:391:62
 Hs.158200:AB011541
- 15 F-HEMBA1001184
 Homo sapiens SH3 domain binding glutamic acid-rich-like protein (SH3BGRL) mRNA, complete cds
 2.7e-24:404:67
 Hs.14368:AF042081
- 20 F-HEMBA1001221
 Human transmembrane protein mRNA, complete cds
 7.7e-44:858:63
 Hs.78531:U19878
- 25 F-HEMBA1001228
 Human germline oligomeric matrix protein (COMP) mRNA, complete cds
 2.2e-85:463:93
 Hs.1584:AC003107
- 30 F-HEMBA1001272
 Antidiuretic hormone receptor
 0.064:616:57
 Hs.2524:L22206
- 35 F-HEMBA1001296
 Homo sapiens delta-catenin mRNA, complete cds
 0.031:410:59
 Hs.80220:U96136
- 40 F-HEMBA1001297
 Homo sapiens putative transcription factor CA150 mRNA, complete cds
 3.0e-15:143:81
 Hs.13063:AF017789
- 45 F-HEMBA1001390
 ESTs, Highly similar to polymerase I-transcript release factor [M.musculus]
 1.6e-49:297:91
 Hs.25581:AI246284
- 50 F-HEMBA1001563
 ESTs
 4.9e-12:160:74
 Hs.162813:AA524616
- 55 F-HEMBA1001621
 Human P2U nucleotide receptor mRNA, complete cds
 0.00098:314:61
 Hs.339:U07225
- F-HEMBA1001878
 Homo sapiens U5 snRNP-specific 40 kDa protein mRNA, complete cds
 3.4e-172:810:98

- Hs.10290:AF090988
- 5 F-HEMBA1001886
Human repressor transcriptional factor (ZNF85) mRNA, complete cds
1.1e-115:849:80
Hs.37138:U35376
- 10 F-HEMBA1002048
Homo sapiens mRNA for APC 2 protein, complete cds
0.96:266:62
Hs.20912:AB012162
- 15 F-HEMBA1002131
Homo sapiens mRNA for KIAA0584 protein, partial cds
1.1e-45:709:66
Hs.106794:AB011156
- 20 F-HEMBA1002163
ASPARTYL-TRNA SYNTHETASE
0.026:568:58
Hs.80758:J05032
- 25 F-HEMBA1002164
Pregnancy-associated plasma protein A
0.0049:274:60
Hs.158229:U28727
- F-HEMBA1002167
- 30 F-HEMBA1002178
Homo sapiens mRNA for KIAA0584 protein, partial cds
8.3e-48:794:65
Hs.106794:AB011156
- 35 F-HEMBA1002195
EST
2.0e-05:177:70
Hs.145935:AI275921
- 40 F-HEMBA1002227
Myristoylated alanine-rich C-kinase substrate
1.2e-138:382:95
Hs.75607:D10522
- 45 F-HEMBA1002239
Homo sapiens mRNA, chromosome I specific transcript KIAA0488
1.2e-47:570:71
Hs.67619:AB007957
- 50 F-HEMBA1002316
EST
1.8e-28:246:79
Hs.136950:AA825638
- 55 F-HEMBA1002420
Homo sapiens GABA-B receptor mRNA, complete cds
1.7e-05:303:63
Hs.12307:AF056085

EP 1 130 094 A2

5 F-HEMBA1002421
Syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan)
4.3e-167:778:98
Hs.1501:J04621

10 F-HEMBA1002524
Human MHC Class I region proline rich protein mRNA, complete cds
8.5e-128:751:89
Hs.41548:U63336

15 F-HEMBA1002551
ESTs
2.4e-25:207:84
Hs.158172:N24325

20 F-HEMBA1002767
Homo sapiens chromosome 1p33-p34 beta-1,4-galactosyltransferase mRNA, complete cds
4.4e-170:798:98
Hs.19154:AF038660

25 F-HEMBA1002985
ESTs
2.6e-09:124:76
Hs.118620:T60326

30 F-HEMBA1002992
ESTs
2.4e-21:121:97
Hs.143571:AI089396

35 F-HEMBA1003047
Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds
1.5e-188:873:99
Hs.148318:AF034611

40 F-HEMBA1003072
ESTs
1.2e-33:387:71
Hs.59628:W91959

45 F-HEMBA1003101
Homo sapiens tyrosylprotein sulfotransferase-2 mRNA, complete cds
1.7e-140:671:98
Hs.26350:AF049891

50 F-HEMBA1003120
Zinc finger protein 91 (HPF7, HTF10)
1.0e-24:143:76
Hs.8597:L11672

55 F-HEMBA1003230
Homo sapiens UP50 mRNA, complete cds
1.8e-184:856:98
Hs.11494:AF093118

F-HEMBA1003294
Human antisecretory factor-1 mRNA, complete cds
5.1e-45:324:83

- Hs.148495:AF050199
- 5 F-HEMBA1003315
Homo sapiens mRNA for TIP49, complete cds
4.2e-19:377:64
Hs.155541:AF070735
- 10 F-HEMBA1003392
Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds
9.2e-185:851:99
Hs.23672:AF074264
- 15 F-HEMBA1003399
H.sapiens BDP1 mRNA for protein-tyrosine-phosphatase
0.00042:297:61
Hs.118929:X79568
- 20 F-HEMBA1003487
Homo sapiens receptor for viral semaphorin protein (VESPR) mRNA, complete cds
0.0011:237:63
Hs.88145:AF030339
- 25 F-HEMBA1003497
ESTs, Weakly similar to similar to zinc finger 5 protein from Gallus gallus, U51640 [H.sapiens]
2.5e-09:303:63
Hs.143723:H86048
- 30 F-HEMBA1003530
Homo sapiens mRNA for ephrin-A2
0.024:396:60
Hs.158306:AJ007292
- 35 F-HEMBA1003602
Homo sapiens DNA from chromosome 19, cosmid R29144
0.0072:663:57
Hs.155647:AC004221
- 40 F-HEMBA1003732
ESTs
1.0e-106:494:100
Hs.157568:AI356515
- 45 F-HEMBA1003945
Homo sapiens clone 638 unknown rRNA, complete sequence
5.9e-78:310:93
Hs.159515:AF091085
- 50 F-HEMBA1004007
PROTO-ONCOGENE TYROSINE-PROTEIN KINASE SRC
0.56:165:64
Hs.115742:AF077754
- 55 F-HEMBA1004067
Fatty acid synthase {3' region} [human, breast and HepG2 cells, mRNA Partial, 2237 nt]
0.048:581:58
Hs.83190:U29344
- F-HEMBA1004085

- ESTs
1.7e-15:92:98
Hs.98138:AI183561
- 5 F-HEMBA1004110
Homo sapiens intersectin short form mRNA, complete cds
1.2e-159:779:96
Hs.66392:AF064244
- 10 F-HEMBA1004250
Human mRNA for KIAA0327 protein, complete cds
2.1e-23:676:59
Hs.149323:AB002325
- 15 F-HEMBA1004391
NEURAL CELL ADHESION MOLECULE L1 PRECURSOR
0.43:157:63
Hs.1757:U52112
- 20 F-HEMBA1004444
H.sapiens mRNA for gp25L2 protein
1.5e-54:544:73
Hs.159569:X90872
- 25 F-HEMBA1004454
Homo sapiens tetraspan NET-4 mRNA, complete cds
1.1e-05:230:62
Hs.20709:AF065389
- 30 F-HEMBA1004505
ESTs
9.1e-61:345:93
Hs.4814:AA631254
- 35 F-HEMBA1004785
Homo sapiens Polycomb 2 homolog (hPc2) mRNA, complete cds
3.7e-18:294:65
Hs.123085:AF013956
- 40 F-HEMBA1004797
ESTs
3.9e-06:107:73
Hs.42302:AI032142
- 45 F-HEMBA1004952
Human cardiotrophin-1 (CTF1) mRNA, complete cds
0.00021:175:68
Hs.25537:U43030
- 50 F-HEMBA1004971
F-HEMBA1004982
Human metabotropic glutamate receptor 8 mRNA, complete cds
0.31:288:60
Hs.86204:U92459
- F-HEMBA1005070
Human mRNA for KIAA0310 gene, complete cds

7.9e-67:370:93
Hs.5716:AB002308

5 F-HEMBA1005084
Homo sapiens mRNA for KIAA0612 protein, partial cds
0.00022:400:59
Hs.112499:AB014512

10 F-HEMBA1005145
Lymphocyte-activation gene 3
3.4e-05:480:59
Hs.74011:X51985

15 F-HEMBA1005230
ESTs
2.3e-103:481:99
Hs.135112:AI090827

20 F-HEMBA1005246
Homo sapiens ALR mRNA, complete cds
2.0e-05:220:62
Hs.153638:AF010403

25 F-HEMBA1005267
ESTs
5.6e-16:305:64
Hs.125699:AA868017

30 F-HEMBA1005337
EST
2.1e-59:304:97
Hs.48956:N64339

35 F-HEMBA1005430
ESTs
6.9e-19:333:65
Hs.116567:AI332643

40 F-HEMBA1005449
Human plectin (PLEC1) mRNA, complete cds
0.026:576:56
Hs.79706:U53204

45 F-HEMBA1005489
Homo sapiens mRNA for KIAA0291 gene, partial cds
0.14:551:59
Hs.104717:AB006629

50 F-HEMBA1005522
COAGULATION FACTOR VII PRECURSOR
1.8e-12:298:64
Hs.36989:M13232

55 F-HEMBA1005545
MUSCARINIC ACETYLCHOLINE RECEPTOR M3
2.6e-143:672:98
Hs.7138:U29589

5 F-HEMBA1005698
ESTs
1.8e-124:611:97
Hs.144441:AI338335

10 F-HEMBA1005913
F-HEMBA1005929
H.sapiens mRNA for serine/threonine protein kinase EMK
1.5e-86:847:72
Hs.157199:X97630

15 F-HEMBA1005945
ESTs, Weakly similar to F17E5.2 [C.elegans]
4.2e-26:159:92
Hs.126571:AI038963

20 F-HEMBA1006016
ESTs
1.3e-22:145:93
Hs.33728:H97503

F-HEMBA1006171

25 F-HEMBA1006276
Homo sapiens KIAA0412 mRNA, partial cds
5.1e-19:371:65
Hs.6200:AB007872

30 F-HEMBA1006299
F-HEMBA1006311

35 F-HEMBA1006335
ESTs
0.00021:327:62
Hs.146044:AI089998

40 F-HEMBA1006357
Homo sapiens secretory carrier membrane protein (SCAMP2) mRNA, complete cds
7.4e-28:389:67
Hs.10761:AF005038

45 F-HEMBA1006430
ESTs
9.7e-92:463:95
Hs.143702:AI084062

50 F-HEMBA1006482
Homo sapiens h-sco1 (SCO1) mRNA, nuclear gene encoding mitochondrial protein, complete cds
6.2e-146:575:98
Hs.14511:AF026852

55 F-HEMBA1006517
ESTs
3.6e-63:381:87
Hs.11611:W21919

- 5 F-HEMBA1006544
 Homo sapiens suppressor of white apricot homolog 2 (SWAP2) mRNA, complete cds
 2.0e-50:503:76
 Hs.43543:AF042800
- 10 F-HEMBA1006572
 Calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
 0.031:611:57
 Hs.96253:U79666
- 15 F-HEMBA1006658
 Homo sapiens mRNA for KIAA0687 protein, partial cds
 1.2e-128:646:95
 Hs.3628:AB014587
- 20 F-HEMBA1006707
 Homo sapiens mRNA for matrilin-4, partial
 1.7e-101:476:98
 Hs.129361:AJ007581
- 25 F-HEMBA1006724
 ESTs
 8.3e-86:450:95
 Hs.10056:AA210796
- 30 F-HEMBA1006749
 Homo sapiens mRNA for matrilin-4, partial
 6.1e-97:457:98
 Hs.129361:AJ007581
- 35 F-HEMBA1006770
 ESTs, Highly similar to BRAIN PROTEIN F41 [Mus musculus]
 1.6e-31:237:85
 Hs.31612:H41366
- 40 F-HEMBA1006902
 Homo sapiens mRNA for matrilin-4, partial
 9.4e-113:541:97
 Hs.129361:AJ007581
- 45 F-HEMBA1006912
 ESTs
 1.4e-94:460:97
 Hs.88672:AA279956
- 50 F-HEMBA1006916
 Homo sapiens Grb14 mRNA, complete cds
 5.2e-120:651:92
 Hs.83070:L76687
- 55 F-HEMBA1006960
 Human DNA binding protein FKHL15 (FKHL15) mRNA, complete cds
 0.011:628:57
 Hs.159234:U89995
- F-HEMBA1007013
 ESTs
 2.6e-05:139:69

- Hs.113817:AA702497
 F-HEMBA1007057
 Homo sapiens hLRp105 mRNA for LDL receptor related protein 105, complete cds
 5 7.5e-12:389:64
 Hs.143641:AB009462
- F-HEMBA1007063
 10 F-HEMBA1007226
 ESTs
 1.8e-35:202:94
 Hs.105140:N32669
- 15 F-HEMBA1007241
 ESTs, Weakly similar to No definition line found [C.elegans]
 4.1e-27:361:67
 Hs.114062:AI421699
- 20 F-HEMBA1007291
 ESTs
 0.96:114:69
 Hs.121411:AA770241
- 25 F-HEMBA1007332
 ESTs, Weakly similar to hTAFII100 [H.sapiens]
 2.5e-81:405:97
 Hs.3727:AA205887
- 30 F-HEMBB1000106
 ESTs
 2.2e-76:393:96
 Hs.151874:AI023405
- 35 F-HEMBB1000276
 EST
 0.81:239:63
 Hs.149811:AI286277
- 40 F-HEMBB1000309
 Homo sapiens zinc finger protein (MBLL) mRNA, complete cds
 2.4e-35:180:100
 Hs.44806:AF061261
- 45 F-HEMBB1000407
 Cyclin-dependent kinase inhibitor 1C (p57, Kip2)
 0.026:218:65
 Hs.106070:U22398
- 50 F-HEMBB1000447
 Homo sapiens JWA protein mRNA, complete cds
 4.6e-160:750:98
 Hs.92384:AF070523
- 55 F-HEMBB1000542
 ESTs, Weakly similar to C01H6.7 [C.elegans]
 6.8e-07:130:77
 Hs.18171:AA524327

5 F-HEMBB1000567
ESTs
8.8e-13:271:71
Hs.19934:AA455673

10 F-HEMBB1000642

15 F-HEMBB1000668
EST
0.83:192:58
Hs.126372:AA912193

20 F-HEMBB1000679
H.sapiens mRNA for TRAMP protein
4.1e-96:727:80
Hs.4147:X63679

25 F-HEMBB1000881
Homo sapiens chromosome 4p homeobox mRNA sequence
2.2e-06:512:60
Hs.104134:M99587

30 F-HEMBB1000905
Homo sapiens mRNA for voltage gated potassium channel
0.93:337:58
Hs.4975:Y15065

35 F-HEMBB1001026
Human p76 mRNA, complete cds
6. 1e-08:410:61
Hs.28757:U81006

40 F-HEMBB1001048
Human Hpast (HPAST) mRNA, complete cds
2.1e-56:524:75
Hs.155119:AF001434

45 F-HEMBB1001200
EST
0.10:300:61
Hs.161647:AA133367

50 F-HEMBB1001407
Homo sapiens PRKY exon 1 and joined CDS
2.6e-40:271:81
Hs.56336:Y15801

55 F-HEMBB1001530
ESTs
1.2e-98:477:98
Hs.135208:AI093908

F-HEMBB1001547

F-HEMBB1001573
EST
2.2e-06:115:75
Hs.138275:R43976

5 F-HEMBB1001847
ESTs
5.3e-79:389:98
Hs.16141:W56079

10 F-HEMBB1001959
Homo sapiens clone 24781 mRNA sequence
1.0e-58:322:93
Hs.108112:AF070640

15 F-HEMBB1001978
EST
4.7e-23:245:74
Hs.136356:AA493225

20 F-HEMBB1002039
EST
2.3e-25:345:70
Hs.128248:AA972858

25 F-HEMBB1002041
Human plectin (PLEC1) mRNA, complete cds
2.2e-08:477:60
Hs.79706:U53204

30 F-HEMBB1002051
Homo sapiens E74-like factor 5 (ELF5) mRNA, complete cds
9.9e-97:454:99
Hs.159267:AF049703

35 F-HEMBB1002120
ESTs
7.6e-10:68:100
Hs.146335:AI262660

40 F-HEMBB1002162
Homo sapiens genethonin 1 mRNA, complete cds
2.2e-68:328:99
Hs.109590:AF062534

45 F-HEMBB1002228
Homo sapiens unknown mRNA, complete cds
5.3e-41:208:98
Hs.11441:AF047439

50 F-HEMBB1002245
Human growth/differentiation factor 1 (GDF-1) mRNA, complete cds
5.6e-05:299:63
Hs.92614:M62302

55 F-HEMBB1002302
F-HEMBB1002427
Homo sapiens GN6ST mRNA for long form of N-acetylglucosamine-6-O-sulfotransferase (GlcNAc6ST), complete
cds
0.84:108:68
Hs.8786:AB014680

- 5 F-HEMBB1002465
 ESTs, Highly similar to ACYL-COA DEHYDROGENASE [Bacillus subtilis]
 3.2e-18:159:84
 Hs.14791:AA741056
- 10 F-HEMBB1002661
 ESTs
 0.023:424:55
 Hs.154029:AI380603
- 15 F-HEMBB1002663
 F-HEMBB1002693
- 20 F-MAMMA1000046
 Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)
 3.2e-43:454:74
 Hs.144563:AF057280
- 25 F-MAMMA1000102
 Homo sapiens mRNA for cathepsin V, complete cds
 0.70:222:65
 Hs.87417:AB001928
- 30 F-MAMMA1000106
 Homo sapiens mRNA for KIAA0754 protein, partial cds
 0.00076:331:61
 Hs.159183:AB018297
- 35 F-MAMMA1000118
 B94 PROTEIN
 1.5e-07:511:61
 Hs.75522:M92357
- 40 F-MAMMA1000141
 ESTs
 2.3e-18:268:73
 Hs.155334:AA827904
- 45 F-MAMMA1000204
 Homo sapiens dysferlin mRNA, complete cds
 2.5e-167:781:98
 Hs.143897:AF075575
- 50 F-MAMMA1000226
 Human involucrin mRNA
 0.0010:414:61
 Hs.157091:M13903
- 55 F-MAMMA1000403
 ESTs
 2.0e-24:163:90
 Hs.44281:AI342377
- F-MAMMA1000449
 ESTs
 0.99:211:60
 Hs.143715:AI167929

EP 1 130 094 A2

- 5 F-MAMMA1000457
NADH-CYTOCHROME B5 REDUCTASE
7.7e-37:551:66
Hs.75666:M28713
- 10 F-MAMMA1000473

F-MAMMA1000496
Homo sapiens PAC clone DJ130H16 from 22q12.1-qter
1.1e-107:543:96
Hs.8003:AC004997
- 15 F-MAMMA1000528
EST
0.22:227:59
Hs.161400:AI423879
- 20 F-MAMMA1000591
H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyl transferase
3.3e-23:470:62
Hs.55823:X92689
- 25 F-MAMMA1000614
H.sapiens mRNA for CCAAT/enhancer binding protein alpha
1.9e-06:492:61
Hs.76171:Y11525
- 30 F-MAMMA1000652
Homo sapiens mRNA, chromosome I specific transcript KIAA0487
1.5e-61:449:75
Hs.92381:AB007956
- 35 F-MAMMA1000681
Homo sapiens mRNA for putative G-protein coupled receptor, EDG6
4.0e-34:636:65
Hs.159543:AJ000479
- 40 F-MAMMA1000706
COAGULATION FACTOR VII PRECURSOR
9.7e-16:378:65
Hs.36989:M13232
- 45 F-MAMMA1000788
ESTs, Weakly similar to M01E11.2 [C.elegans]
3.4e-118:571:97
Hs.78389:AI191127
- 50 F-MAMMA1000810
EST
0.065:211:61
Hs.116798:AA633813
- 55 F-MAMMA1000814
EST
3.1e-08:224:66
Hs.141620:N63316
- F-MAMMA1000881

- Homo sapiens sgk gene
3.5e-08:165:69
Hs.159640:AJ000512
- 5 F-MAMMA1000986
Homo sapiens clone 24796 mRNA sequence
2.3e-115:320:99
Hs.27191:AF070596
- 10 F-MAMMA1000994
Human HOX4C mRNA for a homeobox protein
0.050:178:64
Hs.74061:X59372
- 15 F-MAMMA1001043
Latent transforming growth factor beta binding protein 2
0.0013:376:60
Hs.83337:Z37976
- 20 F-MAMMA1001066
ESTs
1.1e-18:128:77
Hs.114031:AA700958
- 25 F-MAMMA1001094
Homo sapiens clone 243 unknown mRNA, complete sequence
2.0e-182:844:99
Hs.20423:AF091094
- 30 F-MAMMA1001141
Homo sapiens achäete scute homologous protein (ASH1) mRNA, complete cds
6.1e-07:492:58
Hs.1619:L08424
- 35 F-MAMMA1001150
Protein kinase C, mu
8.3e-51:691:67
Hs.2891:X75756
- 40 F-MAMMA1001237
Homo sapiens monocarboxylate transporter (MCT3) mRNA, complete cds
8.2e-08:386:60
Hs.85838:U81800
- 45 F-MAMMA1001284
ESTs
1.1e-91:452:97
Hs.114756:AI279440
- 50 F-MAMMA1001310
Homo sapiens mRNA for KIAA0708 protein, partial cds
0.014:512:57
Hs.117177:AB014608
- 55 F-MAMMA1001344
ESTs, Weakly similar to No definition line found [C.elegans]
8.3e-80:406:96
Hs.121619:AI188389

EP 1 130 094 A2

- 5 F-MAMMA1001418
Human Na+/nucleoside cotransporter (hCNT1a) mRNA, complete cds
1.9e-36:622:63
Hs.97207:U62966
- 10 F-MAMMA1001532
Human kruppel-related zinc finger protein (ZNF184) mRNA, partial cds
2.1e-33:282:68
Hs.158174:U66561
- 15 F-MAMMA1001609
Insulin-like growth factor-binding protein 4
0.00026:596:57
Hs.1516:U20982
- 20 F-MAMMA1001615
Homo sapiens DNA from chromosome 19, cosmid R29144
1.1e-05:504:59
Hs.155647:AC004221
- 25 F-MAMMA1001623
Excision repair protein ERCC6
1.2e-38:274:86
Hs.99924:L04791
- 30 F-MAMMA1001634
ESTs
1.5e-26:176:90
Hs.16187:AI139901
- 35 F-MAMMA1001893
Cyclin-dependent kinase inhibitor 1C (p57, Kip2)
0.00030:170:68
Hs.106070:U22398
- 40 F-MAMMA1001901
ESTs
1.5e-36:201:76
Hs.161660:AA167744
- 45 F-MAMMA1001957
Prostaglandin I2 (prostacyclin) receptor (IP)
0.041:277:61
Hs.393:D38128
- 50 F-MAMMA1001978
EST
4.0e-43:359:81
Hs.136494:AA587773
- 55 F-MAMMA1002070
Human PAC clone DJ515N1 from 22q11.2-q22
5.1e-135:652:97
Hs.26670:AC002073
- F-MAMMA1002080
Calcium channel, voltage-dependent, L type, alpha 1C subunit
0.0019:574:57

- Hs.89925:L04569
- 5 F-MAMMA1002087
Human mRNA for KIAA0009 gene, complete cds
0.71:228:63
Hs.79972:D13634
- 10 F-MAMMA1002091
Homo sapiens CD39L2 (CD39L2) mRNA, complete cds
5.2e-158:743:98
Hs.12330:AF039916
- 15 F-MAMMA1002095
Homo sapiens mRNA for KIAA0703 protein, complete cds
4.9e-55:657:68
Hs.6168:AB014603
- 20 F-MAMMA1002128
Human leucine zipper on the D14S46E locus mRNA, complete cds
0.77:449:59
Hs.89606:M95925
- F-MAMMA1002142
- 25 F-MAMMA1002165
Homo sapiens connective tissue growth factor-like protein precursor, mRNA, complete cds
1.2e-35:182:98
Hs.139340:AF083500
- 30 F-MAMMA1002205
ESTs
4.7e-32:385:71
Hs.46158:AI160121
- 35 F-MAMMA1002224
TRANSCRIPTION INITIATION FACTOR IIE, ALPHA SUBUNIT
1.3e-34:248:85
Hs.3006:X63468
- 40 F-MAMMA1002234
ESTs
1.1e-100:501:97
Hs.158161:AA312511
- 45 F-MAMMA1002586
Human mRNA for KIAA0183 gene, partial cds
0.00041:388:61
Hs.76666:D80005
- 50 F-MAMMA1002633
Landsteiner-Wiener blood group glycoprotein
1.1e-37:477:71
Hs.108287:L27670
- 55 F-MAMMA1003126
Human Hpast (HPAST) mRNA, complete cds
4.1e-84:801:74
Hs.155119:AF001434

5 F-NT2RM1000407
ESTs
4.1e-19:132:92
Hs.133484:D80522

10 F-NT2RM1000462

15 F-NT2RM1000542
Beta-galactosidase (GLB1)
1.3e-17:436:61
Hs.79222:M34423

20 F-NT2RM1000580
ESTs, Weakly similar to similar to M. musculus MER5 and other AHPC/TSA proteins [C.elegans]
6.2e-51:254:98
Hs.132096:AA314601

25 F-NT2RM1000789
Homo sapiens mRNA for hTCF-4
3.5e-96:299:92
Hs.154485:Y11306

30 F-NT2RM1000855
Hydroxysteroid (11-beta) dehydrogenase 2
0.021:178:67
Hs.1376:U26726

35 F-NT2RM1000899
Homo sapiens BAC clone RG119C02 from 7p15
0.037:222:63
Hs.22900:AC004520

40 F-NT2RM2000241
ESTs
2.9e-31:166:97
Hs.156175:AI334328

45 F-NT2RM2000306

50 F-NT2RM2000410
ESTs
3.2e-12:81:97
Hs.72116:AA151564

F-NT2RM2000423
Beta-galactosidase (GLB1)
0.074:163:63

55 F-NT2RM2000497
ESTs, Weakly similar to CHL1 protein [H.sapiens]
3.7e-21:121:97
Hs.97515:AA435715

F-NT2RM2000514

5 F-NT2RM2000565

F-NT2RM2000582
EST
1.7e-42:218:98
Hs.160262:AI146610

10 F-NT2RM2000589

F-NT2RM2000622
Androgen receptor (dihydrotestosterone receptor; testicular feminization; spinal and bulbar muscular atrophy; Kennedy disease)
0.00018:409:62
Hs.99915:M23263

15 F-NT2RM2000632
Homo sapiens TBP-associated factor 172 (TAF-172) mRNA, complete cds
0.00017:331:59
Hs.14244:AF038362

20 F-NT2RM2000773
Human zinc finger protein (MAZ) rnRNA
7.2e-47:274:91
Hs.7647:M94046

25 F-NT2RM2001126
Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds
5.1e-163:663:99
Hs.21301:AF093419

30 F-NT2RM2001558
Homo sapiens protein kinase A binding protein AKAP110 mRNA, complete cds
3.9e-166:770:98
Hs.98397:AF093408

35 F-NT2RM2001626
Human mRNA for KIAA0231 gene, partial cds
2.8e-40:562:67
Hs.7938:D86984

40 F-NT2RM2001643
ESTs
7.9e-112:548:97
Hs.12610:W56112

45 F-NT2RM2001738
FACTOR VIII INTRON 22 PROTEIN
0.32:452:59
Hs.83363:M34677

50 F-NT2RM2001767
Homo sapiens mRNA for B120, complete cds
5.0e-24:131:100
Hs.123090:AB001895

55 F-NT2RM2001792
Homo sapiens mRNA for serum lectin P35, complete cds
8.2e-14:244:67

- Hs.54517:D63160
- 5 F-NT2RM2001818
EST
0.051:152:61
Hs.157619:AI357718
- 10 F-NT2RM2001902
Human p21-activated protein kinase (Pak1) gene, complete cds
4.4e-39:568:66
Hs.62402:U24152
- 15 F-NT2RM2001939
Human G protein-coupled receptor GPR-NGA gene, complete cds
4.2e-141:664:98
Hs.92458:U55312
- 20 F-NT2RM2001941
Dopamine receptor D4
1.3e-14:547:61
Hs.99922:L12398
- 25 F-NT2RM4000100
Human involucrin mRNA
1.1e-09:487:62
Hs.157091:M13903
- F-NT2RM4000115
- 30 F-NT2RM4000198
ESTs
9.3e-101:496:98
Hs.128676:AA464413
- 35 F-NT2RM4000284
Human IgG Fc receptor hFcRn mRNA, complete cds
2.4e-38: 194:98
Hs.110804:U12255
- 40 F-NT2RM4000295
Homo sapiens SOX22 protein (SOX22) mRNA, complete cds
1.7e-06:479:60
Hs.43627:U35612
- 45 F-NT2RM4000326
Phosphorylase kinase, gamma 2 (testis)
0.95:204:63
Hs.87452:M31606
- 50 F-NT2RM4000417
H.sapiens Syt V gene (genomic and cDNA sequence)
0.97:143:67
Hs.23179:X96783
- 55 F-NT2RM4000444
Eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)
0.45:194:64
Hs.90319:Z21507

- 5 F-NT2RM4000587
 Human proto-oncogene (FRAT1) gene, complete cds
 3.8e-05:495:60
 Hs.143005:U58975
- 10 F-NT2RM4000593
 F-NT2RM4000648
 Homo sapiens glycan-4 (GPC4) mRNA, complete cds
 1.0e-50:610:70
 Hs.58367:AF030186
- 15 F-NT2RM4000761
 EST
 0.89:53:79
 Hs.161967:AA494423
- 20 F-NT2RM4000965
 H.sapiens mRNA for PHAPI2b protein
 0.18:148:68
 Hs.84264:U70439
- F-NT2RM4000997
- 25 F-NT2RM4001321
 ESTs
 1.8e-94:467:97
 Hs.12610:W56112
- 30 F-NT2RM4001325
 Homo sapiens mRNA for chondroitin 6-sulfotransferase, complete cds
 2.1e-13:384:64
 Hs.158304:AB012192
- 35 F-NT2RM4001377
 Homo sapiens mRNA for KIAA0638 protein, partial cds
 3.1e-156:719:99
 Hs.77864:AB014538
- 40 F-NT2RM4001735
 F-NT2RM4001768
 ESTs
 0.00012:123:68
 45 Hs.128045:AA970231
- F-NT2RM4001843
- 50 F-NT2RM4002352
 Homo sapiens hLRp105 mRNA for LDL receptor related protein 105, complete cds
 4.4e-157:761:97
 Hs.143641:AB009462
- 55 F-NT2RP1000002
 EST
 0.00023:170:68
 Hs.135504:AI091717

- 5 F-NT2RP1000050
 Histidine-rich calcium binding protein
 0.0047:257:61
 Hs.1480:M60052
- 10 F-NT2RP1000181
 Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene
 6.9e-99:510:94
 Hs.132898:AC004770
- 15 F-NT2RP1000239
 ESTs
 1.7e-34:240:67
 Hs.33020:N31946
- 20 F-NT2RP1000261
 ESTs, Weakly similar to HYPOTHETICAL 25.2 KD PROTEIN IN ACB1-KSS1 INTERGENIC REGION [S.cereviciae]
 9.1e-92:484:94
 Hs.7870:AI078137
- 25 F-NT2RP1000271
 Homo sapiens DNA-binding protein mRNA, complete cds
 1.4e-140:678:97
 Hs.137582:AF038951
- 30 F-NT2RP1000300
 Human endosome-associated protein (EEA1) mRNA, complete cds
 1.0:205:61
 Hs.2864:L40157
- 35 F-NT2RP1000325
 Phosphate carrier, mitochondrial
 7.7e-84:444:93
 Hs.78713:X60036
- 40 F-NT2RP1000448
 ESTs
 9.5e-73:405:93
 Hs.24054:N46499
- 45 F-NT2RP1000465
 ESTs
 8.5e-10:81:87
 Hs.18619:AI202769
- 50 F-NT2RP1000468
 Homo sapiens clone 24781 mRNA sequence
 2.1e-20:133:92
 Hs.108112:AF070640
- 55 F-NT2RP1000551
 Homo sapiens putative interferon-related protein (SM15) mRNA, partial cds
 2.4e-140:742:93
 Hs.75402:U09585
- F-NT2RP1000579
 SUCCINATE DEHYDROGENASE

- 1.1e-141:798:91
Hs.469:L21936
- 5 F-NT2RP1000613
Homo sapiens carbonic anhydrase precursor (CA 12) mRNA, complete cds
5.5e-11:468:58
Hs.5338:AF037335
- 10 F-NT2RP1000679
ESTs
0.79:127:65
Hs.146093:AA100242
- 15 F-NT2RP1000740
Homo sapiens Trio isoform mRNA, complete cds
0.24:160:66
Hs.150625:AF091395
- 20 F-NT2RP1000903
- 25 F-NT2RP1000981
F-NT2RP1001004
Human mRNA for Doc2 beta, complete cds
0.00072:520:57
Hs.54402:D70830
- 30 F-NT2RP1001020
ESTs, Weakly similar to SPORULATION-SPECIFIC PROTEIN 1 [Saccharomyces cerevisiae]
2.1e-73:392:94
Hs.4789:AI418298
- 35 F-NT2RP1001031
Miller-Dieker syndrome chromosome region
4.5e-07:383:61
Hs.77318:L13385
- 40 F-NT2RP1001563
Human eukaryotic translation initiation factor (eIF3) mRNA, complete cds
0.086:398:59
Hs.57783:U78525
- 45 F-NT2RP2000092
Zinc finger protein 136 (clone pHZ-20)
5.5e-56:652:70
Hs.69740:U09367
- 50 F-NT2RP2000178
Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155), complete sequence
0.14:231:62
Hs.159402:AC005609
- 55 F-NT2RP2000240
Homo sapiens KIAA0415 mRNA, complete cds
3.0e-61:554:76
Hs.7289:AB007875
- F-NT2RP2000394

- ESTs
0.0063:210:63
Hs.134272:AI220363
- 5 F-NT2RP2000447
Human (clone SY11) golgin-95 mRNA, complete cds
3.8e-22:498:65
Hs.24049:L06147
- 10 F-NT2RP2000479
ESTs
1.3e-46:298:90
Hs.15641:W63676
- 15 F-NT2RP2000514
Homo sapiens roundabout 1 (robo1) mRNA, complete cds
1.2e-37:543:67
Hs.36702:AF040990
- 20 F-NT2RP2000533
ESTs, Highly similar to HYPOTHETICAL 16.3 KD PROTEIN IN DUR1,2-NGR1 INTERGENIC REGION [Saccharomyces cerevisiae]
5.4e-132:647:96
Hs.18120:AA913148
- 25 F-NT2RP2000610
Homo sapiens antigen NY-CO-16 mRNA, complete cds
0.00027:182:66
Hs.132206:AF039694
- 30 F-NT2RP2000616
ESTs
0.44:235:60
Hs.31714:AA514389
- 35 F-NT2RP2000649
Homo sapiens mRNA for Hs Ste24p, complete cds
6.2e-167:802:97
Hs.25846:AB016068
- 40 F-NT2RP2000663
Homo sapiens mRNA for KIAA0512 protein, complete cds
4.8e-15:305:64
Hs.48924:AB011084
- 45 F-NT2RP2000694
H.sapiens 5T4 gene for 5T4 Oncofetal antigen
1.0e-113:558:96
Hs.82128:AJ012159
- 50 F-NT2RP2000712
ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]
1.5e-83:442:93
Hs.154226:AA468767
- 55 F-NT2RP2000739
Human mRNA for KIAA0326 gene, partial cds
2.1e-25:574:62

Hs.6833:AB002324
 F-NT2RP2000818
 5 F-NT2RP2000903
 H.sapiens 5T4 gene for 5T4 Oncofetal antigen
 3.5e-112:539:97
 Hs.82128:AJ012159
 10 F-NT2RP2001200
 Homo sapiens mRNA for KIAA0676 protein, partial cds
 1.1e-111:540:96
 Hs.115763:AB014576
 15 F-NT2RP2001223
 ESTs
 5.9e-91:461:95
 Hs.103733:AA436929
 20 F-NT2RP2001276
 Homo sapiens mRNA for KIAA0634 protein, partial cds
 2.4e-11:382:62
 Hs.30898:AB014534
 25 F-NT2RP2001388
 F-NT2RP2001469
 ESTs
 7.3e-39:213:95
 30 Hs.151001:AA564706
 F-NT2RP2001480
 Homo sapiens thrombospondin 3 (THBS3) gene, complete cds
 2.9e-141:686:96
 35 Hs.82165:L38969
 F-NT2RP2001495
 Human transporter protein (g17) mRNA, complete cds
 6.0e-37:581:64
 40 Hs.76460:U49082
 F-NT2RP2001514
 F-NT2RP2001529
 45 Homo sapiens mRNA for ZIP-kinase, complete cds
 1.5e-153:757:96
 Hs.25619:AB007144
 F-NT2RP2001538
 50 ESTs, Highly similar to co-repressor protein [M.musculus]
 4.4e-63:329:94
 Hs.22583:AA188168
 F-NT2RP2001562
 55 Homo sapiens GLE1 (GLE1) mRNA, complete cds
 7.5e-119:572:97
 Hs.81449:AF058922

- 5 F-NT2RP2001662
 H.sapiens mRNA for TGIF protein
 2.6e-29:448:67
 Hs.90077:X89750
- 10 F-NT2RP2001755
 ESTs, Highly similar to F-SPONDIN PRECURSOR [Rattus norvegicus]
 1.0e-47:275:92
 Hs.153657:H37929
- 15 F-NT2RP2001769
 Human protein kinase C-L (PRKCL) mRNA, complete cds
 1.9e-09:399:59
 Hs.89616:M55284
- 20 F-NT2RP2001817
 EST
 0.97:133:63
 Hs.145274:AI249468
- 25 F-NT2RP2001878
 Human DNA binding protein FKHL15 (FKHL15) mRNA, complete cds
 3.6e-05:491:60
 Hs.159234:U89995
- 30 F-NT2RP2001903
 Human mRNA for apolipoprotein E receptor 2, complete cds
 0.0023:270:60
 Hs.54481:D86407
- 35 F-NT2RP2001915
 Homo sapiens Pig3 (PIG3) mRNA complete cds
 3.2e-05:493:60
 Hs.50649:AF010309
- 40 F-NT2RP2001921
 F-NT2RP2001948
 ESTs
 0.55:213:61
 Hs.147805:AI221717
- 45 F-NT2RP2001956
 ESTs, Weakly similar to HYPOTHETICAL 25.2 KD PROTEIN IN ACB1-KSS1 INTERGENIC REGION [S.cerevisiae]
 8.1e-45:510:70
 Hs.13144:T67556
- 50 F-NT2RP2002015
 ESTs
 4.3e-20:127:92
 Hs.12610:W56112
- 55 F-NT2RP2002063
 ESTs
 1.0e-08:73:91
 Hs.19814:T81721

F-NT2RP2002188

F-NT2RP2002232

EST

5 0.82:99:67

Hs.148596:AI202232

F-NT2RP2002304

10 Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete cds

0.031:107:71

Hs.82210:U47742

F-NT2RP2002409

15 Homo sapiens lymphocyte secreted C-type lectin precursor, mRNA, complete cds

0.00063:302:65

Hs.105927:AF020044

F-NT2RP2002510

20 ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase; transferase B, alpha 1-3-galactosyltransferase)

4.4e-09:298:64

Hs.144023:U15197

F-NT2RP2002527

25 Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene

5.2e-65:327:96

Hs.132898:AC004770

F-NT2RP2002533

30 Homo sapiens putative tumor suppressor gene 26 protein alpha 2 delta calcium channel subunit mRNA, complete cds

2.1e-142:726:95

Hs.127436:AF040709

F-NT2RP2002564

Homo sapiens mRNA for repressor protein, partial cds

3.5e-55:594:74

Hs.58167:D30612

F-NT2RP2002674

Epoxide hydrolase 2, cytoplasmic

2.5e-07:332:62

Hs.113:L05779

45 F-NT2RP2002721

F-NT2RP2002824

ESTs, Weakly similar to ZK858.6 [C.elegans]

5.2e-28:190:90

50 Hs.120416:AA057428

F-NT2RP2002942

Homo sapiens mRNA for KIAA0806 protein, complete cds

2.0e-146:758:94

55 Hs.24279:AB018349

F-NT2RP2002974

ESTs

4.9e-51:475:77
Hs.137840:AI123378

5 F-NT2RP2002976
ESTs, Weakly similar to No definition line found [C.elegans]
7.8e-50:315:89
Hs.159604:AI380827

10 F-NT2RP2003042
Lecithin-cholesterol acyltransferase
2.4e-25:454:65
Hs.112125:M12625

15 F-NT2RP2003138
H.sapiens mRNA for TGIF protein
2.0e-05:121:75
Hs.90077:X89750

20 F-NT2RP2003179
Homo sapiens mRNA for KIAA0537 protein, complete cds
1.0e-43:587:70
Hs.12836:AB011109

25 F-NT2RP2003210

30 F-NT2RP2003302
Zinc finger protein 136 (clone pHZ-20)
1.8e-64:691:69
Hs.69740:U09367

35 F-NT2RP2003369
Homo sapiens chromosome 7q22 sequence
5.1e-109:539:96
Hs.125742:AF053356

40 F-NT2RP2003383
Homo sapiens mRNA for KIAA0458 protein, complete cds
1.6e-159:801:95
Hs.7414:AB007927

45 F-NT2RP2003390
Homo sapiens SEC63 (SEC63) mRNA, complete cds
2.2e-116:554:98
Hs.31575:AF100141

50 F-NT2RP2003469
ESTs
0.26:127:69
Hs.62649:AA115328

55 F-NT2RP2003545
ESTs, Highly similar to SERINE/THREONINE-PROTEIN KINASE PAK [Rattus norvegicus]
4.2e-111:550:96
Hs.85768:W16504

F-NT2RP2003593
EST
8.7e-43:213:99

- 1 Hs.130657:AI005473
- 2 F-NT2RP2003599
ESTs
5 7.8e-14:84:98
Hs.107171:H53973
- 3 F-NT2RP2003655
10 F-NT2RP2003664
Homo sapiens mRNA for leptin receptor gene-related protein
5.4e-134:630:98
Hs.23581:Y12670
- 15 F-NT2RP2003931
Human mRNA for KIAA0365 gene, partial cds
4.3e-14:101:92
Hs.84123:AB002363
- 20 F-NT2RP2003940
Zinc finger protein 43 (HTF6)
4.6e-99:693:82
Hs.74107:X59244
- 25 F-NT2RP2003950
Cell division cycle 25A
0.00041:419:59
Hs.1634:M81933
- 30 F-NT2RP2004069
ESTs, Weakly similar to HYPOTHETICAL 26.4 KD PROTEIN EED8.8 IN CHROMOSOME II [C.elegans]
1.3e-75:390:94
Hs.13322:AA151730
- 35 F-NT2RP2004108
Zinc finger protein 136 (clone pHZ-20)
4.9e-69:548:78
Hs.69740:U09367
- 40 F-NT2RP2004141
TRICHOHYALIN
4.8e-11:435:63
Hs.82276:L09190
- 45 F-NT2RP2004179
ESTs
0.0054:180:66
Hs.134917:AI092952
- 50 F-NT2RP2004205
Homo sapiens nuclear dual-specificity phosphatase (SBF1) mRNA, partial cds
0.27:474:56
Hs.112049:U93181
- 55 F-NT2RP2004447
Homo sapiens LDL receptor member LR3 mRNA, complete cds
0.016:456:57
Hs.6347:AF077820

EP 1 130 094 A2

- 5 F-NT2RP2004495
Human transporter protein (g17) mRNA, complete cds
1.2e-26:497:61
Hs.76460:U49082
- 10 F-NT2RP2004524
Human bone morphogenetic protein-3b
0.0016:259:64
Hs.2171:D49493
- 15 F-NT2RP2004556
ESTs
1.1e-34:181:97
Hs.27160:AA421991
- 20 F-NT2RP2004606
Tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor)
5.7e-107:587:92
Hs.148726:X03124
- 25 F-NT2RP2004648
TUBULIN ALPHA-4 CHAIN
0.59:186:61
Hs.75318:X06956
- 30 F-NT2RP2004670
Human mRNA for KIAA0369 gene, complete cds
0.097:309:61
Hs.21355:AB002367
- 35 F-NT2RP2004794
ESTs
1.3e-60:310:96
Hs.84926:N50073
- 40 F-NT2RP2004837
F-NT2RP2004847
Zinc finger protein 42 (myeloid-specific retinoic acid-responsive)
1.4e-05:396:60
Hs.78247:M58297
- 45 F-NT2RP2005027
GLUCOSE TRANSPORTER TYPE 3, BRAIN
7.2e-147:713:96
Hs.7594:M20681
- 50 F-NT2RP2005069
Human mRNA for KIAA0355 gene, complete cds
0.14:303:61
Hs.153014:AB002353
- 55 F-NT2RP2005163
ESTs, Weakly similar to No definition line found [C.elegans]
1.4e-23:334:70
Hs.159604:AI380827
- F-NT2RP2005181

Ecotropic retroviral receptor
8.3e-45:501:70
Hs.2928:X57303

5 F-NT2RP2005247
Oxysterol binding protein
4.2e-08:356:62
Hs.143065:M86917

10 F-NT2RP2005378
ESTs
1.7e-100:485:97
Hs.151572:AA588083

15 F-NT2RP2005391
EST
1.0:264:62
Hs.148259:AA905706

20 F-NT2RP2005425
Homo sapiens mRNA for KIAA0803 protein, partial cds
3.3e-118:566:97
Hs.58103:AB018346

25 F-NT2RP2005463

F-NT2RP2005514
ESTs
3.6e-18:193:77
Hs.153344:R26293

30 F-NT2RP2005535
Homo sapiens DNA-binding protein mRNA, complete cds
7.5e-127:726:90
Hs.137582:AF038951

35 F-NT2RP2005541
Glucosamine (N-acetyl)-6-sulfatase (Sanfilippo disease IIID)
1.2e-06:225:64
Hs.2703:Z12173

40 F-NT2RP2005597

F-NT2RP2005632
ESTs
5.6e-67:344:96
Hs.112011:AA987961

45 F-NT2RP2005666
ESTs
5.8e-71:453:87
Hs.122698:AI042484

50 F-NT2RP2005774
Zinc finger protein 136 (clone pHZ-20)
1.3e-45:451:74
Hs.69740:U09367

5 F-NT2RP2005878
ESTs, Highly similar to ESTRADIOL 17 BETA-DEHYDROGENASE 3 [Homo sapiens]
5.9e-10:67:100
Hs.104523:AA584520

10 F-NT2RP2005883
F-NT2RP2005887

15 F-NT2RP2005941
Human novel homeobox mRNA for a DNA binding protein
6.2e-11:464:61
Hs.37035:U07664

20 F-NT2RP2005994
F-NT2RP2006004
Homo sapiens KIAA0405 mRNA, complete cds
1.2e-13:273:63
Hs.48998:AB007865

25 F-NT2RP2006042
Human mRNA for KIAA0144 gene, complete cds
5.6e-12:220:69
Hs.8127:D63478

30 F-NT2RP2006092
Human FE65-like protein (hFE65L) mRNA, partial cds
2.6e-23:353:65
Hs.24957:U62325

35 F-NT2RP2006099
EST
2.5e-28:180:90
Hs.160878:AI361890

40 F-NT2RP2006134
Neogenin (chicken) homolog 1
0.035:219:60
Hs.90408:U61262

45 F-NT2RP2006269
Homo sapiens mRNA for matrilin-3
1.0:147:65
Hs.119534:AJ224741

50 F-NT2RP2006512
ESTs
1.6e-09:70:95
Hs.118981:AA282396

F-NT2RP3000011

55 F-NT2RP3000022
EST
0.016:293:60
Hs.127706:AA961478

- 5 F-NT2RP3000059
Human SH3 domain-containing proline-rich kinase (sprk) mRNA, complete cds
0.0041:608:59
Hs.89449:L32976
- 10 F-NT2RP3000063
Excision repair protein ERCC6
1.0:264:59
Hs.99924:L04791
- 15 F-NT2RP3000125
Human mRNA for KIAA0314 gene, partial cds
6.9e-08:379:59
Hs.155045:AB002312
- 20 F-NT2RP3000148
Human Chromosome 16 BAC clone CIT987SK-A-635H12
4.5e-40:349:73
Hs.108604:AC002310
- 25 F-NT2RP3000169
Homo sapiens MRS1 mRNA, complete cds
1.1e-107:501:99
Hs.30985:AF093239
- 30 F-NT2RP3000171
Homo sapiens methionine synthase reductase (MTRR) mRNA, complete cds
1.0:279:64
Hs.153792:AF025794
- 35 F-NT2RP3000172
Homo sapiens mRNA for ZIP-kinase, complete cds
7.4e-09:463:59
Hs.25619:AB007144
- 40 F-NT2RP3000201
Homo sapiens mRNA for KIAA0687 protein, partial cds
3.0e-171:792:98
Hs.3628:AB014587
- 45 F-NT2RP3000232
ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]
8.6e-24:304:70
Hs.112094:AA447558
- 50 F-NT2RP3000304
Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds
1.1e-172:797:98
Hs.23672:AF074264
- 55 F-NT2RP3000378
Homo sapiens mRNA for KIAA0700 protein, partial cds
4.3e-45:585:66
Hs.13999:AB014600
- F-NT2RP3000427
Protein kinase, cAMP-dependent, catalytic, beta
1.2e-15:97:98

- Hs.87773:M34181
- F-NT2RP3000436
5 Human protein disulfide isomerase-related protein P5 mRNA, partial cds
4.1e-06:353:59
Hs.85200:D49489
- F-NT2RP3000444
10 Homo sapiens mRNA for KIAA0445 protein, complete cds
1.2e-08:542:60
Hs.154139:AB007914
- F-NT2RP3000460
15 ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]
1.3e-17:181:75
Hs.131840:AI016073
- F-NT2RP3000481
20 Homo sapiens RanBP7/importin 7 mRNA, complete cds
5.4e-164:770:98
Hs.5151:AF098799
- F-NT2RP3000616
25 Homo sapiens KIAA0405 mRNA, complete cds
1.5e-32:579:62
Hs.48998:AB007865
- F-NT2RP3000645
30 Human KH type splicing regulatory protein KSRP mRNA, complete cds
4.6e-06:245:64
Hs.91142:U94832
- F-NT2RP3000652
35 Homo sapiens DNA from chromosome 19, BAC 33152
2.6e-135:853:84
Hs.55452:AC003973
- F-NT2RP3000676
40 Homo sapiens mRNA for KIAA0446 protein, complete cds
8.8e-88:420:98
Hs.158286:AB007915
- F-NT2RP3000677
45 ESTs
3.9e-09:67:97
Hs.98819:AA778727
- F-NT2RP3000721
50 ESTs, Weakly similar to No definition line found [C.elegans]
1.2e-57:395:86
Hs.159604:AI380827
- F-NT2RP3000789
55 Homo sapiens putative RNA binding protein KOC (koc) mRNA, complete cds
4.8e-75:833:69
Hs.79440:U97188
- F-NT2RP3000818

- Homo sapiens chromosome 19, fosmid 39554
 5.9e-08:313:63
 Hs.129906:AC004410
- 5 F-NT2RP3000820
 ESTs, Moderately similar to WSB-1 [M.musculus]
 8.8e-127:613:97
 Hs.24630:AI365246
- 10 F-NT2RP3000838
 Homo sapiens mRNA for KIAA0638 protein, partial cds
 8.3e-79:682:79
 Hs.77864:AB014538
- 15 F-NT2RP3000871
 Homo sapiens retinoblastoma-interacting protein (RBBP8) mRNA, complete cds
 1.9e-08:350:60
 Hs.29287:U72066
- 20 F-NT2RP3000907
 Human Ini1 mRNA, complete cds
 0.91:345:59
 Hs.155626:U04847
- 25 F-NT2RP3000921
 Homo sapiens mRNA for KIAA0806 protein, complete cds
 2.0e-65:798:68
 Hs.24279:AB018349
- 30 F-NT2RP3001012
 Homo sapiens mRNA for KIAA0667 protein, partial cds
 1.3e-21:383:64
 Hs.154740:AB014567
- 35 F-NT2RP3001044
 F-NT2RP3001061
 KERATIN, TYPE II CYTOSKELETAL 7
 3.4e-05:256:62
 40 Hs.23881:M99063
- F-NT2RP3001159
 Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene
 1.8e-81:527:70
 45 Hs.132874:AC004770
- F-NT2RP3001170
 Homo sapiens mRNA for KIAA0784 protein, partial cds
 7.3e-183:859:98
 50 Hs.3657:AB018327
- F-NT2RP3001 195
 ESTs
 3.5e-08:282:62
 55 Hs.135168:AI394026
- F-NT2RP3001240
 ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]

	2.8e-64:344:95 Hs.14038:R06800
5	F-NT2RP3001271 Centromere protein B (80kD) 7.6e-08:288:64 Hs.85004:X05299
10	F-NT2RP3001322 ESTs, Weakly similar to W09D10.2 [C.elegans] 1.2e-86:422:98 Hs.26107:R60661
15	F-NT2RP3001388 F-NT2RP3001542
20	F-NT2RP3001560 Protein phosphatase 2C alpha [human, teratocarcinoma, mRNA, 2346 nt] 0.016:190:63 Hs.57764:S87759
25	F-NT2RP3001592 Cyclin-dependent kinase inhibitor 1C (p57, Kip2) 2.3e-13:188:71 Hs.106070:U22398
30	F-NT2RP3001650 Homo sapiens KIAA0415 mRNA, complete cds 1.6e-17:394:66 Hs.7289:AB007875
35	F-NT2RP3001685 F-NT2RP3001738 Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene 1.9e-54:776:65 Hs.132898:AC004770
40	F-NT2RP3001754 Homo sapiens mRNA for B120, complete cds 2.4e-18:106:100 Hs.123090:AB001895
45	F-NT2RP3001858 Homo sapiens mRNA for KIAA0584 protein, partial cds 1.9e-40:770:63 Hs.106794:AB011156
50	F-NT2RP3001976 Zinc finger protein 140 (clone pHZ-39) 7.3e-33:493:68 Hs.154205:U09368
55	F-NT2RP3002015 Homo sapiens OPA-containing protein mRNA, complete cds 0.018:329:62 Hs.85313:AF071309

EP 1 130 094 A2

5 F-NT2RP3002160
Homo sapiens protein phosphatase with EF-hands-2 long form (PPEF-2) mRNA, complete cds
0.53:182:64
Hs.113259:AF023456

10 F-NT2RP3002281
Homo sapiens mRNA for KIAA0765 protein, partial cds
5.2e-151:713:98
Hs.62318:AB018308

15 F-NT2RP3002286
ESTs
0.034:48:95
Hs.124692:AA777421

20 F-NT2RP3002311
Beta-galactosidase (GEB1)
2.3e-28:633:61
Hs.79222:M34423

25 F-NT2RP3002324
ESTs
2.5e-28:296:75
Hs.22822:H06408

30 F-NT2RP3002342
Human transporter protein (g17) mRNA, complete cds
3.2e-37:565:65
Hs.76460:U49082

35 F-NT2RP3002353
Homo sapiens mRNA for KIAA0790 protein, partial cds
0.0055:271:60
Hs.12002:AB018333

40 F-NT2RP3002409
Homo sapiens mRNA for KIAA0719 protein, complete cds
6.4e-191:897:98
Hs.21198:AB018262

45 F-NT2RP3002411
Hydroxysteroid (17-beta) dehydrogenase 3
2.9e-28:604:62
Hs.477:U05659

50 F-NT2RP3002448
Human mRNA for KIAA0233 gene, complete cds
1.6e-08:721:57
Hs.79077:D87071

55 F-NT2RP3002571
Homo sapiens mRNA for KIAA0603 protein, complete cds
9.7e-67:707:71
Hs.16909:AB011175

F-NT2RP3002664
Homo sapiens Trio isoform mRNA, complete cds
0.26:160:66

Hs.150625:AF091395

F-NT2RP3002721
Homo sapiens citrate synthase mRNA, complete cds
2.4e-180:873:96
Hs.132991:AF047042

F-NT2RP3002737
Homo sapiens mRNA for voltage gated potassium channel
7.1e-43:409:75
Hs.4975:Y15065

F-NT2RP3002738
Human BMK1 alpha kinase mRNA, complete cds
0.0070:722:57
Hs.3080:U29725

F-NT2RP3002790
Cyclin-dependent kinase inhibitor 1C (p57, Kip2)
7.2e-17:626:62
Hs.106070:U22398

F-NT2RP3002836
Homo sapiens mRNA for KIAA0463 protein, partial cds
2.2e-153:717:99
Hs.77738:AB007932

F-NT2RP3002887
Human plectin (PLEC1) mRNA, complete cds
2.5e-06:605:59
Hs.79706:U53204

F-NT2RP3002900
H.sapiens mRNA for transmembrane protein rnp24
3.1e-09:346:64
Hs.75914:X92098

F-NT2RP3002958
ESTs
8.3e-117:765:86
Hs.107119:AI198794

F-NT2RP3002983
ESTs
1.4e-07:270:67
Hs.160271:AI149075

F-NT2RP3003000
Homo sapiens T-type calcium channel alpha-1 subunit mRNA, complete cds
2.5e-89:555:88
Hs.122359:AF051946

F-NT2RP3003076
Homo sapiens mRNA for APC 2 protein, complete cds
0.00016:522:60
Hs.20912:AB012162

F-NT2RP3003354

EP 1 130 094 A2

- Homo sapiens secretory carrier membrane protein (SCAMP2) mRNA, complete cds
4.0e-36:625:64
Hs.10761:AF005038
- 5 F-NT2RP3003448
Arginine vasopressin receptor 1B
0.77:149:69
Hs.1372:L37112
- 10 F-NT2RP3003469
ESTs
1.4e-42:239:93
Hs.12610:W56112
- 15 F-NT2RP3003473
ESTs, Highly similar to transcription factor ARF6 chain B [M.musculus]
8.7e-46:281:89
Hs.136172:W28257
- 20 F-NT2RP3003527
Homo sapiens mRNA for protein kinase Dyrk1B
4.6e-162:769:98
Hs.130988:Y17999
- 25 F-NT2RP3003532
OX-2 MEMBRANE GLYCOPROTEIN PRECURSOR
1.5e-146:682:98
Hs.79015:M17229
- 30 F-NT2RP3003535
EST
6.7e-10:330:60
Hs.133239:AI052508
- 35 F-NT2RP3003559
Breakpoint cluster region protein BCR
1.0:143:66
Hs.2557:Y00661
- 40 F-NT2RP3003614
ESTs
3.7e-50:327:88
Hs.148873:T33582
- 45 F-NT2RP3003729
ESTs, Weakly similar to unknown [S.cerevisiae]
1.9e-96:449:99
Hs.100843:W28953
- 50 F-NT2RP3003849
ESTs, Weakly similar to rhophilin [M.musculus]
1.7e-32:197:92
Hs.118457:AA019161
- 55 F-NT2RP3003874
Homo sapiens incomplete cDNA for a myosin class I, myh-1c
8.5e-84:494:90
Hs.109805:AJ001381

EP 1 130 094 A2

5 F-NT2RP3003939
Peroxisomal biogenesis factor 6
1.5e-05:236:62
Hs.30729:D83703

10 F-NT2RP3003963
F-NT2RP3004000
Homo sapiens mRNA for APC 2 protein, complete cds
4.8e-06:669:59
Hs.20912:AB012162

15 F-NT2RP3004025
ESTs
0.0015:68:86
Hs.154835:AI289188

20 F-NT2RP3004067
ESTs, Weakly similar to HYPOTHETICAL 51.2 KD PROTEIN IN LAG1-RPL14B INTERGENIC REGION [S.cerevisiae]
2.1e-76:416:94
Hs.9252:R53360

25 F-NT2RP3004075
ESTs
1.1e-54:298:94
Hs.124051:T15786

30 F-NT2RP3004083
F-NT2RP3004090
Homo sapiens Achaete-Scute homologue 2 (ASCL2) gene, complete cds
2.4e-06:486:62
Hs.135639:U77629

35 F-NT2RP3004119
Human mRNA for KIAA0215 gene, complete cds
4.1e-74:640:75
Hs.82292:D86969

40 F-NT2RP3004130
F-NT2RP3004133
ESTs, Weakly similar to similar to M. musculus MER5 and other AHPC/TSA proteins [C.elegans]
4.6e-52:259:98
Hs.132096:AA314601

45 F-NT2RP3004202
ALPHA-2C-1 ADRENERGIC RECEPTOR
1.0:229:62
Hs.123022:J03853

50 F-NT2RP3004294
Homo sapiens mRNA for KIAA0741 protein, complete cds
2.4e-05:404:59
Hs.3615:AB018284

55 F-NT2RP3004309

EP 1 130 094 A2

- Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene
3.4e-71:756:71
Hs.132874:AC004770
- 5 F-NT2RP3004321
Homo sapiens (clone MG2-5-12) mucin (MG2) mRNA, complete polyA site
0.015:263:60
Hs.103944:L13283
- 10 F-NT2RP3004345
Cyclin-dependent kinase inhibitor 1C (p57, Kip2)
2.3e-13:188:71
Hs.106070:U22398
- 15 F-NT2RP3004355
EST
0.25:130:59
Hs.149436:AI274484
- 20 F-NT2RP3004374
ESTs
1.4e-95:480:96
Hs.12610:W56112
- 25 F-NT2RP3004406
Human breast cancer, estrogen regulated LIV-1 protein (LIV-1) mRNA, partial cds
3.4e-45:505:70
Hs.79136:U41060
- 30 F-NT2RP3004481
Homo sapiens mRNA for KIAA0476 protein, complete cds
0.00065:594:58
Hs.6684:AB007945
- 35 F-NT2RP3004552
Biglycan
0.92:347:57
Hs.821:J04599
- 40 F-NT2RP3004557
Human Ki nuclear autoantigen mRNA, complete cds
2.6e-121:626:94
Hs.152978:U11292
- 45 F-NT2RP3004625
Homo sapiens I-1 receptor candidate protein mRNA, complete cds
3.1e-152:710:98
Hs.26285:AF082516
- 50 F-NT2RP3004640
ESTs, Moderately similar to unknown [H.sapiens]
0.76:195:64
Hs.6487:T65302
- 55 F-NT2RP3004647
Homo sapiens mRNA for KIAA0446 protein, complete cds
6.6e-111:524:98
Hs.158286:AB007915

5 F-NT2RP4000108
 NEUROFILAMENT TRIPLET L PROTEIN
 5.3e-159:862:93
 Hs.159540:X05608

10 F-NT2RP4000634
 Human MEK kinase 3 mRNA, complete cds
 2.3e-54:370:71
 Hs.86201:U78876

15 F-NT2RP4000962
 ESTs, Weakly similar to SPORULATION-SPECIFIC PROTEIN 1 [Saccharomyces cerevisiae]
 2.3e-95:479:96
 Hs.4789:AI418298

20 F-NT2RP4001001
 EST
 0.98:93:64
 Hs.147598:AI217868

25 F-NT2RP4001009
 Homo sapiens mRNA for Hs Ste24p, complete cds
 3.1e-176:828:98
 Hs.25846:AB016068

30 F-NT2RP4001467
 5' nucleotidase (CD73)
 1.1e-160:742:98
 Hs.153952:X55740

35 F-NT2RP4001877
 ESTs, Weakly similar to siah binding protein 1 [H.sapiens]
 3.3e-103:495:98
 Hs.65648:AA600816

40 F-NT2RP4001879
 EST
 0.78:171:61
 Hs.112790:AA609949

45 F-NT2RP4002187
 Hydroxysteroid (17-beta) dehydrogenase 3
 9.9e-27:534:63
 Hs.477:U05659

50 F-NT2RP4002451
 ESTs
 1.5e-11:106:86
 Hs.163724:AA017689

55 F-NT2RP4002715
 EST
 4.2e-07:64:93
 Hs.160901:AI366910

F-NT2RP4002750
 Ecotropic retroviral receptor
 6.6e-51:581:68

Hs.2928:X57303

5 F-OVARC1000003
Solute carrier family 17 (sodium phosphate), member 2
6.9e-65:587:73
Hs.936:L13258

10 F-OVARC1000090
ESTs
4.8e-07:214:65
Hs.87456:AA434484

15 F-OVARC1000105
Human novel homeobox mRNA for a DNA binding protein
0.00095:204:64
Hs.37035:U07664

20 F-OVARC1000137
Human SNARE protein Ykt6 (YKT6) mRNA, complete cds
4.0e-35:184:98
Hs.31531:U95735

25 F-OVARC1000208
Human calcium-dependent group X phospholipase A2 mRNA, complete cds
1.5e-61:365:90
Hs.136004:U95301

30 F-OVARC1000255
Spleen tyrosine kinase
2.2e-88:615:84
Hs.74101:L28824

35 F-OVARC1000275
ESTs, Weakly similar to Rap2 interacting protein 8 [M.musculus]
4.7e-85:424:97
Hs.55165:AA573499

40 F-OVARC1000298
Homo sapiens GABA-B receptor mRNA, complete cds
0.00021:285:61
Hs.12307:AF056085

45 F-OVARC1000307
ESTs
0.00016:226:63
Hs.162935:AI393970

50 F-OVARC1000313
Homo sapiens mRNA for KIAA0573 protein, partial cds
5.5e-121:585:97
Hs.154023:AB011145

55 F-OVARC1000331
Glucose-6-phosphate dehydrogenase
5.3e-18:213:71
Hs.1435:M24470

F-OVARC1000410

EP 1 130 094 A2

- Homo sapiens mRNA for angiopoietin-like factor
1.5e-27:538:62
Hs.146559:Y16132
- 5 F-OVARC1000439
- F-OVARC1000467
ESTs
2.5e-26:173:90
10 Hs.105040:AA292817
- F-OVARC1000529
Homo sapiens mRNA for C8FW phosphoprotein
1.1e-12:391:59
15 Hs.143513:AJ000480
- F-OVARC1000553
Homo sapiens chromosome 19, cosmid R26894
9.0e-111:425:99
20 Hs.157732:AC005594
- F-OVARC1000775
Human chromosome 3p21.1 gene sequence
2.2e-70:380:95
25 Hs.82837:L13435
- F-OVARC1000811
HEPATOCYTE GROWTH FACTOR ACTIVATOR PRECURSOR
1.2e-06:446:61
30 Hs.104:D14012
- F-OVARC1000853
ESTs
7.9e-09:268:63
35 Hs.92700:W37903
- F-OVARC1000873
Homo sapiens mRNA for MIFR-1, complete cds
0.038:343:60
40 Hs.58269:AB010962
- F-OVARC1000916
H.sapiens PISSLRE mRNA
1.3e-56:435:82
45 Hs.77313:X78342
- F-OVARC1000956
Human TBP-associated factor (hTAFII130) mRNA, partial cds
7.7e-05:511:59
50 Hs.24644:U75308
- F-OVARC1000995
ESTs
2.4e-39:205:98
55 Hs.163662:AA514348
- F-OVARC1001030
EST

EP 1 130 094 A2

- 1.1e-44:232:96
Hs.135504:AI091717
- 5 F-OVARC1001049
ESTs
6.1e-78:373:98
Hs.135022:AI417283
- 10 F-OVARC1001086
Homo sapiens cyclin T2a mRNA, complete cds
6.0e-166:761:99
Hs.155478:AF048731
- 15 F-OVARC1001132
ESTs, Weakly similar to GC-RICH SEQUENCE DNA-BINDING FACTOR [Homo sapiens]
7.9e-121:610:96
Hs.26461:AI341685
- 20 F-OVARC1001163
ESTs
5.9e-39:215:94
Hs.126067:AI344351
- 25 F-OVARC1001222
ESTs
2.7e-93:467:95
Hs.10267:W27845
- 30 F-OVARC1001260
Pregnancy-zone protein
1.0:251:58
Hs.74094:X54380
- 35 F-OVARC1001336
Solute carrier family 17 (sodium phosphate), member 2
1.2e-31:304:74
Hs.936:L13258
- 40 F-OVARC1001338
Homo sapiens cam kinase I mRNA, complete cds
3.7e-17:570:60
Hs.118414:L41816
- 45 F-OVARC1001569
Human novel homeobox mRNA for a DNA binding protein
0.038:178:63
Hs.37035:U07664
- 50 F-OVARC1001570
ESTs
4.5e-10:75:93
Hs.120928:AA703165
- 55 F-OVARC1001596
Matrix metalloproteinase 2 (gelatinase A, 72kD gelatinase, 72kD type IV collagenase)
0.0092:287:63
Hs.111301:M55593

EP 1 130 094 A2

- 5 F-OVARC1001607
Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds
5.5e-41:323:80
Hs.154844:U15128
- 10 F-OVARC 1001725
- 15 F-OVARC1001727
EST
3.2e-05:237:61
Hs.119508:AA485732
- 20 F-OVARC1001807
Hormone receptor (growth factor-inducible nuclear protein N10)
3.4e-91:564:88
Hs.1119:D49728
- 25 F-OVARC1001833
ESTs
1.2e-94:444:97
Hs.155256:AA707750
- 30 F-OVARC1001952
Myristoylated alanine-rich C-kinase substrate
2.9e-10:364:64
Hs.75607:D10522
- 35 F-OVARC1001991
Human mRNA for KIAA0176 gene, partial cds
0.0019:224:62
Hs.4935:D79998
- 40 F-OVARC1002058
Human mRNA for KIAA0149 gene, complete cds
5.0e-48:674:67
Hs.57735:D86864
- 45 F-OVARC1002178
Homo sapiens zinc-finger protein of the cerebellum 3 (ZIC3) mRNA, complete cds
0.010:310:61
Hs.111227:AF028706
- 50 F-PLACE1000033
- 55 F-PLACE1000231
Guanine nucleotide binding protein (G protein), alpha 11 (Gq class)
0.00021:235:63
Hs.1686:M69013
- 60 F-PLACE1000258
KRAB zinc finger protein {alternative products}
1.2e-14:241:70
Hs.22556:U37251
- 65 F-PLACE1000442
Zinc finger protein 136 (clone pHZ-20)
7.3e-89:774:76
Hs.69740:U09367

5 F-PLACE1000560
ESTs
1.5e-36:200:96
Hs.86541:AA214554

10 F-PLACE1000740
Homo sapiens secreted apoptosis related protein 3 (SARP3) mRNA, complete cds
6.5e-05:283:62
Hs.113285:AF017988

15 F-PLACE1000907
ESTs, Moderately similar to zinc finger protein [H.sapiens]
8.1e-38:237:89
Hs.139115:AA325104

20 F-PLACE1000912
ESTs
4.6e-61:331:95
Hs.17558:AA155762

25 F-PLACE1000914
Homo sapiens PB39 mRNA, complete cds
3.1e-45:500:69
Hs.18910:AF045584

30 F-PLACE1000927
ESTs, Weakly similar to N-methyl-D-aspartate receptor-associated protein [D.melanogaster]
1.4e-123:655:94
Hs.8661:AI189791

35 F-PLACE1000986
ESTs
1.2e-105:494:99
Hs.19207:AA039595

40 F-PLACE1001016
Calcium channel, voltage-dependent, L type, alpha 1S subunit
0.011:432:59
Hs.1294:L33798

45 F-PLACE1001100
Human clone 23839 mRNA sequence
0.38:342:60
Hs.78362:U79249

50 F-PLACE1001114
Human mRNA for KIAA0303 gene, partial cds
0.085:339:59
Hs.54985:AB002301

55 F-PLACE1041123
ESTs
5.0e-14:505:61
Hs.99272:AI147740

F-PLACE1001183
ESTs, Weakly similar to gene pp21 protein [H.sapiens]
0.66:361:58

Hs.15984:A,I085974

F-PLACE1001229

ESTs, Weakly similar to D9481.15 gene product [S.cerevisiae]

5 9.3e-110:561:96

Hs.125155:W52093

F-PLACE1001231

ESTs, Weakly similar to sodium iodide symporter [H.sapiens]

10 1.0e-17:120:91

Hs.5167:AA053914

F-PLACE1001340

Homo sapiens mRNA for KIAA0719 protein, complete cds

15 4.1e-132:636:97

Hs.21198:AB018262

F-PLACE1001401

ESTs, Weakly similar to IgE receptor beta subunit [H.sapiens]

20 3.1e-100:516:95

Hs.43900:AA418443

F-PLACE 1001407

H.sapiens mRNA for B-HLH DNA binding protein

25 0.00015:244:66

Hs.66744:X99268

F-PLACE1001464

5' nucleotidase (CD73)

30 1.6e-152:742:96

Hs.153952:X55740

F-PLACE1001500

Bloom syndrome

35 5.7e-05:450:58

Hs.36820:U39817

F-PLACE1001516

Homo sapiens Rigui (RIGUI) mRNA, complete cds

40 2.3e-07:663:58

Hs.8114:AF022991

F-PLACE1001536

ESTs

45 4.6e-60:318:97

Hs.13026:H04491

F-PLACE1001564

H.sapiens mRNA for HE6 Tm7 receptor

50 8.8e-41:499:70

Hs.155681:X81892

F-PLACE1001655

Homo sapiens Shab-related delayed-rectifier K+ channel alpha subunit (KCNS3) mRNA, complete cds

55 4.3e-125:585:98

Hs.47584:AF043472

F-PLACE1001788

EP 1 130 094 A2

- Homo sapiens mRNA for HYA22, complete cds
3.2e-22:234:75
Hs.147189:D88153
- 5 F-PLACE1001795
- F-PLACE1001836
ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]
1.1e-18:162:80
- 10 Hs.157223:AA309318
- F-PLACE1001918
Human p76 mRNA, complete cds
1.3e-22:693:60
- 15 Hs.28757:U81006
- F-PLACE1001949
ESTs
0.97:243:63
- 20 Hs.151143:AA576926
- F-PLACE1002080
Homo sapiens mRNA for KIAA0600 protein, partial cds
2.4e-130:622:98
- 25 Hs.9028:AF039691
- F-PLACE1002095
- F-PLACE1002153
Homo sapiens TACC2 protein (TACC2) mRNA, partial cds
2.7e-162:764:98
Hs.90415:AF095791
- 30 F-PLACE1002329
ESTs
1.5e-107:556:95
Hs.28907:AI343292
- F-PLACE1002355
Homo sapiens protease-activated receptor 4 mRNA, complete cds
9.0e-19:190:77
Hs.137574:AF055917
- 35 F-PLACE1002374
Cathepsin L
2.0e-163:716:94
Hs.78056:X12451
- F-PLACE1002518
Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds
7.0e-19:396:64
Hs.28285:AF064801
- 40 F-PLACE1002547
Homo sapiens mRNA for KIAA0719 protein, complete cds
8.3e-173:819:98
Hs.21198:AB018262

5 F-PLACE1002726
Human mRNA for KIAA0362 gene, partial cds
1.0:310:59
Hs.25515:AB002360

10 F-PLACE1002905
ESTs
2.4e-74:415:92
Hs.110298:AA621807

15 F-PLACE1002911
ESTs, Weakly similar to Y53C12A.3 [C.elegans]
0.030:279:58
Hs.107747:AI357868

20 F-PLACE1002967
ESTs
3.3e-120:574:98
Hs.11090:W37646

25 F-PLACE1003135
Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds
1.5e-50:450:75
Hs.72292:AF024636

30 F-PLACE1003163
Homo sapiens DBI-related protein mRNA, complete cds
1.5e-153:722:98
Hs.15250:AF069301

35 F-PLACE1003407
Homo sapiens putative transmembrane protein (CLN5) mRNA, complete cds
2.0e-142:682:97
Hs.30213:AF068227

40 F-PLACE1003428
Biotinidase
8.2e-06:265:62
Hs.78885:AF018631

45 F-PLACE1003438
ESTs
0.018:470:60
Hs.119482:AI361002

50 F-PLACE1003460
ESTs
0.019:211:60
Hs.92700:W37903

55 F-PLACE1003529
130 KD LEUCINE-RICH PROTEIN
0.53:208:63
Hs.87157:M92439

F-PLACE1003573

F-PLACE1003598

EP 1 130 094 A2

Calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
0.00064:302:64
Hs.96253:U79666

- 5 F-PLACE1003644
ESTs
1.3e-06:265:63
Hs.163564:R43678
- 10 F-PLACE1003737

F-PLACE1003772
Human p300/CBP-associated factor (P/CAF) mRNA, complete cds
7.0e-09:448:61
15 Hs.155302:U57317

F-PLACE1003839
Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12
7.7e-109:521:97
20 Hs.154050:AC004131

F-PLACE1003845
ESTs, Moderately similar to similar to thymidine diphosphoglucose 4,6-dehydratase [C.elegans]
1.2e-92:432:100
25 Hs.153778:AI246000

F-PLACE1003852
Homo sapiens mRNA for KIAA0758 protein, partial cds
2.4e-172:814:98
30 Hs.22039:AB018301

F-PLACE1004028

F-PLACE1004078
35 GELSOLIN PRECURSOR, PLASMA
3.1e-49:616:67
Hs.80562:X04412

F-PLACE1004166
40 ESTs
7.6e-79:415:94
Hs.163741:AA551077

F-PLACE1004168
45 F-PLACE1004199
EST
6.8e-15:147:80
Hs.128205:AA972308
50 F-PLACE1004279
Homo sapiens putative renal organic anion transporter 1 (hROAT1) mRNA, complete cds
3.9e-20:456:62
Hs.23965:AF057039
55 F-PLACE1004282

F-PLACE1004305

EP 1 130 094 A2

Homo sapiens mRNA for KIAA0740 protein, complete cds
8.7e-123:612:96
Hs.15099:AB018283

- 5 F-PLACE1004441
Human G protein-coupled receptor (GPR1) gene, complete cds
8.6e-99:501:96
Hs.159248:U13666
- 10 F-PLACE1004450
AMINOPEPTIDASE N
1.1e-09:587:57
Hs.1239:M22324
- 15 F-PLACE1004482

F-PLACE1004492
ESTs
2.1e-25:134:100
20 Hs.154475:AI199037

F-PLACE1004519
ESTs
1.0e-110:518:99
25 Hs.128505:AA306435

F-PLACE1004520
Pregnancy-specific beta 1-glycoprotein 7
1.3e-110:606:92
30 Hs.119662:M34715

F-PLACE1004630
Homo sapiens mRNA for osteoblast specific cysteine-rich protein, complete cds
2.0e-139:749:92
35 Hs.82582:AB008375

F-PLACE1004637

F-PLACE1004648
40 F-PLACE1004816
Homo sapiens mRNA for Hakata antigen, complete cds
1.2e-99:590:90
Hs.9225:D88587
- 45 F-PLACE1004887
Homo sapiens Achaete-Scute homologue 2 (ASCL2) gene, complete cds
5.1e-06:486:62
Hs.135639:U77629
- 50 F-PLACE1005003
Human SNC19 mRNA sequence
1.5e-21:472:63
Hs.56937:U20428
- 55 F-PLACE1005005
Homo sapiens ubiquitin conjugating enzyme G2 (UBE2G2) mRNA, complete cds
4.7e-42:245:93

- Hs.151614:AF032456
- 5 F-PLACE1005031
ESTs, Highly similar to CHLORINE CHANNEL PROTEIN P64 [Bos taurus]
2.9e-43:538:70
Hs.118991:AA675919
- 10 F-PLACE1005239
ESTs
2.4e-42:209:100
Hs.154475:AI199037
- F-PLACE1005250
- 15 F-PLACE1005383
Homo sapiens UP50 mRNA, complete cds
8.5e-128:633:96
Hs.11494:AF093118
- 20 F-PLACE1005410
ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]
1.3e-17:181:75
Hs.131840:AI016073
- 25 F-PLACE1005426
Pregnancy-specific beta-1 glycoprotein 4
2.3e-109:596:93
Hs.108936:X17097
- 30 F-PLACE1005519
Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds
3.3e-55:521:74
Hs.72292:AF024636
- 35 F-PLACE1005539
HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U
5.8e-05:277:63
Hs.103804:AF068846
- 40 F-PLACE1005544
- F-PLACE1005569
EST
0.38:60:75
- 45 Hs.137086:AA912486
- F-PLACE1005601
Homo Sapiens angiotensin II receptor gene, complete cds
0.016:72:84
- 50 Hs.20954:AI054441
- F-PLACE1005660
- F-PLACE1005669
- 55 Homo sapiens N-methyl-D-aspartate receptor 2D subunit precursor (NMDAR2D) mRNA, complete cds
3.5e-08:461:60
Hs.113286:U77783

- 5 F-PLACE1005682
F-PLACE1005725
Huntingtin (Huntington disease)
1.1e-06:401:61
Hs.79391:L12392
- 10 F-PLACE1005736
ESTs
3.6e-63:343:94
Hs.17757:AA875839
- 15 F-PLACE1005745
ESTs, Weakly similar to HYPOTHETICAL 25.2 KD PROTEIN IN ACB1-KSS1 INTERGENIC REGION [S.cerevi-siae]
6.9e-66:351:94
Hs.7870:AI078137
- 20 F-PLACE1005768
ESTs
7.9e-60:318:95
Hs.143856:AI186351
- 25 F-PLACE1005815
Mutated in colorectal cancers
0.0029:199:62
Hs.1345:M62397
- 30 F-PLACE1005878
ESTs, Highly similar to CHLORINE CHANNEL PROTEIN P64 [Bos taurus]
5.0e-38:464:70
Hs.118991:AA675919
- 35 F-PLACE1005927
INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN PRECURSOR
0.010:511:59
Hs.839:M86826
- 40 F-PLACE1006071
EST
0.68:224:59
Hs.161788:AA371859
- 45 F-PLACE1006073
Homo sapiens mRNA for glucuronyltransferase I, complete cds
5.5e-96:464:98
Hs.26492:AB009598
- 50 F-PLACE1006079
Homo sapiens BAC clone RG300E22 from 7q21-q31.1
1.5e-18:402:65
Hs.99348:AC004774
- 55 F-PLACE1006093
Homo sapiens mRNA for protein phosphatase 1 (PPP1R6)
0.0022:306:59
Hs.106471:Y18206

5 F-PLACE1006208
HOMEobox/POU domain protein RDC-1
0.022:425:57
Hs.74095:L20433

10 F-PLACE1006219
ESTs, Moderately similar to similar to thymidine diphosphoglucose 4,6-dehydratase [C.elegans]
1.7e-61:294:100
Hs.153778:AI246000

15 F-PLACE1006277
EST
0.42:60:75
Hs.137086:AA912486

20 F-PLACE1006290
ESTs, Weakly similar to similar to M. musculus MERS and other AHPC/TSA proteins [C.elegans]
1.3e-51:260:98
Hs.132096:AA314601

25 F-PLACE1006443
Homo sapiens PB39 mRNA, complete cds
1.2e-53:553:70
Hs.18910:AF045584

30 F-PLACE1006515
Homo sapiens mRNA for KIAA0576 protein, partial cds
1.3e-141:655:99
Hs.14687:AB011148

35 F-PLACE1006716
EST
7.2e-12:148:75
Hs.162969:AA677315

40 F-PLACE1006786
ESTs
0.0050:125:72
Hs.109156:AA193501

45 F-PLACE1006809
ESTs
4.5e-99:477:98
Hs.135208:AI093908

50 F-PLACE1006959
ESTs
7.4e-72:381:93
Hs.4963:W29030

55 F-PLACE1007028
Homo sapiens p17-Beckwith-Wiedemann region 1 C (BWR1C) mRNA, complete cds
1.8e-18:364:65
Hs.154036:AF035444

F-PLACE1007040
H.sapiens NF-H gene, exon 1 (and joined CDS)
1.4e-09:501:61

- Hs.75735:X15306
- F-PLACE1007077
ESTs, Moderately similar to testis-specific TCP20 [H.sapiens]
5 0.88:192:62
Hs.85818:AI216525
- F-PLACE1007081
Human plectin (PLEC1) mRNA, complete cds
10 0.079:403:60
Hs.79706:U53204
- F-PLACE1007096
YY1 transcription factor
15 0.64:173:64
Hs.97496:M77698
- F-PLACE1007296
ER LUMEN PROTEIN RETAINING RECEPTOR 1
20 4.2e-73:542:83
Hs.78040:X55885
- F-PLACE1007591
EST
25 0.026:136:64
Hs.130897:AI014389
- F-PLACE1007626
Homo sapiens unknown mRNA, complete cds
30 2.6e-105:516:97
Hs.11441:AF047439
- F-PLACE1007702
Homo sapiens mRNA for UTF1, complete cds
35 0.033:297:62
Hs.158307:AB011076
- F-PLACE1007845
ESTs
40 4.8e-22:158:89
Hs.23445:AA489015
- F-PLACE1007881
- F-PLACE1007971
ESTs, Weakly similar to K07F5.14 [C.elegans]
45 1.1e-128:599:99
Hs.157918:AA313781
- F-PLACE1008282
ESTs, Highly similar to HEME-REGULATED EUKARYOTIC INITIATION FACTOR EIF-2-ALPHA KINASE [Oryctolagus cuniculus]
50 2.4e-65:353:94
Hs.130830:W27380
- F-PLACE1008297
- F-PLACE1008359

EP 1 130 094 A2

- Human arginine-rich protein (ARP) gene, complete cds
0.020:197:64
Hs.75412:M83751
- 5 F-PLACE1008469
Homo sapiens PB39 mRNA, complete: cds
5.3e-20:620:60
Hs.18910:AF045584
- 10 F-PLACE1008549
Homo sapiens E74-like factor 5 (ELF5) mRNA, complete cds
1.8e-145:693:98
Hs.159267:AF049703
- 15 F-PLACE1008657
VILLIN
2.3e-10:356:61
Hs.3046:X12901
- 20 F-PLACE1008716
Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds
1.5e-31:191:92
Hs.154844:U15128
- 25 F-PLACE1008744

F-PLACE1008984
Pregnancy-associated plasma protein A
0.0085:268:60
- 30 Hs.158229:U28727

F-PLACE1008985
Signal transducer and activator of transcription 5A
0.0047:249:64
- 35 Hs.14203:U43185

F-PLACE1009067
Human density enhanced phosphatase-1 mRNA, complete cds
2.0e-06:453:60
- 40 Hs.1177:U10886

F-PLACE1009196

F-PLACE1009279
- 45 Homo sapiens mRNA for serin protease with IGF-binding motif, complete cds
1.9e-11:327:64
Hs.75111:D87258
- 50 F-PLACE1009527
Human DNA-binding protein ABP/ZF mRNA, complete cds
6.8e-21:125:96
Hs.86185:U82613
- 55 F-PLACE1009546
TRANSCRIPTION FACTOR RELB
0.051:248:61
Hs.858:M83221

5 F-PLACE1009600
ESTs
1.0:124:64
Hs.52794:W51887

10 F-PLACE1009735
ESTs
0.022:387:61
Hs.132253:AI027207

15 F-PLACE1009982

F-PLACE1010011
Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds
1.3e-09:330:66
Hs.143551:AF048693

20 F-PLACE1010078
ESTs, Weakly similar to HYPOTHETICAL 25.2 KD PROTEIN IN ACB1-KSS1 INTERGENIC REGION [S.cerevisiae]
8.3e-47:474:72
Hs.13144:T67556

25 F-PLACE1010081
Homo sapiens serine/threonine kinase RICK (RICK) mRNA, complete cds
2.2e-151:733:97
Hs.103755:AF027706

30 F-PLACE1010251
Homo sapiens Na+/H+ exchanger regulatory factor 2 (NHERF-2) mRNA, complete cds
0.0037:405:60
Hs.101813:AB016243

35 F-PLACE1010445
ESTs
1.7e-45:235:97
Hs.144501:N39767

40 F-PLACE1010713
Hydroxysteroid (17-beta) dehydrogenase 3
2.8e-20:447:62
Hs.477:U05659

45 F-PLACE1010784
Human protease-activated receptor 3 (PAR3) mRNA, complete cds
0.56:199:59
Hs.159196:U92971

50 F-PLACE 1010827
H.sapiens mRNA for transmembrane protein rnp24
2.9e-09:346:64
Hs.75914:X92098

55 F-PLACE1010968
ESTs
0.00062:52:98
Hs.119408:T87544

- 5 F-PLACE1011045
Homo sapiens E1-like protein mRNA, complete cds
6.0e-129:595:99
Hs.28190:AF094516
- 10 F-PLACE1011116
F-PLACE1011181
ESTs
1.0:301:58
Hs.80285:AI092519
- 15 F-PLACE1011236
Homo sapiens putative renal organic anion transporter 1 (hROAT1) mRNA, complete cds
1.1e-41:776:62
Hs.23965:AF057039
- 20 F-PLACE1011364
ESTs, Weakly similar to HYPOTHETICAL 141.2 KD PROTEIN EED8.9 IN CHROMOSOME II [C.elegans]
3.7e-53:276:96
Hs.106499:W28299
- 25 F-PLACE1011407
ESTs, Moderately similar to ZINC FINGER PROTEIN 140 [H.sapiens]
3.2e-15:228:70
Hs.152174:AI199619
- 30 F-PLACE1011516
ESTs, Weakly similar to HYPOTHETICAL 21.5 KD PROTEIN IN SEC15-SAP4 INTERGENIC REGION [S.cerevisiae]
1.7e-85:444:95
Hs.110978:AA843431
- 35 F-PLACE1011708
Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds
5.9e-145:722:96
Hs.148318:AF034611
- 40 F-PLACE1011824
Human Ste20-like kinase (MST2) mRNA, complete cds
1.6e-101:561:92
Hs.92317:U26424
- 45 F-PLACE1011978
Homo sapiens DNA from chromosome 19, BAC 33152
3.8e-67:733:72
Hs.55452:AC003973
- 50 F-PLACE2000118
Homo sapiens DNA sequence from PAC 393P12 on chromosome Xp11.21. Contains a hypothetical protein KIAA0413 (KIAA0412, KIAA0065, KIAA0569) LIKE Zinc Finger protein pseudogene, a hypothetical Proline-rich protein KIAA0269 LIKE gene and a 60S Ribosomal Protein L7 LIKE pseudogene. Contains ESTs, an STS and a GSS (BAC end sequence)
7.8e-115:568:95
Hs.120856:AL022578
- 55 F-PLACE2000219
EST

8.7e-11:137:75
Hs.98191:AA417044

F-PLACE3000181

5 Human protocadherin 42 mRNA, complete cds for abbreviated PC42
1.5e-128:745:90
Hs.79769:L11370

F-PLACE3000213

10 EST
1.0:219:63
Hs.98452:AA426058

F-PLACE4000354

15 ESTs
1.4e-13:190:71
Hs.138841:R94879

F-PLACE4000455

20 F-SKNMC1000004
Homo sapiens GABA-B receptor mRNA, complete cds
0.00039:275:62
Hs.12307:AF056085

F-SKNMC1000014

25 ESTs
3.3e-38:196:98
Hs.113307:H16716

F-SKNMC1000082

30 Complement component 4A
0.98:324:63
Hs.76682:K02403

F-THYRO1000036

35 Homo sapiens mRNA for putative ATPase, partial
0.98:199:60
Hs.91471:AJ006268

F-THYRO1000061

40 Human kinase Myt1 (Myt1) mRNA, complete cds
1.0:210:62
Hs.77783:AF014118

F-THYRO1000099

45 ESTs
2.5e-119:605:96
Hs.11782:W07369

F-THYRO1000196

50 Homo sapiens Ksp-cadherin (CDH16) mRNA, complete cds
1.6e-126:475:98
Hs.115418:AF016272

F-THYRO1000400

55 Human R kappa B mRNA, complete cds
0.64:223:63

Hs.95262:U08191

F-THYRO1000580

ESTs, Weakly similar to ZINC FINGER PROTEIN 7 [H.sapiens]

5 5.4e-27:248:76

Hs.25465:AA528105

F-THYRO1000584

Alphamannosidase II isozyme

10 2.2e-06:528:60

Hs.155961:L28821

F-THYRO1000678

Gap junction protein, beta 2, 26kD (connexin 26)

15 1.3e-33:266:80

Hs.81795:M86849

F-THYRO1000776

Human involucrin mRNA

20 0.0025:497:59

Hs.157091:M13903

F-THYRO1000795

Mitochondrial 2-oxoglutarate/malate carrier protein

25 4.1e-19:532:62

Hs.3816:AF070548

F-THYRO1000846

Homo sapiens centrosomal Nek2-associated protein 1 (C-NAP1) mRNA, complete cds

30 0.029:387:60

Hs.27910:AF049105

F-THYRO1000866

Homo sapiens SKB1Hs mRNA, complete cds

35 1.1e-92:529:89

Hs.12912:AF015913

F-THYRO1000956

Homo sapiens mRNA for G-protein coupled receptor

40 1.8e-15:474:64

Hs.155235:Y13583

F-THYRO1000964

Human OB binding protein-2 (OB-BP2) mRNA, complete cds

45 0.22:303:61

Hs.117005:U71383

F-THYRO1000999

EST

50 2.0e-05:198:63

Hs.146520:AI130948

F-THYRO1001063

Human mRNA for cerebroside sulfotransferase, complete cds

55 0.51:448:60

Hs.17958:D88667

F-THYRO1001071

EP 1 130 094 A2

- ESTs
2.1e-29:237:83
Hs.155582:AI125241
- 5 F-THYRO1001102
ESTs, Weakly similar to growth arrest inducible gene product [H.sapiens]
4.7e-32:208:88
Hs.7854:W21970
- 10 F-THYRO1001113
Homo sapiens dysferlin mRNA, complete cds
3.2e-53:684:68
Hs.143897:AF075575
- 15 F-THYRO1001128
ESTs
2.1e-120:589:97
Hs.62595:AA306052
- 20 F-THYRO1001205
- F-THYRO1001237
ESTs
0.66:326:60
25 Hs.148352:U80757
- F-THYRO1001242
Protein phosphatase 2C alpha [human, teratocarcinoma, mRNA, 2346 nt]
0.017:188:63
30 Hs.57764:S87759
- F-THYRO1001266
Human sodium iodide symporter mRNA, complete cds
8.6e-43:806:62
35 Hs.103983:U66088
- F-THYRO1001327
ESTs
2.8e-50:264:96
40 Hs.154667:AI343524
- F-THYRO1001456
EST
0.90:84:72
45 Hs.130049:AA902650
- F-THYRO1001457
Protein kinase C, mu
6.0e-53:705:67
50 Hs.2891:X75756
- F-THYRO1001471
ESTs
8.0e-52:278:94
55 Hs.7604:W31115
- F-THYRO1001478
Human mRNA for KIAA0150 gene, partial cds

0.79:150:66
Hs.98508:D63484

5 F-THYRO1001495
Homo sapiens KIAA0415 mRNA, complete cds
9.5e-75:550:82
Hs.7289:AB007875

10 F-THYRO1001523
ESTs
7.2e-19:142:86
Hs.140588:H60533

15 F-THYRO1001529
ESTs
5.7e-24:141:95
Hs.114172:AA703201

20 F-THYRO1001593
H.sapiens mRNA for serine/threonine protein kinase EMK
1.4e-70:643:74
Hs.157199:X97630

25 F-THYRO1001608
Human mRNA for KIAA0227 gene, partial cds
2.6e-07:533:59
Hs.79170:D86980

30 F-THYRO1001641
ESTs
0.87:269:59
Hs.14599:AA522511

35 F-THYRO1001700
Homo sapiens c-Jun N-terminal kinase kinase 2 (JNKK2) mRNA, complete cds
3.3e-05:441:59
Hs.110299:AF013589

40 F-THYRO1001702
Human plectin (PLEC1) mRNA, complete cds
0.00017:346:62
Hs.79706:U53204

45 F-THYRO1001725
Homo sapiens mRNA for procollagen I-N proteinase
1.3e-06:275:64
Hs.120330:AJ003125

50 F-THYRO1001770
Homo sapiens mRNA for HsGAK, complete cds
0.046:265:58
Hs.153227:D88435

55 F-THYRO1001803
EST
0.0085:201:63
Hs.158782:AI376601

5 F-Y79AA1000030
ESTs
0.00051:276:60
Hs.111999:AA465020

10 F-Y79AA1000127
ESTs
1.3e-85:430:96
Hs.49932:W58552

15 F-Y79AA1000207
ESTs
4.5e-81:407:96
Hs.125308:AI376737

20 F-Y79AA1000226
ESTs, Highly similar to HYPOTHETICAL 52.8 KD PROTEIN T05E11.5 IN CHROMOSOME IV [Caenorhabditis elegans]
0.00081:76:84
Hs.11221:AI192291

25 F-Y79AA1000270
Human mRNA for ORF, Xq terminal portion
9.9e-97:590:88
Hs.6551:D16469

30 F-Y79AA1000426
CELL SURFACE GLYCOPROTEIN MUC18 PRECURSOR
0.045:507:59
Hs.82914:X68264

35 F-Y79AA1000521
Homo sapiens mRNA for putative G-protein coupled receptor, EDG6
0.0029:489:58
Hs.159543:AJ000479

40 F-Y79AA1000750
ESTs
9.9e-12:252:65
Hs.52885:H29851

45 F-Y79AA1000776
ESTs
1.4e-50:340:87
Hs.144198:AI017555

50 F-Y79AA1000777
Homo sapiens mRNA for putative transcription factor, partial
3.9e-10:501:61
Hs.26782:AJ009770

55 F-Y79AA1000876
Homo sapiens short form transcription factor C-MAF (c-maf) mRNA, complete cds
1.3e-11:323:66
Hs.30250:AF055376

F-Y79AA1000888
Homo sapiens mRNA for KIAA0469 protein, complete cds

- 1.5e-05:641:58
Hs.7764:AB007938
- 5 F-Y79AA1000959
Homo sapiens Hsp70 binding protein HspBP1 mRNA, complete cds
5.3e-54:277:96
Hs.53066:AF093420
- 10 F-Y79AA1000967
Human mRNA for KIAA0369 gene, complete cds
8.1e-10:517:61
Hs.21355:AB002367
- 15 F-Y79AA1001013
ESTs
2.4e-44:259:93
Hs.109468:W52074
- 20 F-Y79AA1001056
ESTs, Moderately similar to maternal transcript Maid [M.musculus]
4.7e-07:90:87
Hs.36794:AI038407
- 25 F-Y79AA1001062
ESTs, Weakly similar to tumor necrosis factor-alpha-induced protein B12 [H.sapiens]
1.6e-60:320:96
Hs.13982:W27344
- 30 F-Y79AA1001090
H.sapiens DAP-kinase mRNA
2.3e-06:465:59
Hs.153924:X76104
- 35 F-Y79AA1001212
Homo sapiens SL15 protein mRNA, complete cds
1.5e-163:763:98
Hs.6710:AF038961
- 40 F-Y79AA1001264
Homo sapiens mRNA for MSJ-1, complete cds
5.3e-15:367:64
Hs.3845:AB014888
- 45 F-Y79AA1001272
Human plectin (PLEC1) mRNA, complete cds
6.3e-05:325:63
Hs.79706:U53204
- 50 F-Y79AA1001328
Homo sapiens Delta mRNA, complete cds
1.8e-07:271:61
Hs.144631:AF003522
- 55 F-Y79AA1001426
Aldehyde dehydrogenase 7
0.94:485:56
Hs.83155:U10868

5 F-Y79AA1001427
 NADH-CYTOCHROME B5 REDUCTASE
 1.7e-56:649:69
 Hs.75666:M28713

10 F-Y79AA1001430
 Homo sapiens mRNA for KIAA0469 protein, complete cds
 2.8e-124:577:99
 Hs.7764:AB007938

15 F-Y79AA1001523
 Homo sapiens transcription intermediary factor 1 (TIF1) mRNA, complete cds
 1.1e-92:496:93
 Hs.128763:AF009353

20 F-Y79AA1001530
 Human beta-tubulin gene (5-beta) with ten Alu family members
 1.0e-131:669:95
 Hs.108014:X00734

25 F-Y79AA1001592
 ESTs
 1.2e-88:212:97
 Hs.131180:AA594251

30 F-Y79AA1001727
 F-Y79AA1001787
 Human mRNA for KIAA0315 gene, partial cds
 0.48:248:63
 Hs.3989:AB002313

35 F-Y79AA1001793
 ESTs
 1.4e-67:192:98
 Hs.118559:AA887084

40 F-Y79AA1001795
 Homo sapiens mRNA for GAIT4 protein
 5.3e-89:431:98
 Hs.21495:AL031228

45 F-Y79AA1001799
 NUCLEAR FACTOR RIP140
 0.54:182:62
 Hs.155017:X84373

50 F-Y79AA1001803
 ESTs, Highly similar to MELANOMA-ASSOCIATED ANTIGEN XP [Homo sapiens]
 0.72:169:63
 Hs.94011:AA627644

55 F-Y79AA1001863
 EST
 1.0:114:63
 Hs.152260:AA489703

F-Y79AA1002022

B94 PROTEIN
 5.7e-13:469:65
 Hs.75522:M92357

5 F-Y79AA1002058
 Homo sapiens clone 24733 mRNA sequence
 1.7e-154:740:98
 Hs.21970:AF052149

10 F-Y79AA1002121
 EST
 0.14:104:66
 Hs.100070:M91493

15 F-Y79AA1002129
 ESTs
 5.1e-90:431:98
 Hs.40719:AI183452

20 F-Y79AA1002213

F-Y79AA1002334
 ESTs
 5.0e-20:187:80

25 Hs.111900:AA397579

F-Y79AA1002373
 ESTs
 4.5e-37:192:98

30 Hs.118559:AA887084

F-Y79AA1002376
 Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds
 1.2e-36:657:64

35 Hs.65248:AF063228

F-Y79AA1002378
 Homo sapiens KIAA0426 mRNA, complete cds
 4.9e-38:424:72

40 Hs.97476:AB007886

F-Y79AA1002381
 CELL DIVISION PROTEIN KINASE 3
 8.4e-17:580:61

45 Hs.100009:X66357

Homology search result 9

50 [0302] The result of the homology search in the Human Unigene(<http://www.ncbi.nlm.nih.gov/UniGene>) using the clone sequences of the 3'-ends.

55 Indicated are from the top,
 the name of the clone sequence,
 title of the top hit data,
 the P-value: the length of the sequence used for comparison (nucleotide):similarity (%),
 the Accession No. of the top hit data.

[0303] Blank indicates that the 3'-end sequence corresponding to the 5'-end was not determined in the clone.

EP 1 130 094 A2

[0304] Data were not shown for the clones in which the P-value was higher than 1.

5	R-HEMBA1000006 ESTs 1.0:85:71 Hs.130699:AA621478
10	R-HEMBA1000121 ESTs 1.3e-111:545:97 Hs.153432:AA098922
15	R-HEMBA1000128 ESTs, Weakly similar to HYPOTHETICAL 30.6 KD PROTEIN IN SCP160-MRPL8 INTERGENIC REGION PRE-CURSOR [S.cerevisiae] 3.0e-98:532:93 Hs.7745:H92988
20	R-HEMBA1000275 ESTs 6.5e-11:81:81 Hs.163492:AI334460
25	R-HEMBA1000300 Homo sapiens mRNA for putative lipoic acid synthetase, partial 1.2e-39:309:81 Hs.53531:AJ224162
30	R-nnnnnnnnnnnnn ESTs 4.9e-95:455:98 Hs.154009:AI284184
35	R-HEMBA1000462 Homo sapiens clone 243 unknown mRNA, complete sequence 3.6e-91:313:94 Hs.20423:AF091094
40	R-HEMBA1000477 ESTs 4.7e-111:541:97 Hs.84526:AI341541
45	R-HEMBA1000590 Homo sapiens mRNA for matrilin-4, partial 2.6e-102:547:93 Hs.129361:AJ007581
50	R-HEMBA1000634 ESTs 0.85:189:62 Hs.131268:AA909162
55	R-HEMBA1000671 ESTs 6.5e-84:432:96 Hs.31991:T78668

5 R-HEMBA1000713
 Homo sapiens 10kD protein (BC10) mRNA, complete cds
 4.0e-119:575:97
 Hs.5300:AF053470

10 R-HEMBA1000732
 EST
 3.9e-81:435:92
 Hs.146718:AI146722

15 R-nnnnnnnnnnnnnn
 R-HEMBA1000875
 EST
 0.023:207:62
 Hs.148275:AA907849

20 R-HEMBA1000940
 Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds
 7.4e-31:211:81
 Hs.97203:U83171

25 R-HEMBA1000962
 ESTs
 1.1e-104:515:97
 Hs.8978:W63573

30 R-HEMBA1001 184
 EST
 7.1e-07:382:62
 Hs.124559:AA847550

35 R-HEMBA1001221
 ESTs, Weakly similar to transmembrane protein [H.sapiens]
 1.2e-95:487:95
 Hs.22791:AI056665

40 R-HEMBA1001228
 Human germline oligomeric matrix protein (COMP) mRNA, complete cds
 4.0e-42:170:92
 Hs.1584:AC003107

45 R-HEMBA1001272
 ESTs
 5.7e-71:514:84
 Hs.26966:N74056

50 R-HEMBA1001296
 EST
 1.7e-93:494:95
 Hs.102465:N27272

55 R-HEMBA1001297
 Homo sapiens putative transcription factor CA150 mRNA, complete cds
 1.5e-93:466:96
 Hs.13063:AF017789

R-HEMBA1001390

EP 1 130 094 A2

- ESTs
1.6e-42:181:89
Hs.139190:N55515
- 5 R-HEMBA1001563
Homo sapiens DEC-205 mRNA, complete cds
8.4e-42:311:83
Hs.153563:AF011333
- 10 R-HEMBA1001621
ESTs, Highly similar to PROBABLE G PROTEIN-COUPLED RECEPTOR APJ [Homo sapiens]
4.2e-56:386:86
Hs.9305:W84893
- 15 R-HEMBA1001878
Homo sapiens U5 snRNP-specific 40 kDa protein mRNA, complete cds
1.1e-80:433:93
Hs.10290:AF090988
- 20 R-HEMBA1001886
Zinc finger protein 141 (clone pHZ-44)
5.9e-61:530:80
Hs.159596:L15309
- 25 R-HEMBA1002048
ESTs
0.95:127:63
Hs.98690:AA431162
- 30 R-HEMBA1002131
- R-HEMBA1002163
ESTs, Weakly similar to K09E9.2 [C.elegans]
5.9e-36:225:90
Hs.26813:AI339473
- 35 R-HEMBA1002167
ESTs
1.5e-35:325:80
Hs.124171:N98933
- 40 R-HEMBA1002178
MICROSOMAL DIPEPTIDASE PRECURSOR
0.99:243:61
Hs.109:J05257
- 45 R-HEMBA1002195
Deoxyhypusine synthase
1.9e-19:109:100
Hs.79064:U79262
- 50 R-HEMBA1002227
Myristoylated alanine-rich C-kinase substrate
2.0e-116:567:97
Hs.75607:D10522
- 55 R-HEMBA1002316
Homo sapiens mRNA for putative GTP-binding protein

EP 1 130 094 A2

- 8.2e-20:160:85
Hs.101033:Y14391
- 5 R-HEMBA1002420
ESTs, Weakly similar to T03G11.6 gene product [C.elegans]
2.7e-78:402:97
Hs.108354:W19984
- 10 R-HEMBA1002421
Syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan)
1.9e-91:443:97
Hs.1501:J04621
- 15 R-HEMBA1002524
Human MHC Class I region proline rich protein mRNA, complete cds
1.0e-111:551:96
Hs.41548:U63336
- 20 R-HEMBA1002551
ESTs
3.4e-107:553:96
Hs.92071:W80592
- 25 R-HEMBA1002767
Homo sapiens chromosome 1p33-p34 beta-1,4-galactosyltransferase mRNA, complete cds
5.5e-108:568:95
Hs.19154:AF038660
- 30 R-HEMBA1002985
ESTs
4.4e-39:211:96
Hs.126894:AA932538
- 35 R-HEMBA1003047
Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds
1.6e-115:571:96
Hs.148318:AF034611
- 40 R-HEMBA1003072
EST
0.044:220:61
Hs.136349:AA490873
- 45 R-HEMBA1003101
Homo sapiens tyrosylprotein sulfotransferase-2 mRNA, complete cds
1.2e-117:575:97
Hs.26350:AF049891
- 50 R-HEMBA1003120
Zinc finger protein 10 (KOX 1)
5.8e-41:412:73
Hs.2479:X78933
- 55 R-HEMBA1003230
Homo sapiens UP50 mRNA, complete cds
4.2e-44:258:93
Hs.11494:AF093118

EP 1 130 094 A2

5 R-HEMBA1003294
ESTs
4.3e-84:410:98
Hs.113517:AA418756

10 R-HEMBA1003315
ESTs, Weakly similar to TIP49 [R.norvegicus]
7.3e-73:476:87
Hs.6455:AA515838

15 R-HEMBA1003392
Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds
8.3e-117:557:98
Hs.23672:AF074264

20 R-HEMBA1003399
ESTs, Highly similar to MVP1 PROTEIN [Saccharomyces cerevisiae]
8.0e-94:526:92
Hs.12169:N38744

25 R-HEMBA1003487
ESTs
4.5e-84:417:96
Hs.21835:AA458524

30 R-HEMBA1003497
ESTs
1.4e-72:346:99
Hs.129837:AA778570

35 R-HEMBA1003530
ESTs
8.5e-82:459:91
Hs.22140:R41751

40 R-HEMBA1003602
ESTs
1.0e-101:592:90
Hs.124342:AA829829

45 R-HEMBA1003732
ESTs
2.1e-111:530:99
Hs.101660:AA481200

50 R-HEMBA1003945
Calcineurin B
2.9e-83:410:97
Hs.1335:M30773

55 R-HEMBA1004007
Homo sapiens PYRIN (MEFV) mRNA, complete cds
3.8e-57:382:77
Hs.113283:AF018080

R-HEMBA1004085
ESTs
3.0e-59:396:87

Hs.102480:AA520980

- 5 R-nnnnnnnnnnnnn
Homo sapiens intersectin short form mRNA, complete cds
2.0e-116:569:97
Hs.66392:AF064244
- 10 R-HEMBA1004250
ESTs
1.6e-97:469:97
Hs.125529:AA883986
- 15 R-HEMBA1004391
EST
0.085:113:63
Hs.157582:AI356856
- 20 R-HEMBA1004444
ESTs
2.3e-88:430:98
Hs.141680:N98441
- 25 R-HEMBA1004454
ESTs
1.7e-71:338:100
Hs.103913:AA740543
- 30 R-HEMBA1004505
ESTs
2.2e-63:329:95
Hs.4814:AA631254
- 35 R-HEMBA1004785
EST
1.0:77:67
Hs.144066:AA905236
- 40 R-HEMBA1004797
ESTs
4.1e-11:71:100
Hs.27206:AA626782
- 45 R-HEMBA1004952
ESTs
6.0e-93:435:99
Hs.115120:AA935633
- 50 R-HEMBA1004971
ESTs
0.98:152:58
Hs.112621:AA608964
- 55 R-HEMBA1004982
ESTs
2.3e-109:516:98
Hs.14877:AA749081
- R-HEMBA1005070

EP 1 130 094 A2

- Human mRNA for KIAA0310 gene, complete cds
4.0e-96:381:91
Hs.5716:AB002308
- 5 R-HEMBA1005084
ESTs
1.0:75:80
Hs.62119:AA043299
- 10 R-HEMBA1005145
Homo sapiens LIM protein mRNA, complete cds
1.6e-58:278:84
Hs.154103:AF061258
- 15 R-HEMBA1005230
ESTs
3.7e-65:336:95
Hs.124946:AI026708
- 20 R-HEMBA1005246

R-HEMBA1005267
Human protein immuno-reactive with anti-PTH polyclonal antibodies mRNA, partial cds
7.8e-75:536:81
Hs.44566:U28831
- 25 R-HEMBA1005337
EST
8.7e-58:291:97
Hs.48956:N64339
- 30 R-HEMBA1005430
ESTs
7.6e-83:388:100
Hs.28968:AA524690
- 35 R-HEMBA1005449
ESTs
5.0e-47:317:86
Hs.23650:H21144
- 40 R-HEMBA1005489
ESTs
1.8e-96:504:94
Hs.8028:AA053817
- 45 R-HEMBA1005522
EST
1.0:98:64
Hs.157385:AI364194
- 50 R-HEMBA1005545
MUSCARINIC ACETYLCHOLINE RECEPTOR M3
6.3e-117:579:96
Hs.7138:U29589
- 55 R-HEMBA1005698
ESTs

	1.6e-113:562:96 Hs.12942:AI042353
5	R-HEMBA1005913 ESTs 2.8e-109:564:94 Hs.28827:AI125541
10	R-HEMBA1005929 Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds 9.6e-63:497:77 Hs.97203:U83171
15	R-HEMBA1005945 ESTs 1.1e-74:412:92 Hs.32246:AA464020
20	R-HEMBA1006016 ESTs 1.4e-18:162:82 Hs.149448:AI082465
25	R-HEMBA1006171 EST 0.049:94:69 Hs.159919:AA961766
30	R-HEMBA1006276 ESTs 6.3e-22:257:75 Hs.138847:N64493
35	R-HEMBA1006299 ESTs, Weakly similar to R06B9.b [C.elegans] 3.9e-107:596:91 Hs.30432:W28988
40	R-HEMBA1006311 Homo sapiens SALL1 gene, partial 0.99:273:60 Hs.123094:X98833
45	R-HEMBA1006335 ESTs 2.5e-72:447:89 Hs.23579:W38893
50	R-HEMBA1006357 ESTs 6.3e-15:187:74 Hs.161714:AA229078
55	R-HEMBA1006430 Homo sapiens tumor necrosis factor superfamily member LIGHT mRNA, complete cds 2.9e-47:303:88 Hs.129708:AF064090

EP 1 130 094 A2

R-HEMBA1006482
Homo sapiens h-sco1 (SCO1) mRNA, nuclear gene encoding mitochondrial protein, complete cds
5.5e-107:537:96
Hs.14511:AF026852

5 R-HEMBA1006517
ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]
2.7e-43:173:86
Hs.141505:N30650

10 R-HEMBA1006544
Homo sapiens mRNA for small GTP-binding protein, complete cds
5.8e-60:329:80
Hs.115325:D84488

15 R-HEMBA1006572
ESTs
7.2e-94:450:99
Hs.123933:AA758566

20 R-HEMBA1006658
Homo sapiens mRNA for KIAA0687 protein, partial cds
2.3e-112:570:94
Hs.3628:AB014587

25 R-HEMBA1006707
Homo sapiens mRNA for matrilin-4, partial
1.7e-79:389:97
Hs.129361:AJ007581

30 R-HEMBA1006724

R-HEMBA1006749
Homo sapiens mRNA for matrilin-4, partial
1.0e-89:472:94
Hs.129361:AJ007581

35 R-HEMBA1006770
ESTs, Moderately similar to CAGH4 [H.sapiens]
2.0e-112:554:96
Hs.41641:AA428519

40 R-HEMBA1006902
Homo sapiens mRNA for matrilin-4, partial
3.0e-113:540:98
Hs.129361:AJ007581

45 R-HEMBA1006912
H.sapiens mRNA for phosphoinositide 3-kinase
5.9e-45:297:86
Hs.101238:Y11312

50 R-HEMBA1006916
Homo sapiens Grb14 mRNA, complete cds
5.8e-116:346:99
Hs.83070:L76687

55 R-HEMBA1006960

EP 1 130 094 A2

ESTs
1.7e-110:519:99
Hs.22015:AI359551

5 R-HEMBA1007013
ESTs
0.53:280:59
Hs.143532:AI087321

10 R-HEMBA1007057

R-HEMBA1007063
EST
3.2e-41:310:83

15 Hs.163333:AA879053

R-HEMBA1007241
ESTs
1.8e-103:492:98

20 Hs.127478:AI188768

R-HEMBA1007291
Human mRNA for KIAA0266 gene, complete cds
8.7e-46:283:89

25 Hs.78878:D87455

R-HEMBA1007332
ESTs, Weakly similar to hTAFII100 [H.sapiens]
2.8e-17:161:80

30 Hs.3727:AA205887

R-HEMBB1000106
ESTs
1.3e-100:491:97

35 Hs.27774:AA576731

R-HEMBB1000276

R-HEMBB1000309
EST
1.0:150:64

40 Hs.125409:AA879096

R-HEMBB1000407
ESTs, Weakly similar to C47D12.2 [C.elegans]
4.1e-110:535:97

45 Hs.14328:AA503393

R-HEMBB1000447
Homo sapiens JWA protein mRNA, complete cds
5.6e-109:533:97

50 Hs.92384:AF070523

R-HEMBB1000542
ESTs, Weakly similar to C01H6.7 [C.elegans]
1.6e-88:497:91

55 Hs.18171:AA524327

5 R-HEMBB1000567
 Insulin-like growth factor 2 (somatomedin A)
 8.9e-61:369:88
 Hs.155487:J03242

10 R-HEMBB1000642
 ESTs
 2.2e-44:308:84
 Hs.141318:N71080

15 R-HEMBB1000668
 ESTs, Weakly similar to hTAFII100 [H.sapiens]
 2.5e-102:520:95
 Hs.3830:AA167691

20 R-HEMBB1000679
 ESTs
 6.7e-36:188:97
 Hs.154218:AA169554

25 R-HEMBB1000881
 ESTs
 8.4e-105:519:96
 Hs.110967:AA570505

30 R-HEMBB1000905
 ESTs
 1.1e-94:454:98
 Hs.52515:AA464314

35 R-HEMBB1001026
 ESTs
 0.22:93:69
 Hs.119510:AA630235

40 R-HEMBB1001048
 EST
 0.42:127:66
 Hs.147466:AI215091

45 R-HEMBB1001200
 ESTs
 3.7e-07:330:62
 Hs.10109:AI148628

50 R-HEMBB1001407
 MHC class II transactivator
 3.8e-35:414:71
 Hs.3076:U18259

55 R-HEMBB1001530
 ESTs
 2.4e-95:455:98
 Hs.8956:AI146421

R-HEMBB1001547
 ESTs
 1.0e-111:533:98

Hs.33979:AI074147

5 R-HEMBB1001573
ESTs, Moderately similar to LL5 protein [R.norvegicus]
1.7e-06:64:95
Hs.131327:AI148746

10 R-HEMBB1001847
ESTs
1.4e-54:280:96
Hs.109755:AA180809

15 R-HEMBB1001959
Homo sapiens clone 24781 mRNA sequence
1.5e-104:504:97
Hs.108112:AF070640

20 R-HEMBB1001978
Homo sapiens mRNA for TRAFS, complete cds
7.0e-28:220:84
Hs.29736:AB000509

25 R-HEMBB1002039
ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]
1.5e-34:423:72
Hs.154912:N63897

30 R-HEMBB1002041
ESTs, Weakly similar to transmembrane protein [H.sapiens]
7.0e-122:575:98
Hs.22791:AI056665

35 R-HEMBB1002051
ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME III [Caenorhabditis elegans]
4.2e-43:298:84
Hs.141429:AA631915

40 R-HEMBB1002120
ESTs
1.4e-91:438:99
Hs.145014:AI218562

45 R-HEMBB1002162
ESTs
1.0e-34:238:86
Hs.164036:AA845659

50 R-HEMBB1002228
Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds
1.7e-59:583:77
Hs.129735:AF010144

55 R-HEMBB1002245
ESTs
9.1e-66:383:91
Hs.8989:R71365

5 R-HEMBB1002302
ESTs
3.6e-54:329:89
Hs.37706:AA005120

10 R-HEMBB1002427
ESTs
4.2e-83:400:98
Hs.130783:AI263114

15 R-HEMBB1002465
EST
9.9e-38:231:90
Hs.133443:AI061405

20 R-HEMBB1002661
ESTs
2.5e-101:472:99
Hs.26878:AI421289

25 R-HEMBB1002663
Small inducible cytokine A5 (RANTES)
7.1e-43:268:88
Hs.155464:AF088219

30 R-MAMMA1000046
EST
3.9e-06:196:65
Hs.155522:AA829725

35 R-MAMMA1000102
Human G protein-coupled receptor (STRL22) mRNA, complete cds
1.1e-31:237:83
Hs.46468:U45984

40 R-MAMMA1000106
ESTs
1.3e-65:333:95
Hs.130749:AI284219

45 R-MAMMA1000118
ESTs
7.3e-95:465:97
Hs.119286:AA126730

50 R-MAMMA1000141
ESTs
4.2e-94:515:93
Hs.8116:H23508

55 R-MAMMA1000204
Homo sapiens dysferlin mRNA, complete cds
2.3e-108:542:96

Hs.143897:AF075575

- 5 R-MAMMA1000226
ESTs
2.1e-112:535:98
Hs.105761:AA903862
- 10 R-MAMMA1000403
ESTs
1.5e-36:162:83
Hs.152413:AA780515
- 15 R-MAMMA1000449
EST
1.5e-40:347:78
Hs.163333:AA879053
- 20 R-MAMMA1000457
Homo sapiens clone 638 unknown mRNA, complete sequence
2.6e-117:570:97
Hs.5825:AF091084
- 25 R-MAMMA1000473
ESTs
1.3e-62:308:99
Hs.53565:W02102
- 30 R-MAMMA1000496
Phosphodiesterase 4C, cAMP-specific (dunce (*Drosophila*)-homolog phosphodiesterase E1)
0.051:125:68
Hs.189:AC005759
- 35 R-MAMMA1000528
ESTs
2.4e-12:216:71
Hs.134105:AI078038
- 40 R-MAMMA1000591
ESTs
5.0e-104:509:98
Hs.151678:AA032243
- 45 R-MAMMA1000614
Homo sapiens mRNA for KIAA0665 protein, complete cds
0.57:251:62
Hs.119004:AB014565
- 50 R-MAMMA1000652
ESTs
0.93:49:87
Hs.13248:R54144
- 55 R-MAMMA1000681
ESTs
1.3e-87:434:97
Hs.46668:N47089
- R-MAMMA1000706

EP 1 130 094 A2

- Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds
3.7e-48:232:100
Hs.18953:AF067223
- 5 R-MAMMA1000788
ESTs
3.7e-108:559:94
Hs.38969:AA130220
- 10 R-MAMMA1000810
ESTs
1.2e-45:347:80
Hs.146811:AA410788
- 15 R-MAMMA1000814
ESTs
1.1e-18:288:70
Hs.140608:N53448
- 20 R-MAMMA1000881
ESTs
1.9e-107:557:96
Hs.141602:N63562
- 25 R-MAMMA1000986
ESTs
3.8e-46:342:83
Hs.132722:AA618531
- 30 R-MAMMA1000994
Homo sapiens mRNA for ISLR, complete cds
1.2e-109:552:96
Hs.102171:AB003184
- 35 R-MAMMA1001043
ESTs
2.3e-88:445:96
Hs.20450:AI094818
- 40 R-MAMMA1001066
Homo sapiens KIAA0414 mRNA, partial cds
1.5e-43:282:81
Hs.127649:AB007874
- 45 R-MAMMA1001094
Homo sapiens clone 243 unknown mRNA, complete sequence
3.0e-116:566:97
Hs.20423:AF091094
- 50 R-MAMMA1001141
ESTs
1.2e-104:496:98
Hs.29669:AI285856
- 55 R-MAMMA1001150
ESTs, Highly similar to MYOSIN LIGHT CHAIN KINASE [Dictyostelium discoideum]
1.9e-59:284:100
Hs.9915:AI300083

5 R-MAMMA1001237
ESTs
0.45:206:62
Hs.121366:AA758653

10 R-MAMMA1001284
ESTs
6.3e-40:279:85
Hs.109765:AI096738

15 R-MAMMA1001310
ESTs, Moderately similar to !!!! ALU SUBFAMTLY J WARNING ENTRY !!!! [H.sapiens]
5.1e-98:498:96
Hs.27264:AA159597

20 R-MAMMA1001418
Human mRNA for platelet-activating factor acetylhydrolase 2, complete cds
1.2e-41:302:85
Hs.86188:D87845

25 R-MAMMA1001532
ESTs
3.9e-22:331:71
Hs.141840:AA028117

30 R-MAMMA1001609
Small inducible cytokine A5 (RANTES)
1.5e-31:277:78
Hs.155464:AF088219

35 R-MAMMA1001615
ESTs
1.1e-72:376:95
Hs.135569:AA923461

40 R-MAMMA1001623
ESTs
7.9e-106:505:98
Hs.22908:AI224910

45 R-MAMMA1001634
Homo sapiens PYRIN (MEFV) mRNA, complete cds
1.9e-44:428:76
Hs.113283:AF018080

50 R-MAMMA1001893
ESTs
8.0e-67:367:92
Hs.19210:W26097

55 R-MAMMA1001901
Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492
4.7e-35:342:69
Hs.127338:AB007961

R-MAMMA1001957
Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2
5.5e-47:383:79

- Hs.1361:M55053
- R-MAMMA1001978
ESTs
5 6.6e-108:560:95
Hs.8859:AA191552
- R-MAMMA1002070
- 10 R-MAMMA1002080
ESTs, Weakly similar to GTP-BINDING PROTEIN YPTM1 [Zea mays]
9.8e-105:542:94
Hs.10092:AI189282
- 15 R-MAMMA1002087
ESTs
4.0e-19:153:84
Hs.136678:AA730474
- 20 R-MAMMA1002095
ESTs
6.8e-34:196:93
Hs.48119:AA454227
- 25 R-MAMMA1002128
ESTs, Highly similar to ABC1 PROTEIN PRECURSOR [Saccharomyces cerevisiae]
9.0e-96:503:94
Hs.39088:AA194773
- 30 R-MAMMA1002142
ESTs
5.6e-21:145:90
Hs.62119:AA043299
- 35 R-MAMMA1002165
ESTs
1.6e-35:351:76
Hs.140413:N47721
- 40 R-MAMMA1002205
Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds
6.4e-42:217:79
Hs.133089:AF064019
- 45 R-MAMMA1002224
ESTs
0.50:170:64
Hs.144140:H04293
- 50 R-MAMMA1002234
- R-MAMMA1002586
ESTs
5.0e-105:529:96
55 Hs.4814:AA631254
- R-MAMMA1002633
ESTs

7.3e-97:470:98
Hs.38039:AI360128

5 R-MAMMA1003126
ESTs

6.1e-114:567:97
Hs.20733:AI417917

10 R-NT2RM4000100
ESTs

3.6e-71:343:99
Hs.92186:AI080282

15 R-NT2RM4000115
ESTs

1.5e-86:405:100
Hs.129151:AA988192

20 R-NT2RM4000198
ESTs

8.4e-83:462:93
Hs.96772:AI369496

25 R-NT2RM4000284
Human IgG Fc receptor hFcRn mRNA, complete cds

5.4e-95:440:100
Hs.110804:U12255

30 R-NT2RM4000295
ESTs

1.1e-112:544:97
Hs.21452:AA581881

35 R-NT2RM4000326
EST

4.0e-59:301:96
Hs.86264:AA206496

40 R-NT2RM4000417
ESTs

2.0e-88:489:93
Hs.29098:AA521439

45 R-NT2RM4000444
ESTs

6.4e-90:497:92
Hs.6129:U66676

50 R-NT2RM4000587
ESTs

1.0e-97:473:98
Hs.24947:AA039350

55 R-NT2RM4000593
ESTs

9.8e-109:554:95
Hs.7579:AA775865

5 R-NT2RM4000648
 ESTs, Moderately similar to GLYCAN-1 PRECURSOR [Homo sapiens]
 7.6e-39:262:85
 Hs.118407:AA001322

10 R-NT2RM4000761
 ESTs
 6.4e-86:433:95
 Hs.153428:AI246519

15 R-NT2RM4000965
 ESTs
 2.8e-102:523:96
 Hs.61790:AA421156

20 R-NT2RM4000997
 R-NT2RM4001321
 ESTs
 2.4e-66:315:100
 Hs.75425:AA149434

25 R-NT2RM4001325
 ESTs
 0.99:104:62
 Hs.116257:AA628680

30 R-NT2RM4001377
 Homo sapiens mRNA for KIAA0638 protein, partial cds
 9.3e-113:553:96
 Hs.77864:AB014538

35 R-NT2RM4001735
 Homo sapiens clone 23904 mRNA sequence
 1.5e-107:553:94
 Hs.67364:AF052129

40 R-NT2RM4001768
 EST
 1.6e-14:82:85
 Hs.140922:R51520

45 R-NT2RM4001843
 ESTs
 2.1e-123:579:98
 Hs.3741:AI057614

50 R-NT2RM4002352
 Homo sapiens hLRp105 mRNA for LI(L receptor related protein 105, complete cds
 1.8e-109:557:95
 Hs.143641:AB009462

55 R-NT2RP2000092
 ESTs
 3.3e-08:286:65
 Hs.79881:AA401302

R-NT2RP2000178

EP 1 130 094 A2

- ESTs, Weakly similar to MITOCHONDRIAL LON PROTEASE HOMOLOG PRECURSOR [H.sapiens]
2.3e-95:462:98
Hs.47305:AA195153
- 5 R-NT2RP2000240
ESTs
1.3e-55:272:98
Hs.125522:AI299693
- 10 R-NT2RP2000394
ESTs
2.4e-107:528:96
Hs.28555:W55892
- 15 R-NT2RP2000447
ESTs, Moderately similar to dynamin, internal form 2, short C-terminal form [H.sapiens]
1.6e-67:357:94
Hs.128788:AA424076
- 20 R-NT2RP2000479
ESTs
2.6e-48:312:86
Hs.146811:AA410788
- 25 R-NT2RP2000514
EST
3.2e-63:348:93
Hs.44542:N33966
- 30 R-NT2RP2000533
ESTs
0.017:307:57
Hs.97873:AA402799
- 35 R-NT2RP2000616
ESTs
1.0e-91:475:95
Hs.50344:AI300539
- 40 R-NT2RP2000649
Homo sapiens mRNA for Hs Ste24p, complete cds
1.4e-66:322:98
Hs.25846:AB016068
- 45 R-NT2RP2000663
ESTs
8.2e-59:311:96
Hs.9728:T98746
- 50 R-NT2RP2000712
EST
1.7e-27:239:76
Hs.161561:W60681
- 55 R-NT2RP2000739
ESTs, Weakly similar to zinc finger protein [H.sapiens]
6.3e-86:462:93
Hs.13323:AA897542

5 R-NT2RP2000818
ESTs
7.3e-99:485:97
Hs.100525:AI310204

10 R-NT2RP2000903
H.sapiens 5T4 gene for 5T4 Oncofetal antigen
1.2e-100:505:96
Hs.82128:AJ012159

15 R-NT2RP2001200
Homo sapiens mRNA for KIAA0676 protein, partial cds
6.6e-59:306:95
Hs.115763:AB014576

20 R-NT2RP2001223
ESTs
1.2e-94:475:95
Hs.27556:AA115361

25 R-NT2RP2001276
ESTs, Moderately similar to regulatory protein [M.musculus]
4.7e-65:354:92
Hs.105547:AI361036

30 R-NT2RP2001388
ESTs
5.5e-83:459:93
Hs.15713:AA485755

35 R-NT2RP2001469
ESTs, Weakly similar to teg292 protein [M.musculus]
2.0e-30:233:83
Hs.68791:AA527270

40 R-NT2RP2001480
Homo sapiens thrombospondin 3 (THBS3) gene, complete cds
2.1e-84:426:95
Hs.82165:L38969

45 R-NT2RP2001495
ESTs, Weakly similar to transporter protein [H.sapiens]
1.7e-14:130:84
Hs.18272:N78499

50 R-NT2RP2001514
ESTs, Weakly similar to PROBABLE CATION-TRANSPORTING ATPASE YEL031W [Saccharomyces cerevisiae]
3.3e-45:242:95
Hs.9275:AA973284

55 R-NT2RP2001538
EST
1.4e-05:111:73
Hs.137268:T39311

R-NT2RP2001562
EST
0.50:35:91

Hs.140505:AA804211

R-NT2RP2001662

Homo sapiens clone 24615 mRNA sequence

5 1.0e-95:485:95

Hs.94785:AF055012

R-NT2RP2001755

Homo sapiens mRNA for KIAA0762 protein, partial cds

10 4.2e-105:576:92

Hs.5378:AB018305

R-NT2RP2001769

ESTs

15 4.2e-102:548:93

Hs.14014:AA745592

R-NT2RP2001817

ESTs

20 6.0e-97:472:97

Hs.31176:AI037953

R-NT2RP2001878

ESTs

25 3.3e-94:475:95

Hs.144655:AI279798

R-NT2RP2001903

ESTs

30 1.7e-88:461:95

Hs.112218:AI038601

R-NT2RP2001915

ESTs

35 7.8e-96:480:96

Hs.100890:AA779892

R-NT2RP2001921

ESTs

40 2.5e-88:466:94

Hs.104859:AA779101

R-NT2RP2001948

ESTs

45 1.9e-81:439:91

Hs.105463:AA583017

R-NT2RP2001956

ESTs

50 8.7e-85:477:91

Hs.12101:AA677423

R-NT2RP2002015

ESTs

55 3.5e-85:431:95

Hs.75425:AA149434

R-NT2RP2002063

EP 1 130 094 A2

EST
0.0083:199:62
Hs.48699:N63049

5 R-NT2RP2002188
ESTs
1.5e-108:559:94
Hs.47320:AA057440

10 R-NT2RP2002232
ESTs
2.5e-113:576:95
Hs.7099:AI089774

15 R-nnnnnnnnnnnnn
Human mRNA for KIAA0383 gene, partial cds
8.0e-102:511:96
Hs.27590:AB002381

20 R-NT2RP2002409
ESTs
3.2e-84:432:95
Hs.128443:AI281991

25 R-NT2RP2002510
ESTs
1.3e-42:303:82
Hs.146811:AA410788

30 R-NT2RP2002527
Thromboxane A2 receptor
2.9e-23:164:88
Hs.89887:D38081

35 R-NT2RP2002533
Homo sapiens putative tumor suppressor gene 26 protein alpha 2 delta calcium channel subunit mRNA, complete cds
4.0e-117:580:96
Hs.127436:AF040709

40 R-NT2RP2002564
Human zinc-finger protein C2H2-150 mRNA, complete cds
4.0e-111:569:94
Hs.108139:U38864

45 R-NT2RP2002674
ESTs, Weakly similar to putative p150 [H.sapiens]
0.010:293:60
Hs.140964:AI214400

50 R-NT2RP2002721
ESTs
5.6e-10:165:69
Hs.108745:H95644

55 R-NT2RP2002824
EST
0.0055:209:58

Hs.136259:AA347883

R-NT2RP2002942

ESTs

5 9.2e-82:422:96

Hs.140952:R59211

R-NT2RP2002974

ESTs

10 5.6e-99:507:96

Hs.43314:AA160543

R-NT2RP2002976

ESTs

15 2.9e-78:397:91

Hs.83575:N28730

R-NT2RP2003042

ESTs

20 2.7e-107:526:97

Hs.6770:AA972732

R-NT2RP2003179

ESTs

25 2.9e-59:335:92

Hs.87019:AA760977

R-NT2RP2003210

ESTs

30 2.1e-80:419:94

Hs.25354:N28667

R-NT2RP2003302

ESTs, Moderately similar to ZINC FINGER PROTEIN 7 [Homo sapiens]

35 2.1e-92:443:98

Hs.112508:AA599140

R-NT2RP2003369

ESTs

40 9.7e-84:462:92

Hs.155116:C16874

R-NT2RP2003383

Homo sapiens mRNA for KIAA0458 protein, complete cds

45 1.3e-112:549:97

Hs.7414:AB007927

R-NT2RP2003390

Homo sapiens SEC63 (SEC63) mRNA, complete cds

50 4.9e-56:286:96

Hs.31575:AF100141

R-NT2RP2003469

Human mRNA for KIAA0355 gene, complete cds

55 6.6e-40:302:83

Hs.153014:AB002353

R-NT2RP2003545

- ESTs
8.0e-121:572:98
Hs.23643:AI299952
- 5 R-NT2RP2003593
EST
1.0:124:62
Hs.59890:AA001879
- 10 R-NT2RP2003599
EST
5.2e-06:319:60
Hs.147887:AI223203
- 15 R-NT2RP2003655
ESTs
9.3e-107:519:97
Hs.5831:AA176450
- 20 R-NT2RP2003664
Homo sapiens mRNA for leptin receptor gene-related protein
5.3e-112:549:96
Hs.23581:Y12670
- 25 R-NT2RP2003931
Human mRNA for KIAA0365 gene, partial cds
1.7e-113:571:96
Hs.84123:AB002363
- 30 R-NT2RP2003940
EST
3.0e-71:385:93
Hs.162657:AA603590
- 35 R-NT2RP2003950
Homo sapiens clone 24778 unknown mRNA
5.0e-98:494:95
Hs.25306:AF070572
- 40 R-NT2RP2004069
Human kpn1 repeat mrna (cdna clone pcd-kpn1-8), 3' end
6.3e-54:556:74
Hs.103948:K00627
- 45 R-NT2RP2004108
ESTs, Moderately similar to ZINC FINGER PROTEIN ZFP-36 [Homo sapiens]
6.9e-92:442:98
Hs.14831:AI261191
- 50 R-NT2RP2004141
ESTs
8.3e-29:171:93
Hs.25700:AI338437
- 55 R-NT2RP2004179
ESTs
3.1e-71:461:88
Hs.6748:R68509

5 R-NT2RP2004205
ESTs
2.6e-44:397:78
Hs.95115:AA206594

10 R-NT2RP2004447
ESTs
4.0e-101:494:97
Hs.51655:AA523276

15 R-NT2RP2004495
ESTs, Weakly similar to transporter protein [H.sapiens]
6.1e-71:417:92
Hs.18272:N78499

20 R-NT2RP2004524
ESTs
1.8e-93:482:95
Hs.119285:AI225008

25 R-NT2RP2004556
Homo sapiens mRNA for KIAA0459 protein, partial cds
8.8e-48:353:82
Hs.28169:AB007928

30 R-NT2RP2004606
Tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor)
3.5e-116:576:96
Hs.148726:X03124

35 R-NT2RP2004648
ESTs
5.9e-114:600:93
Hs.3741:AI057614

40 R-NT2RP2004670
ESTs
1.7e-92:488:94
Hs.6262:T89093

45 R-NT2RP2004794
EST
0.44:205:57
Hs.147759:AI220726

50 R-NT2RP2004837
ESTs
6.9e-111:576:94
Hs.12305:AA166889

55 R-NT2RP2004847
ESTs
8.3e-94:445:99
Hs.53996:AI268861

R-NT2RP2005027
GLUCOSE TRANSPORTER TYPE 3, BRAIN
2.5e-104:508:97

Hs.7594:M20681

R-NT2RP2005069
ESTs, Highly similar to vacuolar protein sorting homolog r-vps33b [R.norvegicus]
5 4.7e-111:541:97
Hs.26510:AA700425

R-NT2RP2005163
ESTs
10 6.8e-64:327:89
Hs.83575:N28730

R-NT2RP2005181
ESTs, Moderately similar to HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 [H.sapiens]
15 1.6e-106:527:97
Hs.86362:AA205485

R-NT2RP2005247
MHC class II transactivator
20 7.9e-35:465:69
Hs.3076:U18259

R-NT2RP2005378
ESTs
25 3.4e-110:566:94
Hs.23060:N64748

R-NT2RP2005391
ESTs
30 5.5e-82:463:92
Hs.118793:AA192438

R-NT2RP2005425
Homo sapiens mRNA for KIAA0803 protein, partial cds
35 2.6e-101:526:94
Hs.58103:AB018346

R-NT2RP2005463
ESTs, Weakly similar to weakly similar to S. cervisiae PTM1 precursor [C.elegans]
40 7.6e-111:554:97
Hs.16492:N95400

R-NT2RP2005514
ESTs
45 1.8e-97:490:95
Hs.109677:AA447864

R-NT2RP2005535
EST
50 5.1e-40:399:73
Hs.127142:AA937570

R-NT2RP2005541
ESTs
55 5.2e-114:573:96
Hs.70823:AI378619

R-NT2RP2005597

EP 1 130 094 A2

- ESTs, Weakly similar to rotated abdomen protein [D.melanogaster]
3.7e-109:543:96
Hs.99654:AA670164
- 5 R-nnnnnnnnnnnnn
ESTs
1.1 e-100:501:97
Hs.112011:AA987961
- 10 R-NT2RP2005666
ESTs
2.7e-106:560:94
Hs.42814:AA205754
- 15 R-NT2RP2005774
Homo sapiens apoptosis-related mRNA, 3'UTR, partial sequence
7.0e-96:440:96
Hs.139345:AF035364
- 20 R-NT2RP2005878
ESTs
2.8e-89:479:93
Hs.142305:R42591
- 25 R-NT2RP2005883
ESTs
1.0e-85:431:96
Hs.6909:AA928115
- 30 R-NT2RP2005887
ESTs
5.5e-109:566:94
Hs.12305:AA166889
- 35 R-nnnnnnnnnnnnn
Paired box homeotic gene 6 (aniridia, keratitis)
1.6e-116:578:96
Hs.89506:M93650
- 40 R-NT2RP2005994
EST
0.0061:129:68
Hs.160756:AI310589
- 45 R-NT2RP2006004
ESTs, Weakly similar to KIAA0405 [H.sapiens]
4.7e-45:303:86
Hs.14146:W92235
- 50 R-NT2RP2006042
EST
0.64:84:71
Hs.133275:AI053487
- 55 R-NT2RP2006092
ESTs, Weakly similar to HYPOTHETICAL PROTEIN KIAA0168 [H.sapiens]
1.1e-75:384:95
Hs.32822:AI194045

5 R-NT2RP2006099
ESTs
6.9e-35:224:82
Hs.139446:AA461080

10 R-NT2RP2006134
EST
1.3e-95:445:100
Hs.162033:AA514590

15 R-NT2RP2006269
Human mRNA for KIAA0315 gene, partial cds
0.96:343:60
Hs.3989:AB002313

20 R-NT2RP2006512
Homo sapiens clone 23904 mRNA sequence
1.5e-107:531:96
Hs.67364:AF052129

25 R-NT2RP3000011
ESTs
7.3e-92:508:91
Hs.112041:W26001

30 R-NT2RP3000022
EST
0.78:175:63
Hs.135650:AA902912

35 R-NT2RP3000059
ESTs
6.2e-99:475:98
Hs.123136:AA631067

40 R-NT2RP3000063
ESTs
9.7e-105:554:94
Hs.7542:AA121663

45 R-nnnnnnnnnnnnn
Human mRNA for KIAA0314 gene, partial cds
5.0e-17:307:65
Hs.155045:AB002312

50 R-NT2RP3000148
ESTs
6.4e-101:527:94
Hs.58461:W80378

55 R-NT2RP3000169
Homo sapiens MRS1 mRNA, complete cds
1.4e-111:551:96
Hs.30985:AF093239

R-NT2RP3000171
EST
0.45:205:57

Hs.147759:AI220726

- 5 R-NT2RP3000172
ESTs
2.0e-89:494:93
Hs.6262:T89093
- 10 R-NT2RP3000201
Human mRNA for KIAA0355 gene, complete cds
1.1e-40:305:83
Hs.153014:AB002353
- 15 R-NT2RP3000232
ESTs, Weakly similar to kruppel-related zinc finger protein [H.sapiens]
5.7e-65:386:90
Hs.4841:AI279875
- 20 R-NT2RP3000304
Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds
1.1e-109:541:97
Hs.23672:AF074264
- 25 R-NT2RP3000378
EST
2.0e-05:112:74
Hs.137268:T39311
- 30 R-NT2RP3000436
EST
1.2e-08:347:62
Hs.158830:AI377454
- 35 R-NT2RP3000444
ESTs
3.3e-70:314:99
Hs.57973:AI263207
- 40 R-NT2RP3000460
EST
1.9e-50:294:92
Hs.7260:T23737
- 45 R-NT2RP3000481
PROBABLE G PROTEIN-COUPLED RECEPTOR GPR6
1.0:183:59
Hs.46332:U18549
- 50 R-NT2RP3000616
ESTs
3.0e-71:309:93
Hs.41296:N71923
- 55 R-NT2RP3000645
ESTs
1.5e-101:550:92
Hs.21910:AA020743
- R-NT2RP3000652

- ESTs
6.6e-88:411:100
Hs.43134:AA766138
- 5 R-NT2RP3000676
Homo sapiens mRNA for KIAA0446 protein, complete cds
1.0e-104:542:94
Hs.158286:AB007915
- 10 R-NT2RP3000677
ESTs
0.33:307:59
Hs.133022:AI374739
- 15 R-NT2RP3000721
ESTs
1.6e-75:390:90
Hs.83575:N28730
- 20 R-NT2RP3000789
ESTs
1.5e-71:340:99
Hs.37776:H93038
- 25 R-NT2RP3000818
ESTs
1.9e-52:330:88
Hs.111052:H80504
- 30 R-NT2RP3000820
EST
9.1e-05:82:74
Hs.124352:AA830406
- 35 R-NT2RP3000838
Homo sapiens mRNA for KIAA0638 protein, partial cds
1.5e-100:522:94
Hs.77864:AB014538
- 40 R-NT2RP3000871
ESTs
3.9e-76:424:91
Hs.121642:AA772262
- 45 R-NT2RP3000907
ESTs, Weakly similar to PROBABLE CATION-TRANSPORTING ATPASE YEL031W [Saccharomyces cerevisiae]
4.5e-95:493:94
Hs.9275:AA973284
- 50 R-NT2RP3000921
ESTs
4.1e-52:283:94
Hs.49714:AA442453
- 55 R-NT2RP3001012
Homo sapiens mRNA for CMP-sialic acid transporter, complete cds
0.60:250:61
Hs.82921:D87969

5 R-NT2RP3001044
ESTs
3.5e-106:547:95
Hs.12305:AA166889

10 R-NT2RP3001061
ESTs
1.3e-96:453:99
Hs.4916:AI149707

15 R-NT2RP3001159
ESTs, Weakly similar to T13F2.1 [C.elegans]
3.8e-47:302:90
Hs.6281:AA523081

20 R-NT2RP3001170
Homo sapiens mRNA for KIAA0784 protein, partial cds
2.8e-118:561:98
Hs.3657:AB018327

25 R-NT2RP3001195
ESTs
1.5e-40:461:72
Hs.152438:AI334078

30 R-NT2RP3001240
EST
1.9e-50:294:92
Hs.7260:T23737

35 R-NT2RP3001271
ESTs
1.1e-77:432:92
Hs.12211:AA908631

40 R-NT2RP3001322
ESTs
0.25:331:60
Hs.44330:N32264

45 R-NT2RP3001542
EST
0.0032:432:58
Hs.148107:AA693476

50 R-NT2RP3001560
EST
3.5e-50:281:93
Hs.101727:H16171

55 R-NT2RP3001592
ESTs
3.2e-65:344:93
Hs.28964:AA715101

R-NT2RP3001685
EST
3.0e-37:165:81

Hs.160895:AI365871
 R-NT2RP3001738
 ESTs, Weakly similar to T13F2.1 [C.elegans]
 5 3.8e-47:302:90
 Hs.6281 :AA523081

R-NT2RP3001754
 EST
 10 0.00043:104:69
 Hs.148331:AA911426

R-NT2RP3001858
 ESTs
 15 7.6e-93:502:93
 Hs.153524:AA533582

R-NT2RP3001976
 ESTs
 20 5.0e-104:516:96
 Hs.35461:AA777644

R-NT2RP3002015

25 R-NT2RP3002160
 ESTs
 1.4e-34:178:99
 Hs.130783:AI263114

30 R-NT2RP3002281
 Homo sapiens mRNA for KIAA0765 protein, partial cds
 3.5e-83:446:93
 Hs.62318:AB018308

35 R-NT2RP3002286
 ESTs
 2.1e-103:513:97
 Hs.58570:AA521423

40 R-NT2RP3002311
 ESTs
 1.4e-108:538:96
 Hs.3741:AI057614

45 R-NT2RP3002324
 ESTs
 3.7e-102:483:99
 Hs.99668:AA829521

50 R-NT2RP3002342
 ESTs, Weakly similar to transporter protein [H.sapiens]
 2.0e-60:339:95
 Hs.18272:N78499

55 R-NT2RP3002353
 ESTs
 6.8e-98:484:97
 Hs.9732:AA527784

5 NNNNNNNNNNNNNN
 Homo sapiens mRNA for KIAA0788 protein, partial cds
 2.7e-29:214:85
 Hs.2397:Z70200

10 NNNNNNNNNNNNNN
 ESTs
 3.0e-72:389:94
 Hs.32246:AA464020

15 R-NT2RP3002448
 ESTs, Weakly similar to Y48E1B.t [C.elegans]
 1.0e-19:131:75
 Hs.8715:H58021

20 R-NT2RP3002571
 ESTs
 1.1e-78:407:95
 Hs.27356:AA740928

25 R-NT2RP3002664
 ESTs
 1.2e-56:341:90
 Hs.23308:AA115020

30 R-NT2RP3002721
 EST
 2.8e-41:302:82
 Hs.124936:AA825548

35 R-NT2RP3002737
 EST
 1.7e-51:267:97
 Hs.161348:AI422470

40 R-NT2RP3002738
 ESTs, Weakly similar to enhancer of filamentation 1 [H.sapiens]
 1.7e-106:530:96
 Hs.4894:AI191323

45 R-NT2RP3002836
 ESTs
 4.6e-49:282:92
 Hs.107979:AA146994

50 R-NT2RP3002887
 ESTs
 6.3e-98:516:94
 Hs.11900:AA535065

55 R-NT2RP3002900
 ESTs
 2.0e-29:155:99
 Hs.153329:AA112325

R-NT2RP3002958

EP 1 130 094 A2

Homo sapiens clone 23851 mRNA sequence
6.6e-119:575:98
Hs.10065:AF035313

5 R-NT2RP3002983
ESTs
1.1e-61:374:90
Hs.17834:AA128246

10 R-NT2RP3003000
Homo sapiens T-type calcium channel alpha-1 subunit mRNA, complete cds
4. 1e-65:358:94
Hs.122359:AF051946

15 R-NT2RP3003076
ESTs
2.6e-95:507:93
Hs.21910:AA020743

20 R-NT2RP3003354
ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]
2.1e-78:385:96
Hs.92177:AI207792

25 R-NT2RP3003448
ESTs
6.7e-105:521:96
Hs.106833:AA470128

30 R-NT2RP3003469
ESTs
1.1e-91:461:96
Hs.75425: AA149434

35 R-NT2RP3003473

R-NT2RP3003527
Homo sapiens mRNA for protein kinase Dyrk1B
1.6e-92:445:97
Hs.130988:Y17999

40 R-NT2RP3003532
ESTs
0.022:193:63
Hs.122593:Z99400

45 R-nnnnnnnnnnnnn
EST
0.036:279:59
Hs.158745:AI375513

50 R-NT2RP3003559
ESTs
9.8e-106:513:97
Hs.44970:AI061464

55 R-NT2RP3003614
Homo sapiens mRNA, chromosome 1 specific transcript KIAA0510

0.00016:113:69
Hs.92660:AB007979

5 R-NT2RP3003729
ESTs
1.2e-43:289:86
Hs.106401:R50967

10 R-NT2RP3003849
ESTs
5.4e-91:435:98
Hs.144840:AI221746

15 R-NT2RP3003874
ESTs
0.21:323:59
Hs.42919:AA805764

20 R-NT2RP3003963
ESTs
1.7e-90:438:97
Hs.105894:AA564110

25 R-NT2RP3004000
ESTs
2.9e-101:559:91
Hs.21910:AA020743

30 R-NT2RP3004025
ESTs
2.3e-108:517:98
Hs.15356:AA911109

35 R-NT2RP3004075
ESTs
7.4e-84:453:93
Hs.22412:AA523036

40 R-NT2RP3004083
ESTs, Weakly similar to R06B9.b [C.elegans]
4.2e-84:474:91
Hs.30432:W28988

45 R-NT2RP3004090
ESTs
1.0:207:61
Hs.92832:AA631027

50 R-NT2RP3004119
EST
1.8e-50:248:99
Hs.162023:AA506128

55 R-NT2RP3004130
ESTs
1.1e-103:520:96
Hs.10491:W28968

EP 1 130 094 A2

5 R-NT2RP3004133
ESTs
4.7e-104:545:93
Hs.15727:H98190

10 R-NT2RP3004202
ESTs
1.1e-98:471:98
Hs.61884:AI335985

15 R-NT2RP3004294
ESTs, Weakly similar to R06B9.b [C.elegans]
2.4e-96:500:94
Hs.30432:W28988

20 R-NT2RP3004309
ESTs, Weakly similar to T13F2.1 [C.elegans]
3.5e-48:308:90
Hs.6281:AA523081

25 R-NT2RP3004321
ESTs
2.6e-99:494:97
Hs.19306:N53491

30 R-NT2RP3004345
ESTs
5.4e-95:444:99
Hs.107149:AI379497

35 R-NT2RP3004355
ESTs
3.9e-99:490:97
Hs.43410:N23651

40 R-NT2RP3004374
ESTs
1.2e-90:462:95
Hs.75425:AA149434

45 R-NT2RP3004406
ESTs
1.9e-100:502:96
Hs.24936:AA479402

50 R-NT2RP3004481
ESTs
1.6e-53:370:87
Hs.11953:AA194120

55 R-NT2RP3004552
ESTs, Weakly similar to gene SEZ-6 [M.musculus]
7.8e-92:488:93
Hs.6314:AA522619

R-NT2RP3004625
Homo sapiens I-1 receptor candidate protein mRNA, complete cds
2.6e-50:352:84

Hs.26285:AF082516

- 5 R-NT2RP3004640
ESTs
1.1e-105:551:94
Hs.83348:AA527170
- 10 R-NT2RP3004647
Homo sapiens mRNA for KIAA0446 protein, complete cds
4.9e-111:555:96
Hs.158286:AB007915
- 15 R-NT2RP4000108
ESTs
2.9e-94:479:96
Hs.6625:AA115182
- 20 R-NT2RP4000634
ESTs
3.0e-120:572:98
Hs.28827:AI125541
- 25 R-NT2RP4000962
ESTs, Weakly similar to SPORULATION-SPECIFIC PROTEIN 1 [Saccharomyces cerevisiae]
6.0e-17:98:98
Hs.4789:AI418298
- 30 R-NT2RP4001001
ESTs
3.1e-117:567:97
Hs.4931:AA523860
- 35 R-NT2RP4001009
Homo sapiens mRNA for Hs Ste24p, complete cds
1.6e-83:404:98
Hs.25846:AB016068
- 40 R-NT2RP4001467
5' nucleotidase (CD73)
5.9e-113:545:97
Hs.153952:X55740
- 45 R-NT2RP4001877
ESTs, Highly similar to GONADOTROPIN-RELEASING HORMONE RECEPTOR [Rattus norvegicus]
2.2e-67:375:93
Hs.16389:AA206356
- R-NT2RP4001879
- 50 R-NT2RP4002187
EST
0.010:117:70
Hs.160416:AI394161
- 55 R-NT2RP4002451
EST
1.3e-62:386:87
Hs.57082:H25761

5 R-NT2RP4002715
ESTs
6.9e-111:552:96
Hs.12305:AA166889

10 R-NT2RP4002750
ESTs, Moderately similar to HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 [H.sapiens]
7.0e-109:532:97
Hs.86362:AA205485

15 R-OVARC1000003
ESTs
1.3e-74:391:95
Hs.105039:AA477819

20 R-OVARC1000090
Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds
9.9e-44:471:75
Hs.129735:AF010144

25 R-OVARC1000105
60S RIBOSOMAL PROTEIN L38
8.8e-14:83:100
Hs.2017:Z26876

30 R-OVARC1000137
ESTs
3.0e-84:387:95
Hs.22028:AA167715

35 R-OVARC1000208
Human mRNA for KIAA0392 gene, partial cds
2.8e-51:313:89
Hs.40100:AB002390

40 R-OVARC1000255
Spleen tyrosine kinase
2.8e-106:510:98
Hs.74101:L28824

45 R-OVARC1000275
ESTs, Highly similar to PROBABLE PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE FAB [Saccharomyces cerevisiae]
6.9e-105:556:94
Hs.5748:AA608559

50 R-OVARC1000298
ESTs, Weakly similar to T03G11.6 gene product [C.elegans]
2.4e-56:338:90
Hs.108354:W19984

55 R-OVARC1000307
ESTs
2.4e-101:563:93
Hs.24479:N25972

R-OVARC1000313
Homo sapiens mRNA for KIAA0573 protein, partial cds

EP 1 130 094 A2

5.0e-98:534:93
Hs.154023:AB011145

5 R-OVARC1000331
Homo sapiens chromosome 9, P1 clone 11659
1.0e-55:281:97
Hs.3439:AC004472

10 R-OVARC1000410
Homo sapiens clone 23767 and 23782 mRNA sequences
3.3e-90:462:94
Hs.8025:AF007150

15 R-OVARC1000439
ESTs, Highly similar to HYPOTHETICAL 64.3 KD GTP-BINDING PROTEIN C02F5.3 IN CHROMOSOME III
[*Caenorhabditis elegans*]
1.6e-99:510:95
Hs.7471:AI143226

20 R-OVARC1000467

R-OVARC1000529
ESTs
5.7e-93:461:96

25 Hs.21396:AA114834

R-OVARC1000553
ESTs
4.3e-51:351:87

30 Hs.42979:W31096

R-OVARC1000775

R-OVARC1000811
ESTs
1.3e-82:441:95
Hs.73452:AA581386

40 R-OVARC1000853
ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]
3.1e-95:492:95
Hs.6853:AA401703

45 R-OVARC1000873
ESTs
2.4e-46:281:91
Hs.43857:R91358

50 R-OVARC1000916
H.sapiens PISSLRE mRNA
1.9e-112:588:94
Hs.77313:X78342

55 R-OVARC1000956
Homo sapiens mRNA for MDC3, complete cds
0.18:259:62
Hs.7164:AB009672

5 R-OVARC1000995
EST
6.6e-43:343:81
Hs.149580:AI281881

10 R-OVARC1001030
ESTs, Weakly similar to neuroendocrine-specific protein C [H.sapiens]
1.5e-21:116:100
Hs.65450:AA055913

15 R-OVARC1001049
ESTs
1.2e-70:369:95
Hs.42949:N21131

20 R-OVARC1001086
Homo sapiens cyclin T2a mRNA, complete cds
1.3e-106:569:94
Hs.155478:AF048731

25 R-OVARC1001132
INITIATION FACTOR IF-2, MITOCHONDRIAL PRECURSOR
0.16:170:64
Hs.149894:L34600

30 R-OVARC1001163
ESTs
1.9e-39:219:94
Hs.126067:AI344351

35 R-OVARC1001222
ESTs
0.62:177:63
Hs.141162:H66213

40 R-OVARC1001260
ESTs
2.1e-79:425:94
Hs.105039:AA477819

45 R-OVARC1001336
ESTs
9.2e-75:439:91
Hs.105039:AA477819

50 R-OVARC1001338
ESTs
2.3e-19:139:92
Hs.7978:W05059

55 R-OVARC1001569
ESTs
2.4e-83:412:97
Hs.21396:AA114834

R-OVARC1001570
ESTs
2.6e-49:280:94

Hs.3854:R12478

- 5 R-OVARC1001596
EST
8.2e-15:93:97
Hs.136918:AA811543
- 10 R-OVARC1001607
ESTs
0.019:413:56
Hs.24684:AA587245
- 15 R-OVARC1001725
ESTs
1.4e-96:504:95
Hs.23754:N29716
- R-OVARC1001727
- 20 R-OVARC1001807
Hormone receptor (growth factor-inducible nuclear protein N10)
8.5e-78:425:94
Hs.1119:D49728
- 25 R-OVARC1001833
ESTs
1.0e-63:325:96
Hs.126912:AA469087
- 30 R-OVARC1001991
ESTs
1.3e-92:467:95
Hs.26506:AI348000
- 35 R-OVARC1002058
ESTs
2.5e-89:512:91
Hs.58093:W63576
- 40 R-OVARC1002178
ESTs
3.3e-99:487:96
Hs.136527:AI419398
- 45 R-PLACE1000033
ESTs
0.012:202:59
Hs.157400:AI370528
- 50 R-PLACE1000231
ESTs
2.9e-56:285:96
Hs.36688:AA603479
- 55 R-PLACE1000258
EST
3.4e-50:353:83
Hs.146794:AI149478

5 R-PLACE1000442
 ESTs, Moderately similar to ZINC FINGER PROTEIN ZFP-36 [Homo sapiens]
 5.5e-91:437:98
 Hs.14831:AI261191

10 R-PLACE1000560
 ESTs
 3.7e-60:317:94
 Hs.65713:AI269328

15 R-PLACE1000740
 ESTs
 4.2e-67:362:94
 Hs.163434:T79849

20 R-PLACE1000912
 ESTs
 3.4e-57:329:92
 Hs.121907:R66773

25 R-PLACE1000914
 ESTs
 2.6e-71:419:89
 Hs.90809:AA010979

30 R-PLACE1000927
 ESTs, Weakly similar to N-methyl-D-aspartate receptor-associated protein [D.melanogaster]
 7.8e-111:545:97
 Hs.8661:AI189791

35 R-PLACE1000986
 ESTs
 1.5e-91:431:99
 Hs.42458:AA452296

40 R-PLACE1001016
 ESTs
 3.4e-45:231:97
 Hs.121013:AA324765

45 R-PLACE1001100
 Homo sapiens nephrin (NPHS1) mRNA, complete cds
 3.5e-43:321:83
 Hs.128834:AF035835

50 R-PLACE1001114
 Human clone 23732 mRNA, partial cds
 1.6e-42:305:83
 Hs.81281:U79258

55 R-PLACE1001123
 ESTs, Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-28.4 KD [Saccharomyces cerevisiae]
 1.2e-51:310:90
 Hs.7773:AA127629

R-PLACE1001183
 Human mRNA for KIAA0308 gene, partial cds

0.88:182:65
Hs.10351:AB002306

5 R-PLACE1001229
ESTs
5.2e-90:471:95
Hs.18271:N92774

10 R-PLACE1001231

15 R-PLACE1001340
Homo sapiens mRNA for KIAA0719 protein, complete cds
6.6e-53:265:98
Hs.21198:AB018262

20 R-PLACE1001401
ESTs
1.9e-72:362:96
Hs.20161:AA056410

25 R-PLACE1001407
ESTs
2.1e-36:249:85
Hs.23579:W38893

30 R-PLACE1001464
5' nucleotidase (CD73)
1.0e-91:457:96
Hs.153952:X55740

35 R-PLACE1001500
ESTs, Weakly similar to DNA helicase Q1 [H.sapiens]
2.0e-19:150:87
Hs.154199:AA155882

40 R-PLACE1001516
EST
1.9e-11:109:82
Hs.137486:AA425225

45 R-PLACE1001536
Human BRCA2 region, mRNA sequence CG016
0.28:146:63
Hs.112434:U50529

50 R-PLACE1001564
ESTs
6.3e-14:109:88
Hs.26519:AA442703

55 R-PLACE1001655
Homo sapiens Shab-related delayed-rectifier K+ channel alpha subunit (KCNS3) mRNA, complete cds
1.2e-118:578:97
Hs.47584:AF043472

R-PLACE1001788
ESTs
8.4e-38:205:95

5 Hs.23800:AA524095
R-PLACE1001795
ESTs, Weakly similar to HYPOTHETICAL 30.6 KD PROTEIN IN SCP160-MRPL8 INTERGENIC REGION PRE-CURSOR [S.cerevisiae]
2.5e-77:392:96
Hs.7745:H92988

10 R-PLACE1001836
ESTs
1.5e-49:296:90
Hs.17691:H60366

15 R-PLACE1001918
ESTs, Weakly similar to multispanning membrane protein [H.sapiens]
2.0e-42:304:85
Hs.110439:N93209

20 R-PLACE1001949
R-PLACE1002080
Small inducible cytokine A5 (RANTES)
8.5e-41:296:82
Hs. 155464:AF088219

25 R-PLACE1002095
ESTs
8.5e-25:227:81
Hs.110488:AA034235

30 R-PLACE1002153
Homo sapiens TACC2 protein (TACC2) mRNA, partial cds
1.5e-101:514:95
Hs.90415:AF095791

35 R-PLACE1002329
ESTs
8.7e-48:257:94
Hs.126062:AA411593

40 R-PLACE1002355
ESTs
7.7e-71:362:95
Hs.120866:AI076780

45 R-PLACE1002374
Cathepsin L
8.4e-103:501:97
Hs.78056:X12451

50 R-PLACE1002518
ESTs
6.9e-97:471:97
Hs.104893:AA576941

55 R-PLACE1002547
Homo sapiens mRNA for KIAA0719 protein, complete cds
6.5e-55:276:97

Hs.21198:AB018262

- 5 R-PLACE1002726
Human DNA-binding protein ABP/ZF mRNA, complete cds
3.8e-39:212:94
Hs.86185:U82613
- 10 R-PLACE1002905
Homo sapiens mRNA for KIAA0563 protein, complete cds
2.9e-41:330:81
Hs.15731:AB011135
- R-PLACE1002911
- 15 R-PLACE1002967
ESTs
1.0e-43:384:77
Hs.132722:AA618531
- 20 R-PLACE1003135
ESTs
8.2e-94:462:97
Hs.23643:AI299952
- 25 R-PLACE1003163
Homo sapiens DBI-related protein mRNA, complete cds
3.5e-110:541:96
Hs.15250:AF069301
- 30 R-PLACE1003407
Homo sapiens putative transmembrane protein (CLN5) mRNA, complete cds
5.5e-49:287:91
Hs.30213:AF068227
- 35 R-PLACE1003428
ESTs, Moderately similar to BIOTINIDASE PRECURSOR [Homo sapiens]
6.8e-83:406:97
Hs.17586:AA461448
- 40 R-PLACE1003438
ESTs
2.9e-83:463:92
Hs.11067:H30385
- 45 R-PLACE1003460
ESTs
7.0e-27:187:87
Hs.18763:H56292
- 50 R-nnnnnnnnnnnnn
ESTs
1.7e-52:265:97
Hs.114049:AI091839
- 55 R-PLACE1003573
Human mRNA for KIAA0160 gene, partial cds
0.13:102:69
Hs.79880:D63881

5 R-PLACE1003598
ESTs
8.0e-39:210:95
Hs.26286:AA040823

10 R-PLACE1003644
EST
0.47:84:73
Hs.105856:AA551478

15 R-PLACE1003737
ESTs
1.1e-77:366:100
Hs.62699:AA707766

20 R-PLACE1003772
Human mRNA for KIAA0355 gene, complete cds
6.1e-27:551:65
Hs.153014:AB002353

25 R-PLACE1003839
ESTs
0.019:244:59
Hs.137825:AA778400

30 R-PLACE1003845
EST
5.3e-79:416:93
Hs.150153:AI300555

35 R-PLACE1003852
Homo sapiens mRNA for KIAA0758 protein, partial cds
2.2e-87:439:96
Hs.22039:AB018301

40 R-PLACE1004028
Sialyltransferase 4A (beta-galactosidase alpha-2,3-sialyltransferase)
0.73:128:71
Hs.60617:L13972

45 R-PLACE1004078
ESTs
1.7e-69:353:96
Hs.142075:AA654529

50 R-PLACE1004166
ESTs
1.7e-64:362:92
Hs.10177:AA191619

55 R-nnnnnnnnnnnnn
EST
0.98:59:71
Hs.132255:AI027216

R-PLACE1004199
ESTs
1.3e-55:279:97

Hs.147585:AI217699

- 5 R-PLACE1004279
ESTs
3.7e-68:373:93
Hs.145531:H87181
- 10 R-PLACE1004282
- 15 R-PLACE1004305
Homo sapiens mRNA for KIAA0740 protein, complete cds
6.4e-79:377:99
Hs.15099:AB018283
- 20 R-PLACE1004441
ESTs
1.8e-46:244:95
Hs.107082:R63714
- 25 R-PLACE1004450
- 30 R-PLACE1004482
ESTs
1.2e-92:491:93
Hs.17840:AI269915
- 35 R-PLACE1004492
ESTs
6.1e-54:278:95
Hs.55862:A1341676
- 40 R-PLACE1004519
ESTs
3.1e-25:133:100
Hs.47378:AI193598
- 45 R-PLACE1004520
Pregnancy-specific beta-1 glycoprotein 4
2.8e-66:390:89
Hs.108936:X17097
- 50 R-PLACE1004630
ESTs
7.3e-58:338:92
Hs.155506:AI281549
- 55 R-PLACE1004637
ESTs
1.1e-37:309:82
Hs.20102:AA150165
- R-PLACE1004648
ESTs
2.3e-67:340:96
Hs.69321:AA633240
- R-PLACE1004816
Homo sapiens mRNA for Hakata antigen, complete cds

- 1.8e-104:586:90
Hs.9225:D88587
- 5 R-PLACE1004887
ESTs, Weakly similar to GOLIATH PROTEIN [D.melanogaster]
2.6e-30:222:86
Hs.18557:AA203416
- 10 R-PLACE1005003
ESTs
0.99:123:68
Hs.146244:AI276718
- 15 R-PLACE1005005
Homo sapiens ubiquitin conjugating enzyme G2 (UBE2G2) mRNA, complete cds
6.8e-58:299:95
Hs.151614:AF032456
- 20 R-PLACE1005031
ESTs
4.7e-57:325:92
Hs.31196:H13265
- 25 R-PLACE1005239
Homo sapiens mRNA for HIRIP3 protein, clone pH4-17
1.4e-86:450:93
Hs.26484:AJ223351
- 30 R-PLACE1005250
ESTs, Moderately similar to maternal transcript Maid [M.musculus]
1.7e-106:521:97
Hs.36794:AI038407
- 35 R-PLACE1005383
Homo sapiens UP50 mRNA, complete cds
6.3e-79:471:88
Hs.11494:AF093118
- 40 R-PLACE1005410
EST
2.3e-49:296:90
Hs.7260:T23737
- 45 R-PLACE1005426
Pregnancy-specific beta-1 glycoprotein 4
8.0e-109:576:93
Hs.108936:X17097
- 50 R-PLACE1005519
ESTs
5.4e-108:569:93
Hs.23643:AI299952
- 55 R-PLACE1005539
ESTs, Weakly similar to p20 protein [R.norvegicus]
4.5e-05:107:77
Hs.56874:W61026

5 R-PLACE1005544
ESTs
4.2e-57:280:98
Hs.155391:AA451633

10 R-PLACE1005569
ESTs
2.7e-90:470:94
Hs.8904:AI129815

15 R-PLACE1005601

R-PLACE1005660
ESTs, Highly similar to HYPOTHETICAL 64.3 KD GTP-BINDING PROTEIN C02F5.3 IN CHROMOSOME III
[*Caenorhabditis elegans*]
1.4e-91:483:93
Hs.7471:AI143226

20 R-PLACE1005669
ESTs
1.7e-84:438:95
Hs.18271:N92774

25 R-PLACE1005682
ESTs
6.3e-80:482:88
Hs.128679:AI160081

30 R-PLACE1005725
ESTs
1.5e-98:519:93
Hs.11360:AI147467

35 R-PLACE1005736
ESTs
3.1e-110:561:95
Hs.24111:AI346026

40 R-PLACE1005745
ESTs
2.4e-96:473:97
Hs.126935:AA603217

45 R-PLACE1005768
Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2
4.0e-46:387:77
Hs.1361:M55053

50 R-PLACE1005815
Homo sapiens PYRIN (MEFV) mRNA, complete cds
7.1e-56:324:79
Hs.113283:AF018080

55 R-PLACE1005878
ESTs
3.1e-75:388:94
Hs.153483:AA569128

5 R-PLACE1005927
ESTs
4.3e-64:403:87
Hs.126899:N50907

10 R-PLACE1006071
ESTs
5.3e-96:510:93
Hs.24398:AI262946

15 R-PLACE1006073
Homo sapiens mRNA for glucuronyltransferase I, complete cds
3.0e-97:504:93
Hs.26492:AB009598

20 R-PLACE1006079
ESTs
3.1e-79:453:90
Hs.134194:AI142137

25 R-PLACE1006093
ESTs
1.3e-78:378:98
Hs.129327:AI201040

30 R-nnnnnnnnnnnnn
R-PLACE1006219
EST
1.6e-75:412:92
Hs.150153:AI300555

35 R-PLACE1006277
ESTs
2.8e-92:493:93
Hs.8904:AI129815

40 R-PLACE1006290
ESTs
2.8e-92:433:99
Hs.23445:AA489015

45 R-PLACE1006443
ESTs
2.5e-73:419:91
Hs.90809:AA010979

50 R-PLACE1006515
Homo sapiens mRNA for KIAA0576 protein, partial cds
6.9e-78:413:94
Hs.14687:AB011148

55 R-PLACE1006716
ESTs
4.8e-44:262:88
Hs.8503:AI393886

R-PLACE1006786

ESTs
6.3e-89:431:98
Hs.42458:AA452296

5 R-PLACE1006809
ESTs
1.6e-68:377:92
Hs.8956:AI146421

10 R-PLACE1006959
EST
0.00065:211:63
Hs.136605:AA665784

15 R-PLACE1007028
ESTs
7.4e-92:475:94
Hs.110222:AA532444

20 R-PLACE1007040
ESTs
5.1e-103:509:97
Hs.71190:AA524036

25 R-PLACE1007077
ESTs
1.0e-98:529:93
Hs.24398:AI262946

30 R-PLACE1007081
Human growth factor independence-1 (Gfi-1) mRNA, complete cds
0.57:238:61
Hs.73172:U67369

35 R-PLACE1007096
ESTs
1.2e-88:466:94
Hs.8268:N70144

40 R-PLACE1007296
EST
4.3e-53:338:86
Hs.147274:AI206582

45 R-PLACE1007591
EST
4.6e-76:384:97
Hs.94445:N90719

50 R-PLACE1007626
Homo sapiens unknown mRNA, complete cds
5.0e-30:179:91
Hs.11441:AF047439

55 R-PLACE1007702
ESTs
1.0e-52:341:87
Hs.103382:AA026923

5 R-PLACE1007845
ESTs
2.2e-102:541:93
Hs.15727:H98190

10 R-PLACE1007881
ESTs
4.1e-75:398:93
Hs.55560:AI142804

15 R-PLACE1007971
ESTs
2.8e-43:304:85
Hs.82933:AA058963

20 R-PLACE1008282
ESTs, Highly similar to HEME-REGULATED EUKARYOTIC INITIATION FACTOR EIF-2-ALPHA KINASE [Oryctolagus cuniculus]
2.2e-74:393:94
Hs.77613:AI367385

25 R-PLACE1008297
ESTs
6.5e-101:506:96
Hs.44274:AA523749

30 R-PLACE1008359
ESTs
1.8e-94:469:96
Hs.160551:AI281417

35 R-PLACE1008469
ESTs
7.0e-74:421:90
Hs.90809:AA010979

40 R-PLACE1008549
ESTs
2.0e-81:474:90
Hs.11713:T65960

45 R-PLACE1008657
ESTs
9.5e-89:512:89
Hs.142075:AA654529

50 R-PLACE1008716
Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds
5.6e-100:504:95
Hs.154844:U15128

55 R-PLACE1008744
ESTs, Highly similar to COMPLEMENT RECEPTOR TYPE 2 PRECURSOR [Homo sapiens]
2.3e-107:528:96
Hs.8963:AI379350

R-PLACE1008984
ESTs

2.0e-76:464:89
Hs.40094:D12041

5 R-PLACE1008985
EST, Highly similar to SYNAPTOTAGMIN B [Discopyge ommata]
2.2e-59:343:90
Hs.161031:H72014

10 R-PLACE1009067
ESTs
7.7e-90:503:92
Hs.55067:AA037664

15 R-PLACE1009196
EST
0.011:243:60
Hs.149839:AI287601

20 R-PLACE1009279
Homo sapiens mRNA for serin protease with IGF-binding motif, complete cds
5.4e-27:553:62
Hs.75111:D87258

25 R-PLACE1009527
Human DNA-binding protein ABP/ZF mRNA, complete cds
2.7e-92:497:91
Hs.86185:U82613

30 R-PLACE1009546
ESTs
5.9e-80:461:90
Hs.134292:AA603031

35 R-PLACE1009600
ESTs
5.5e-98:509:93
Hs.21015:AA428288

40 R-PLACE1009735
ESTs
1.1e-85:462:93
Hs.48563:AA526595

45 R-nnnnnnnnnnnnnnn
ESTs
6.8e-82:499:87
Hs.43498:AA570507

50 R-PLACE1010011
ESTs, Moderately similar to synaptonemal complex protein [M.musculus]
2.7e-15:171:78
Hs.31655:AI075991

55 R-PLACE1010078
ESTs
1.2e-48:267:92
Hs.12101:AA677423

EP 1 130 094 A2

- 5 R-PLACE1010081
Homo sapiens serine/threonine kinase RICK (RICK) mRNA, complete cds
3.0e-106:560:93
Hs.103755:AF027706
- 10 R-PLACE1010251
ESTs
0.00049:248:60
Hs.154164:AI246893
- 15 R-PLACE1010445
ESTs
1.5e-90:496:92
Hs.163999:AA778110
- 20 R-PLACE1010713
Interleukin 1 receptor antagonist
4.1e-07:307:59
Hs.81134:U65590
- 25 R-PLACE1010784
ESTs, Weakly similar to putative G-protein-coupled receptor [H.sapiens]
1.5e-21:206:78
Hs.29202:R71586
- 30 R-PLACE1010827
- R-PLACE 1010968
ESTs
2.6e-75:385:95
Hs.109884:AA766018
- 35 R-PLACE1011045
Homo sapiens E1-like protein mRNA, complete cds
5.3e-92:453:96
Hs.28190:AF094516
- 40 R-PLACE1011116
Homo sapiens embryonic lung protein (HUEL) mRNA, complete cds
1.5e-73:385:94
Hs.44053:AF006621
- R-PLACE1011236
- 45 R-PLACE1011364
ESTs
2.3e-47:289:89
Hs.6163:W26652
- 50 R-PLACE1011407
ESTs
1.1e-09:191:64
Hs.118620:T60326
- 55 R-PLACE1011516
ESTs, Weakly similar to HYPOTHETICAL 21.5 KD PROTEIN IN SEC15-SAP4 INTERGENIC REGION [S.cerev-
siae]
6.3e-75:441:88

Hs.110978:AA843431

R-PLACE1011708

5 Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds
 7.7e-93:521:91
 Hs.148318:AF034611

R-PLACE1011824

10 ESTs
 0.013:199:62
 Hs.44343:AA532514

R-PLACE1011978

15 EST
 4.0e-97:462:98
 Hs.116391:AA644085

R-PLACE2000118

20 ESTs
 1.2e-83:468:92
 Hs.110578:AA115763

R-PLACE2000219

25 Homo sapiens KIAA0414 mRNA, partial cds
 2.0e-44:344:81
 Hs.127649:AB007874

R-PLACE3000181

30 Human protocadherin 42 mRNA, 3' end of cds for alternative splicing PC42-8
 1.3e-82:441:94
 Hs.115642:L11369

R-PLACE3000213

35 ESTs, Highly similar to COMPLEMENT RECEPTOR TYPE 2 PRECURSOR [Homo sapiens]
 2.3e-114:557:97
 Hs.8963:AI379350

R-PLACE4000354

40 ESTs, Highly similar to COMPLEMENT RECEPTOR TYPE 2 PRECURSOR [Homo sapiens]
 3.4e-105:518:97
 Hs.8963:AI379350

R-PLACE4000455

45 ESTs
 9.0e-57:289:96
 Hs.42458:AA452296

R-THYRO1000036

50 Collagen, type IX, alpha 3
 1.3e-100:527:93
 Hs.53563:L41162

R-THYRO1000061

55 ESTs
 1.8e-87:460:94
 Hs.124869:H98977

R-THYRO1000099

- ESTs
1.2e-34:193:94
Hs.149488:AI243816
- 5 R-THYRO1000196
Homo sapiens Ksp-cadherin (CDH16) mRNA, complete cds
3.7e-106:530:96
Hs.115418:AF016272
- 10 R-THYRO1000400
Human HU-K4 mRNA, complete cds
0.99:227:60
Hs.74573:U60644
- 15 R-THYRO1000580
Homo sapiens mRNA for KIAA0628 protein, complete cds
0.21:126:67
Hs.43133:AB014528
- 20 R-THYRO1000584
ESTs, Weakly similar to golgi alpha-mannosidaseII [H.sapiens]
3.0e-106:529:96
Hs.12183:AA888145
- 25 R-THYRO1000678
EST
2.9e-62:304:99
Hs.48956:N64339
- 30 R-THYRO1000776
ESTs
1.3e-102:533:94
Hs.4866:AA582196
- 35 R-THYRO1000795
ESTs
3.3e-98:529:92
Hs.55263:AI344338
- 40 R-THYRO1000846
ESTs
1.6e-105:522:96
Hs.135106:AI335251
- 45 R-THYRO1000866
Homo sapiens SKB1Hs mRNA, complete cds
1.3e-43:251:92
Hs.12912:AF015913
- 50 R-THYRO1000956
ESTs, Highly similar to PROBABLE G PROTEIN-COUPLED RECEPTOR APJ [Homo sapiens]
5.2e-106:548:94
Hs.9305:W84893
- 55 R-THYRO1000964
R-THYRO1000999
ESTs

EP 1 130 094 A2

1.9e-18:150:84
Hs.111583:AA463590

5 R-THYRO1001063
ESTs
1.5e-95:464:97
Hs.142684:AA902402

10 R-THYRO1001071
ESTs
2.5e-104:496:98
Hs.6071:AA868544

15 R-THYRO1001102

15 R-THYRO1001113
ESTs, Weakly similar to FER-1 [C.elegans]
7.1e-90:446:97
Hs.8076:AA115644

20 R-THYRO1001128
ESTs
1.9e-16:270:68
Hs.140194:N35720

25 R-THYRO1001205
Small inducible cytokine A5 (RANTES)
1.9e-58:400:84
Hs.155464:AF088219

30 R-THYRO1001237
ESTs
1.5e-104:532:96
Hs.6603:AA772122

35 R-THYRO1001242
EST
1.7e-50:281:93
Hs.101727:H16171

40 R-THYRO1001266
Homo sapiens mRNA for KIAA0650 protein, partial cds
0.00037:403:60
Hs.8118:AB014550

45 R-THYRO1001327
ESTs
1.2e-96:530:93
Hs.28786:AA034412

50 R-THYRO1001456
ESTs, Weakly similar to Similar to phytoene desaturase [C.elegans]
3.3e-43:257:92
Hs.97031:AA773647

55 R-THYRO1001457
ESTs, Highly similar to MYOSIN LIGHT CHAIN KINASE [Dictyostelium discoideum]
4.8e-59:284:99

- Hs.9915:AI300083
- R-THYRO1001471
ESTs
5 1.1e-67:378:93
Hs.52113:R40587
- R-THYRO1001478
- 10 R-THYRO1001495
H.sapiens mRNA for Zinc-finger protein (ZNFpT17)
1.6e-63:434:84
Hs.32954:X65233
- 15 R-THYRO1001523
ESTs
5.8e-75:388:96
Hs.6527:R21517
- 20 R-THYRO1001529
ESTs
1.1e-25:184:87
Hs.18441:AA005104
- 25 R-THYRO1001593
ESTs
4.7e-34:182:98
Hs.8312:AA813022
- 30 R-THYRO1001608
ESTs
2.8e-107:547:95
Hs.23765:AA524283
- 35 R-THYRO1001641
Homo sapiens clone 24448 unknown mRNA, partial cds
1.1e-111:562:96
Hs.4973:AF070638
- 40 R-THYRO1001700
ESTs
1.3e-78:407:95
Hs.86987:N99896
- 45 R-THYRO1001702
ESTs
4.3e-98:566:92
Hs.119447:AA524436
- 50 R-THYRO1001725
ESTs
1.3e-84:424:96
Hs.38039:AI360128
- 55 R-THYRO1001770
ESTs
1.0e-62:325:97
Hs.20137:R08273

EP 1 130 094 A2

5 R-THYRO1001803
ESTs
6.8e-90:456:96
Hs.134438:R42585

10 R-Y79AA1000030
ESTs, Weakly similar to HYPOTHETICAL PROTEIN KIAA0168 [H.sapiens]
2.4e-98:515:94
Hs.32822:AI194045

15 R-Y79AA1000127
ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]
1.1e-57:307:95
Hs.83513:W05849

20 R-Y79AA1000207
EST
1.0e-97:411:96
Hs.141431:N21286

25 R-Y79AA1000226
ESTs, Highly similar to HYPOTHETICAL 52.8 KD PROTEIN T05E11.5 IN CHROMOSOME IV [Caenorhabditis elegans]
7.2e-102:545:94
Hs.11221:AI192291

30 R-Y79AA1000270
Human mRNA for ORF, Xq terminal portion
3.3e-107:564:93
Hs.6551:D16469

35 R-Y79AA1000426
H.sapiens mRNA for activin beta-C chain
2.5e-10:217:66
Hs.83267:X82540

40 R-Y79AA1000521
Homo sapiens N-methyl-D-aspartate receptor 2D subunit precursor (NMDAR2D) mRNA, complete cds
0.73:257:59
Hs.113286:U77783

45 R-Y79AA1000750
ESTs
4.3e-75:391:95
Hs.157192:W84862

50 R-Y79AA1000776
ESTs
3.5e-56:303:95
Hs.118559:AA887084

55 R-Y79AA1000777
ESTs, Weakly similar to LIS-1 protein [H.sapiens]
9.5e-98:515:95
Hs.59461:W93217

R-Y79AA1000876
EST

- 2.7e-23:173:84
Hs.135872:AI037885
- 5 R-Y79AA1000959
Homo sapiens Hsp70 binding protein HspBP1 mRNA, complete cds
3.4e-80:453:92
Hs.53066:AF093420
- 10 R-Y79AA1000967
ESTs
7.3e-86:461:93
Hs.6262:T89093
- 15 R-Y79AA1001013
ESTs
1.4e-115:566:97
Hs.108408:N31922
- 20 R-Y79AA1001056
ESTs, Moderately similar to maternal transcript Maid [M.musculus]
8.7e-111:557:95
Hs.36794:AI038407
- 25 R-Y79AA1001062
ESTs
0.0021:365:59
Hs.106129:AA292171
- 30 R-Y79AA1001090
ESTs
5.0e-52:255:99
Hs.106214:AI123831
- 35 R-Y79AA1001212
Homo sapiens SL15 protein mRNA, complete cds
1.8e-83:407:97
Hs.6710:AF038961
- 40 R-Y79AA1001264
ESTs, Highly similar to DNAJ PROTEIN HOMOLOG 2 [Homo sapiens]
2.8e-111:552:96
Hs.62489:AI057091
- 45 R-Y79AA1001272
Zinc finger protein, X-linked
0.019:317:59
Hs.2074:X59739
- 50 R-Y79AA1001328
ESTs
3.6e-67:385:92
Hs.127792:AI421472
- 55 R-Y79AA1001426
ESTs
2.0e-13:92:93
Hs.105607:AA478379

	R-Y79AA1001430
	Homo sapiens mRNA for KIAA0469 protein, complete cds
5	2.0e-112:555:96
	Hs.7764:AB007938
	R-Y79AA1001523
	EST
	1.7e-07:120:73
10	Hs.130984:AI015430
	R-Y79AA1001530
	Homo sapiens RRM RNA binding protein Gry-rbp (GRY-RBP) mRNA, complete cds
	0.030:169:63
15	Hs.155489:AF037448
	R-Y79AA1001592
	ESTs
	5.0e-60:340:91
20	Hs.87019:AA760977
	R-Y79AA1001727
	ESTs
	6.1e-101:547:93
25	Hs.7404:W29012
	R-Y79AA1001787
	ESTs
	8.8e-84:449:95
30	Hs.128866:AA977749
	R-Y79AA1001795
	Homo sapiens mRNA for GalT4 protein
	9.9e-110:541:97
35	Hs.21495:AL031228
	R-Y79AA1001799
	ESTs, Highly similar to MITOCHONDRIAL RNA SPLICING PROTEIN MSR4 [Saccharomyces cerevisiae]
	1.6e-94:567:90
40	Hs.34401:AA447775
	R-Y79AA1001803
	ESTs, Highly similar to SECRETOGRAININ III PRECURSOR [Mus musculus]
	1.2e-86:509:90
45	Hs.22215:AI371482
	R-Y79AA1001863
	ESTs
	1.4e-23:268:73
50	Hs.131613:AI190576
	R-Y79AA1002022
	ESTs
	8.9e-97:462:98
55	Hs.6140:D52151
	R-nnnnnnnnnnnnnn
	R-nnnnnnnnnnnnnn

EP 1 130 094 A2

Homo sapiens DNA recombination and repair protein (MRE11B) mRNA, complete cds
0.00075:456:59
Hs.153855:AF022778

- 5 R-Y79AA1002213
Human mRNA for KIAA0392 gene, partial cds
6.2e-45:304:85
Hs.40100:AB002390
- 10 R-Y79AA1002334
ESTs
7.7e-91:495:92
Hs.90804:W28091
- 15 R-Y79AA1002373
Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end
5.2e-98:545:91
Hs.103948:K00627
- 20 R-Y79AA1002376
ESTs
2.0e-91:455:97
Hs.153375:AI287812
- 25 R-Y79AA1002378
ESTs, Highly similar to ZINC FINGER PROTEIN ZFP-35 [Mus musculus]
9.4e-15:131:83
Hs.20082:W89121
- 30 R-Y79AA1002381
ESTs, Highly similar to CELL DIVISION CONTROL PROTEIN 2 HOMOLOG [Plasmodium falciparum (isolate k1/thailand)]
1.5e-104:531:95
Hs.26322:AA156858
- 35 Homology search result 10
- [0305] Data obtained by the homology search for full length nucleotide sequences and deduced amino acid sequences. In the result of the search shown below, both units, aa and bp, are used as length units for the sequences to be compared. Each data includes Clone name, Definition in matching data, P value, Length of sequence to be compared, Homology, and Accession number (No.) of matching data. These items are shown in this order, separated by a double-slash mark, //.
- 40 C-HEMBA1000006//Homo sapiens mRNA; cDNA DKFZp564G1762 (from clone DKFZp564G1762).//0//1230bp//
92%//AB026894
C-nnnnnnnnnnnn//GAMETOGENESIS EXPRESSED PROTEIN GEG-154.//2.30E-71//344aa//50%//P50636
C-HEMBA1000121//HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III.//4.80E-05//83aa//27%//
P34679
C-HEMBA1000128//PATHOGENESIS-RELATED PROTEIN 1 PRECURSOR (PR-1).//3.20E-07//89aa//34%//
50 P33154
C-HEMBA1000275
C-HEMBA1000300
C-HEMBA1000349//ATP-BINDING CASSETTE TRANSPORTER 1.//5.30E-65//352aa//39%//P41233
C-HEMBA1000443//Homo sapiens CGI-96 protein mRNA, complete cds.//4.70E-129//686bp//91%//AF151854
55 C-HEMBA1000590//Homo sapiens mRNA for matrilin-4, partial.//2.00E-273//1254bp//99%//AJ007581
C-HEMBA1000634//Homo sapiens T-cell activation protein (PGR1) gene, complete cds.//0//994bp//99%//
AF116272
C-HEMBA1000713//Homo sapiens 10kD protein (BC10) mRNA, complete cds.//0//1254bp//99%//AF053470

EP 1 130 094 A2

C-HEMBA1000745//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//2.00E-07//445aa//27%//P02454
C-HEMBA1000907
C-HEMBA1000940//GAP JUNCTION ALPHA-3 PROTEIN (CONNEXIN 44) (CX44).//2.90E-39//362aa//31%//
P41987
5 C-HEMBA1000962
C-HEMBA1001221//AGRIN PRECURSOR.//2.50E-25//294aa//29%//P31696
C-HEMBA1001228//Human germline oligomeric matrix protein (COMP) mRNA, complete cds.//7.80E-286//
1105bp//94%//L32137
C-HEMBA1001297
10 C-HEMBA1001390//Mus musculus polymerase I-transcript release factor mRNA, complete cds.//2.50E-57//
464bp//82%//AF036249
C-HEMBA1001563
C-HEMBA1001621//PROBABLE G PROTEIN-COUPLED RECEPTOR APJ//3.50E-123//259aa//89%//P35414
15 C-nnnnnnnnnnnn//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//2.40E-85//293aa//50%//
P51523
C-HEMBA1001878//Homo sapiens U5 snRNP-specific 40 kDa protein mRNA, complete cds.//0//1488bp//99%//
AF090988
C-HEMBA1002131//PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE 1//4.10E-10//140aa//
30 30%//P24802
C-HEMBA1002163//HYPOTHETICAL 40.7 KD PROTEIN IN DAK1-ORC1 INTERGENIC REGION.//9.40E-28//
309aa//30%//Q04651
C-HEMBA1002164
C-HEMBA1002167//Rattus norvegicus neuroligin 1 mRNA, complete cds.//1.30E-305//1643bp//91%//U22952
C-HEMBA1002178//PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE 1 PRECURSOR (EC
25 1.14.11.4) (LYSYL HYDROXYLASE 1) (LH1).//3.70E-10//140aa//30%//P24802
C-nnnnnnnnnnnn//Human glycyl-tRNA synthetase mRNA, complete cds.//0//2380bp//99%//U09587
C-HEMBA1002195//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//8.80E-23//221aa//31%//Q00808
C-HEMBA1002227//Homo sapiens mRNA for 80K-L protein, complete cds.//0//1324bp//98%//D10522
30 C-HEMBA1002239
C-HEMBA1002316
C-HEMBA1002420
C-HEMBA1002421//Human heparan sulfate proteoglycan (HSPG) core protein, 3' end.//0//2097bp//99%//J04621
C-HEMBA1002524//Human MHC Class I region proline rich protein mRNA, complete cds.//0//1763bp//95%//
U63336
35 C-HEMBA1002551//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).//9.80E-08//110aa//
37%//P49695
C-HEMBA1002767//Homo sapiens chromosome 1p33-p34 beta-1,4-galactosyltransferase mRNA, complete cds.//
0//1497bp//99%//AF038660
C-HEMBA1002992//UBIQUITIN-LIKE PROTEIN DSK2.//2.00E-21//216aa//35%//P48510
40 C-HEMBA1003047//Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds.//0//1768bp//
99%//AF034611
C-HEMBA1003072//Gallus gallus single-strand DNA-binding protein csdp mRNA, partial cds.//3.30E-93//927bp//
73%//U68380
C-HEMBA1003101//Homo sapiens tyrosylprotein sulfotransferase-2 mRNA, complete cds.//0//1854bp//99%//
45 AF049891
C-HEMBA1003230//Homo sapiens fibulin-5.//5.60E-308//1398bp//99%//AJ133490
C-HEMBA1003294
C-HEMBA1003315//Mus musculus mRNA for DNA helicase, complete cds.//6.30E-250//1426bp//88%//AB013912
C-HEMBA1003392//Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds.//0//1721bp//
50 100%//AF074264
C-HEMBA1003399//MVP1 PROTEIN.//2.30E-15//279aa//23%//P40959
C-HEMBA1003487
C-HEMBA1003530//S.scrofa mRNA for BM88 antigen.//1.20E-60//900bp//66%//X82027
C-HEMBA1003602//Homo sapiens CGI-67 protein mRNA, complete cds.//3.50E-70//732bp//66%//AF151825
55 C-HEMBA1003732//SFT2 PROTEIN.//1.50E-06//162aa//30%//P38166
C-HEMBA1003945//Homo sapiens hypothetical 43.2 Kd protein mRNA, complete cds.//8.90E-287//757bp//97%//
AF077030
C-HEMBA1004110//Homo sapiens intersectin short form mRNA, complete cds.//0//2033bp//99%//AF064243

EP 1 130 094 A2

C-HEMBA1004250//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//6.40E-51//
277aa//35%//P33450
C-HEMBA1004391//TUMOR SUPPRESSOR PROTEIN DCC PRECURSOR.//5.60E-20//194aa//26%//P70211
C-HEMBA1004444//GLYCOPROTEIN 25L PRECURSOR (GP25L).//4.60E-41//148aa//52%//P27869
5 C-HEMBA1004454
C-HEMBA1004505//MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ISOFORM 1 (EC
3.2.1.113) (MAN(9)-ALPHA-MANNOSIDASE).//2.70E-45//239aa//43%//P53624
C-HEMBA1004797
10 C-HEMBA1004982//TETRACYCLINE RESISTANCE PROTEIN, CLASS E (TETA(E)).//6.30E-10//149aa//26%//
Q07282
C-HEMBA1005070//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//1.10E-05//187aa//
29%//P17437
C-HEMBA1005084//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE- PRO-
TEIN KINASE 1).//1.20E-07//102aa//37%//P18160
15 C-HEMBA1005145
C-HEMBA1005430
C-HEMBA1005449//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSI-
DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//5.40E-10//224aa//24%//P13983
C-HEMBA1005489
20 C-HEMBA1005522//COAGULATION FACTOR VII PRECURSOR (EC 3.4.21.21).//7.70E-15//78aa//51%//P98139
C-HEMBA1005545//MUSCARINIC ACETYLCHOLINE RECEPTOR M3.//0//2121aa//100%//U29589
C-HEMBA1005698//Homo sapiens vesicle trafficking protein (SEC22C) mRNA, complete cds.//6.60E-163//
753bp//99%//AF039568
C-HEMBA1005913
25 C-HEMBA1005929//H.sapiens mRNA for serine/threonine protein kinase EMK.//6.50E-92//1092bp//69%//X97630
C-HEMBA1005945//Oryctolagus cuniculus peroxisomal Ca-dependent solute carrier mRNA, complete Gds.//
1.90E-44//666bp//65%//AF004161
C-HEMBA1006016
C-HEMBA1006171
30 C-HEMBA1006299
C-HEMBA1006311
C-HEMBA1006335
C-HEMBA1006430//Human putative transmembrane protein precursor (B5) mRNA, complete cds.//2.40E-70//
1108bp//65%//L38961
35 C-HEMBA1006482//Homo sapiens h-scol (SCO1) mRNA, nuclear gene encoding mitochondrial protein, complete
cds.//0//1101bp//98%//AF026852
C-HEMBA1006572//ODD-SKIPPED PROTEIN.//2.60E-39//85aa//83%//P23803
C-HEMBA1006707//Homo sapiens mRNA for matrilin-4, partial.//0//2003bp//99%//AJ007581
C-HEMBA1006724
40 C-HEMBA1006902//Homo sapiens mRNA for matrilin-4, partial.//4.80E-275//1799bp//85%//AJ007581
C-HEMBA1006916//Homo sapiens Grb14 mRNA, complete cds.//3.00E-277//1010bp//95%//L76687
C-HEMBA1006960
C-HEMBA1007013
C-HEMBA1007057
45 C-HEMBA1007241
C-HEMBA1007291
C-HEMBA1007332
C-HEMBB1000276
C-HEMBB1000447//Homo sapiens JWA protein mRNA, complete cds.//0//2059bp//99%//AF070523
50 C-HEMBB1000642
C-HEMBB1000668//Homo sapiens mRNA for KIAA0893 protein, complete cds.//0//2375bp//99%//AB020700
C-HEMBB1000679//C.familiaris mRNA for TRAM-protein.//4.10E-210//1149bp//80%//X63678
C-HEMBB1000881//Danio rerio mRNA for MINDIN2, complete cds.//1.70E-67//948bp//66%//AB006085
C-HEMBB1000905//TRANSCRIPTIONAL REPRESSOR RCO-1.//1.00E-11//311aa//27%//P78706
55 C-HEMBB1001026//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHE-
ROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPO-
NENT).//5.30E-11//142aa//30%//P32802
C-HEMBB1001048//Human Hpast (HPAST) mRNA, complete cds.//6.50E-39//448bp//75%//AC000159

C-HEMBB1001200
 C-HEMBB1001407
 C-HEMBB1001530//SLS1 PROTEIN PRECURSOR //9.80E-10//273aa//27%//Q99158
 C-HEMBB1001573
 5 C-nnnnnnnnnnnn//Homo sapiens orphan G protein-coupled receptor (GPR34) gene, complete cds //1.50E-251//
 1146bp//99%//AF118670
 C-HEMBB1001847//NEUROGENIC PROTEIN BIG BRAIN //4.70E-06//258aa//24%//P23645
 C-HEMBB1001978
 C-HEMBB1002162//Homo sapiens genethonin 1 mRNA, complete cds //8.30E-67//328bp//99%//AP062354
 10 C-HEMBB1002228
 C-HEMBB1002245//PROSTAGLANDIN F2-ALPHA RECEPTOR REGULATORY PROTEIN PRECURSOR
 (PROSTAGLANDIN F2-ALPHA RECEPTOR ASSOCIATED PROTEIN) //0//879aa//89%//Q62786
 C-HEMBB1002427//FUCOSYLGlycoprotein alpha-N-acetylgalactosaminyltransferase (EC
 15 2.4.1.40) (histo-blood group A transferase) (A transferase) / Fucosylglycoprotein 3-
 alpha-galactosyltransferase (EC 2.4.1.37) (histo-blood group B transferase) (B transferase) (NAGAT) //1.80E-70//221aa//50%//P16442
 C-HEMBB1002465//ACYL-COA DEHYDROGENASE (EC 1.3.99.-) //2.30E-53//249aa//48%//P45857
 C-HEMBB1002663
 C-HEMBB1002693
 20 C-MAMMA1000046
 C-MAMMA1000118
 C-nnnnnnnnnnnn//Homo sapiens SNC73 protein (SNC73) mRNA, complete cds //1.50E-312//1594bp//93%//
 AF067420
 C-MAMMA1000449
 25 C-MAMMA1000457//Human NADH-cytochrome b5 reductase mRNA, 3' end //9.50E-79//829bp//71%//M16462
 C-MAMMA1000591//POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN-
 UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYL GALACTOS-
 AMINYLTRANSFERASE) (GALNAC-T1) //1.20E-115//515aa//49%//Q07537
 C-MAMMA1000681//PROBABLE G PROTEIN-COUPLED RECEPTOR EDG-1 //9.40E-82//311aa//52%//O08530
 30 C-MAMMA1001043//MRC OX-45 SURFACE ANTIGEN PRECURSOR (BCM1 SURFACE ANTIGEN)(BLAST-1)
 (CD48) //2.90E-12//239aa//28%//P10252
 C-MAMMA1001893
 C-NT2RM2000241
 35 C-NT2RM2000306//PUTATIVE GTP-BINDING PROTEIN W08E3.3 //4.50E-130//362aa//68%//P91917
 C-NT2RM2000410
 C-NT2RM2000423//BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE) //1.80E-38//308aa//35%//
 P48982
 C-NT2RM2000497//CHL1 PROTEIN //9.90E-24//296aa//29%//P22516
 C-NT2RM2000514//Homo sapiens mRNA for KIAA0875 protein, partial cds //0//2381bp//99%//AB020682
 40 C-NT2RM2000622
 C-NT2RM2001126//Homo sapiens mRNA for multi PDZ domain protein //0//1600bp//99%//AJ0001319
 C-NT2RM2001902//Homo sapiens mRNA for PAK4 protein //5.40E-216//988bp//99%//AJ011855
 C-NT2RM2001939//Human G protein-coupled receptor GPR-NGA gene, complete cds //0//1559bp//98%//U55312
 C-NT2RM2001941//MUSCARINIC ACETYLCHOLINE RECEPTOR M1 //7.40E-38//193aa//34%//P08482
 45 C-NT2RM4000198
 C-NT2RM4000284//Human IgG Fc receptor hFcRn mRNA, complete cds //1.30E-257//603bp//96%//U12255
 C-NT2RM4000295
 C-NT2RM4000326//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2) //9.00E-100//434aa//43%//
 P51523
 50 C-NT2RM4000444//ANTIGEN PEPTIDE TRANSPORTER 1 (APT1) //1.70E-112//493aa//44%//P36370
 C-NT2RM4000587
 C-NT2RM4000648//K-GLYPCAN PRECURSOR //4.00E-193//531aa//66%//P51655
 C-NT2RM4000997//MONO- AND DIACYLGLYCEROL LIPASE PRECURSOR (EC 3.1.1.-) (MDGL) //1.80E-10//
 189aa//30%//P25234
 55 C-NT2RM4001321
 C-NT2RM4001325//CHONDROITIN 6-SULFOTRANSFERASE (EC 2.8.2.17) (C6ST) //2.90E-48//343aa//34%//
 Q92179
 C-NT2RM4001735

EP 1 130 094 A2

C-NT2RM4002352//Homo sapiens hLRp105 mRNA for LDL receptor related protein 105, complete cds./0//
2184bp//99%//AB009462
C-NT2RP1000002
C-NT2RP1000050
5 C-NT2RP1000181//Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds./3.30E-121//1394bp//69%//
AF126799
C-NT2RP1000261//ORM1 PROTEIN./2.40E-17//137aa//35%//P53224
C-NT2RP1000300//Human transporter protein (g17) mRNA, complete cds./3.80E-26//758bp//62%//U49082
C-NT2RP1000325//H.sapiens gene for phosphate carner./0//439bp//98%//X77337
10 C-NT2RP1000448
C-NT2RP1000551//Homo sapiens putative interferon-related protein (SM15) mRNA, partial cds./0//1761bp//
99%//U09585
C-NT2RP1000579//Human succinate dehydrogenase flavoprotein subunit (SDH) mRNA, complete cds./0//
1951bp//94%//L21936
15 C-NT2RP1000613//CARBONIC ANHYDRASE VI (EC 4.2.1.1) (SALIVARY) (CARBONATE DEHYDRATASE VI).//
3.40E-52//304aa//40%//P08060
C-NT2RP1000903
C-NT2RP1000981//CELL SURFACE A33 ANTIGEN PRECURSOR./3.60E-14//286aa//27%//Q99795
C-NT2RP1001004//F-SPONDIN PRECURSOR./9.20E-43//322aa//35%//P35446
20 C-NT2RP1001020//SERINE/THREONINE-PROTEIN KINASE PAK-BETA (EC 2.7.1.-) (BETA-PAK) (P21-ACTI-
VATED KINASE 3) (CDC42/RAC EFFECTOR KINASE PAK-B).//9.70E-22//227aa//31%//Q61036
C-NT2RP1001563//TESTIS-SPECIFIC PROTEIN TPX-1 PRECURSOR (AUTOANTIGEN 1) (25 KD ACROSOM-
AL AUTOANTIGEN) (AA1).//9.70E-19//201aa//31%//Q60477
25 C-NT2RP2000394//Gallus gallus p52 pro-apoptotic protein mRNA, complete cds./1.60E-90//956bp//70%//
AF029071
C-NT2RP2000479
C-NT2RP2000514//Homo sapiens roundabout 2 (robo2) mRNA, partial cds./3.00E-185//855bp//99%//AF040991
C-NT2RP2000533//Homo sapiens cornichon protein mRNA, complete cds./1.30E-290//1324bp//99%//AF070654
30 C-NT2RP2000649//Homo sapiens mRNA for Hs Ste24p, complete cds./0//2847bp//99%//AB016068
C-NT2RP2000663
C-NT2RP2000694//Homo sapiens 5T4 oncofetal trophoblast glycoprotein gene./0//2278bp//99%//AJ012159
C-NT2RP2000903//Homo sapiens 5T4 oncofetal trophoblast glycoprotein gene./0//2276bp//100%//AJ012159
C-NT2RP2001480//Homo sapiens thrombospondin 3 (THBS3) gene, complete cds./0//2547bp//99%//L38969
C-NT2RP2001495//Human transporter protein (g17) mRNA, complete cds./2.20E-65//641bp//65%//U49082
35 C-NT2RP2001514//PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38).//1.20E-133//429aa//
41%//P39986
C-NT2RP2001529//Homo sapiens mRNA for ZIP-kinase, complete cds./0//2079bp//99%//AB007144
C-NT2RP2001769//SERINE/THREONINE-PROTEIN KINASE ORB6 (EC 2.7.1.-).//9.10E-47//185aa//44%//
O13310
40 C-NT2RP2001878
C-NT2RP2001903//CALPAIN, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM- ACTIVATED NEU-
TRAL PROTEINASE) (CANP) (MU/M-TYPE).//3.80E-58//475aa//34%//P00789
C-NT2RP2001915
C-NT2RP2001956//ORM1 PROTEIN./3.90E-19//137aa//37%//P53224
45 C-NT2RP2002063//GNS1 PROTEIN./3.60E-18//231aa//33%//P25358
C-NT2RP2002188//Rattus norvegicus neuroligin 3 mRNA, complete cds./2.50E-226//1284bp//89%//U41663
C-NT2RP2002232//HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I./1.90E-93//420aa//
43%//Q09782
50 C-NT2RP2002304//Human mRNA for KIAA0383 gene, partial cds./0//1640bp//99%//AB002381
C-NT2RP2002409
C-NT2RP2002510
C-NT2RP2002527//CYTOCHROME B5./1.30E-11//92aa//38%//P40312
C-NT2RP2002533//Homo sapiens alpha 2 delta calcium channel subunit isoform I mRNA, complete cds./0//
2365bp//99%//AF042792
55 C-NT2RP2002564//Human zinc-finger protein C2H2-150 mRNA, complete cds./0//2237bp//99%//U38864
C-NT2RP2002674//SOLUBLE EPOXIDE HYDROLASE (SEH) (EC 3.3.2.3) (EPOXIDE HYDRATASE) (CY-
TOSOLIC EPOXIDE HYDROLASE) (CEH).//5.50E-38//201aa//39%//P34913
C-NT2RP2002721//REGULATORY PROTEIN UHPC./1.60E-23//153aa//30%//P27669

EP 1 130 094 A2

C-NT2RP2002824//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPO-
NENT).//3.50E-63//404aa//33%//P32802
5 C-NT2RP2002942//Homo sapiens mRNA for KIAA0806 protein, complete cds.//0//2090bp//99%//AB018349
C-NT2RP2002974//HOMEobox PROTEIN SIX5 (DM LOCUS-ASSOCIATED HOMEODOMAIN PROTEIN HOMOLOG) (FRAGMENT).//8.20E-241//555aa//84%//P70178
C-NT2RP2002976
10 C-NT2RP2003042//PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR (EC 2.3.1.43) (LECITHIN-CHOLESTEROL ACYLTRANSFERASE) (PHOSPHOLIPID-CHOLESTEROL ACYLTRANSFERASE) (FRAGMENT).//2.10E-109//385aa//52%//P53760
C-NT2RP2003179//PUTATIVE SERINE/THREONINE-PROTEIN KINASE EMK (EC 2.7.1.-).//2.60E-67//256aa//49%//Q05512
15 C-NT2RP2003210//Homo sapiens fatty acid transport protein (FATP) mRNA, complete cds.//9.80E-272//1265bp//98%//AF055899
C-NT2RP2003369//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//5.90E-20//204aa//34%//Q15404
C-NT2RP2003383//Homo sapiens mRNA for KIAA0458 protein, complete cds.//0//2565bp//99%//AB007927
C-NT2RP2003469//GALACTOSE-PROTON SYMPORT (GALACTOSE TRANSPORTER).//1.10E-45//324aa//29%//P37021
20 C-NT2RP2003545//Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds.//5.40E-48//578bp//71%//AF024636
C-NT2RP2003593
C-NT2RP2003599
25 C-NT2RP2003655//HYPOTHETICAL 26.3 KD PROTEIN IN OYE2-GND1 INTERGENIC//4.80E-15//93aa//47%//P38869
C-NT2RP2003931
C-NT2RP2004141
C-NT2RP2004179
30 C-NT2RP2004205//BUTYROPHILIN PRECURSOR (BT).//1.60E-21//276aa//32%//Q62556
C-NT2RP2004447
C-NT2RP2004495//Human transporter protein (g17) mRNA, complete cds.//9.80E-64//642bp//64%//U49082
C-NT2RP2004524
C-NT2RP2004556
35 C-NT2RP2004606//Human fibroblast collagenase inhibitor mRNA, complete cds.//2.10E-166//768bp//99%//M12670
C-NT2RP2004648//Mouse beta-galactosidase (BGAL) gene, complete cds.//1.20E-33//1136bp//59%//M57734
C-NT2RP2004670//Rattus norvegicus vesicla-associate calmodulin-binding protein mRNA, complete cds.//0//1250bp//86%//L22557
40 C-NT2RP2004794//HYPOTHETICAL 24.5 KD PROTEIN IN SAP185-BCK1 INTERGENIC REGION//2.70E-09//203aa//26%//P40857
C-NT2RP2004837
C-NT2RP2004847//ZINC FINGER PROTEIN 135.//8.00E-35//193aa//40%//P52742
C-nnnnnnnnnnnn//Homo sapiens SCG10-like-protein (SCLIP) mRNA, complete cds.//2.90E-170//813bp//98%//AF069709
45 C-NT2RP2005027
C-NT2RP2005163
C-NT2RP2005181//Mus musculus cationic amino acid transporter (CAT3) mRNA, complete cds.//5.30E-315//2126bp//81%//U70859
C-NT2RP2005247//ZINC-FINGER PROTEIN RFP (RET FINGER PROTEIN).//5.00E-53//296aa//37%//Q62158
50 C-NT2RP2005425//Homo sapiens mRNA for AKAP450 protein.//0//4341bp//99%//AJ131693
C-NT2RP2005463//PROTEIN PTM1 PRECURSOR.//7.40E-15//284aa//28%//P32857
C-NT2RP2005514
C-NT2RP2005541//N-ACETYLGLUCOSAMINE-6-SULFATASE PRECURSOR (EC 3.1.6.14) (G6S) (GLUCOSAMINE-6-SULFATASE).//4.70E-24//78aa//51%//P15586
55 C-NT2RP2005632
C-NT2RP2005878//PUTATIVE STEROID DEHYDROGENASE KIK-I (EC 1.1.1.-).//3.60E-55//238aa//50%//O57314
C-NT2RP2005883//DOPAMINE-BETA-MONOXYGENASE PRECURSOR (EC 1.14.17.1) (DOPAMINE BETA-

EP 1 130 094 A2

HYDROXYLASE) (DBH).//6.70E-72//512aa//34%//P15101
 C-NT2RP2005887
 C-NT2RP2005941//Human paired box gene (PAX6) homologue, complete cds.//1.40E-308//1396bp//99%//
 M93650
 5 C-NT2RP2005994//HYPOTHETICAL 51.5 KD PROTEIN D2024.3 IN CHROMOSOME IV.//3.50E-35//144aa//
 47%//P49191
 C-NT2RP2006042//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSI-
 DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//9.40E-15//501aa//25%//P08640
 10 C-NT2RP2006269//DOLICHYL-PHOSPHATE-MANNOSE--PROTEIN MANNOSYLTRANSFERASE 2 (EC
 2.4.1.109).//2.30E-78//679aa//32%//P31382
 C-NT2RP2006512//GNS 1 PROTEIN.//2.00E-21//290aa//29%//P25358
 C-NT2RP3000059//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID) (FRAGMENT).//
 15 3.70E-12//133aa//32%//Q01485
 C-NT2RP3000063//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).//
 5.00E-29//596aa//30%//P19246
 C-NT2RP3000125//RETINOBLASTOMA BINDING PROTEIN 2 (RBBP-2).//6.30E-08//70aa//41%//P29375
 C-NT2RP3000169//Homo sapiens MRS1 mRNA, complete cds.//0//1519bp//97%//AF093239
 C-NT2RP3000172//CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123) (CAM KI-
 NASE I).//1.30E-80//359aa//44%//Q14012
 20 C-NT2RP3000201//Homo sapiens mRNA for KIAA0687 protein, partial cds.//2.00E-305//1224bp//99%//AB014587
 C-NT2RP3000436//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//6.20E-27//
 90aa//42%//P38660
 C-NT2RP3000460//Canis familiaris sec61 homologue mRNA, complete cds.//1.80E-198//643bp//89%//M96629
 C-NT2RP3000616//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN).//5.20E-26//
 25 227aa//36%//Q06828
 C-NT2RP3000721//HYPOTHETICAL 149.7 KD PROTEIN IN IRE1-KSP1 INTERGENIC REGION.//1.10E-22//
 171aa//36%//P38800
 C-NT2RP3000820//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).//1.90E-30//269aa//
 30 33%//P49695
 C-NT2RP3000871
 C-NT2RP3000907//PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38).//2.20E-134//296aa//
 42%//P39986
 C-NT2RP3001012//Homo sapiens mRNA for KIAA0829 protein, partial cds.//0//2906bp//98%//AB020636
 C-NT2RP3001044
 35 C-NT2RP3001061//Homo sapiens mRNA for KIAA0853 protein, partial cds.//0//3591bp//99%//AB020660
 C-NT2RP3001170//Homo sapiens mRNA; cDNA DKFZp586K2120 (from clone DKFZp586K2120).//0//2421bp//
 99%//AL080163
 C-NT2RP3001195//GALACTOSE-PROTON SYMPORT (GALACTOSE TRANSPORTER).//4.70E-48//339aa//
 29%//P37021
 40 C-NT2RP3001240//Canis familiaris sec61 homologue mRNA, complete cds.//1.20E-301//1141bp//89%//M96629
 C-NT2RP3001322//PROBABLE CALCIUM-TRANSPORTING ATPASE 3 (EC 3.6.1.38) (ENDOPLASMIC RETIC-
 ULUM CA2+-ATPASE).//1.70E-21//220aa//30%//P39524
 C-NT2RP3001388//SYNAPTOTAGMIN IV.//2.00E-118//430aa//54%//P50232
 C-nnnnnnnnnnnn//Human mRNA for KIAA0315 gene, partial cds.//0//2971bp//99%//AB002313
 45 C-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0017 protein, complete cds.//0//3243bp//99%//D87686
 C-NT2RP3001560//Homo sapiens cleft lip and palate transmembrane protein 1 (CLPTM1) mRNA, complete cds.//
 0//2468bp//99%//AF037339
 C-NT2RP3001592//N2,N2-DIMETHYLGUANOSINE TRNA METHYLTRANSFERASE PRECURSOR (EC
 2.1.1.32).//1.30E-18//279aa//27%//P15565
 50 C-NT2RP3001738//CYTOCHROME B5.//1.30E-11//133aa//33%//P00169
 C-NT2RP3001754
 C-NT2RP3001858
 C-NT2RP3002160//Canis familiaris forssman synthetase mRNA, complete cds.//5.00E-152//789bp//84%//U66140
 C-NT2RP3002311//BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE).//9.80E-103//547aa//
 55 43%//P48982
 C-NT2RP3002342//Human transporter protein (g17) mRNA, complete cds.//1.70E-65//641bp//65%//U49082
 C-NT2RP3002448
 C-NT2RP3002721//Porcine citrate synthase mRNA, complete cds.//9.10E-281//1454bp//93%//M21197

EP 1 130 094 A2

C-NT2RP3002738//Homo sapiens enhancer of filamentation (HEF1) mRNA, complete cds./.2.20E-47//763bp//
 65%//L43821
 C-NT2RP3002790
 C-NT2RP3002836//Homo sapiens mRNA for KIAA0463 protein, partial cds./.0//1617bp//99%//AB007932
 C-NT2RP3002958//TRANS-GOLGI NETWORK INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR//
 8.00E-08//197aa//26%//P19814
 C-NT2RP3003000//Homo sapiens T-type calcium channel alpha-1 subunit mRNA, complete cds./.0//3160bp//
 96%//AF051946
 C-NT2RP3003076
 10 C-NT2RP3003354//SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 3//.5.10E-55//208aa//51%//
 O35609
 C-NT2RP3003469
 C-NT2RP3003527//Homo sapiens mRNA for protein kinase Dyrk1B//.0//2483bp//99%//Y17999
 C-NT2RP3003535//UDP-N-ACETYLGLUCOSAMINE--PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE
 15 110 KD SUBUNIT (EC 2.4.1.-) (O-GLCNAC TRANSFERASE P110 SUBUNIT).//8.80E-18//368aa//25%//P56558
 C-NT2RP3003559
 C-NT2RP3003614
 C-NT2RP3003729
 20 C-NT2RP3003849//PROTEIN KINASE C, BRAIN ISOZYME (EC 2.7.1.-) (PKC) (DPKC53E(BR)). PKC1//1.20E-
 13//126aa//34%//P05130
 C-NT2RP3003874//Homo sapiens incomplete cDNA for a mutated allele of a myosin class I, myh-1c://.0//2160bp//
 98%//AJ001381
 C-NT2RP3003963
 C-NT2RP3004000
 25 C-NT2RP3004075
 C-NT2RP3004083
 C-NT2RP3004090//GOLIATH PROTEIN (G1 PROTEIN).//9.00E-33//179aa//47%//Q06003
 C-NT2RP3004130//CELL SURFACE ANTIGEN 114/A10 PRECURSOR//8.10E-06//71aa//42%//P19467
 C-NT2RP3004133//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//2.50E-48//198aa//37%//P43636
 30 C-NT2RP3004202
 C-NT2RP3004309//Homo sapiens mRNA; cDNA DKFZp586C201 (from clone DKFZp586C201).//.0//2584bp//
 99%//AL050118
 C-NT2RP3004321
 C-NT2RP3004355
 35 C-NT2RP3004374
 C-NT2RP3004406//HYPOTHETICAL 37.4 KD PROTEIN IN IRR1-TIM44 INTERGENIC REGION//3.20E-15//
 165aa//33%//P40544
 C-NT2RP3004552//COMPLEMENT RECEPTOR TYPE 1 PRECURSOR (C3B/C4B RECEPTOR) (CD35 ANTI-
 GEN).//8.50E-24//263aa//33%//P17927
 40 C-NT2RP3004557//Human Ki nuclear autoantigen mRNA, complete cds./.0//2181bp//96%//U11292
 C-NT2RP3004625//Homo sapiens mRNA for KIAA0975 protein, partial cds./.0//1339bp//99%//AB023192
 C-NT2RP3004640//Bos taurus tuftelin mRNA, complete cds./.0//1204bp//88%//AF105228
 C-NT2RP3004647//PUTATIVE MITOCHONDRIAL CARRIER YMR166C//2.00E-15//220aa//27%//Q03829
 C-NT2RP4000108//Human gene for neurofilament subunit NF-L//.0//1998bp//99%//AF176680
 45 C-NT2RP4000962//SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-).//2.60E-18//225aa//32%//P08458
 C-NT2RP4001009//Homo sapiens mRNA for farnesylated-proteins converting enzyme 1//.0//2965bp//99%//
 Y13834
 C-NT2RP4001467//Human placental cDNA coding for 5'nucleotidase (EC 3.1.3.5).//.0//2140bp//99%//X55740
 50 C-OVARC1000090
 C-OVARC1000105//UBIQUITIN-CONJUGATING ENZYME E2-28.4 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN
 LIGASE) (UBIQUITIN CARRIER PROTEIN).//4.20E-47//171aa//56%//P33296
 C-OVARC1000137
 C-OVARC1000208
 C-OVARC1000255//H.sapiens syk mRNA for protein-tyrosine kinase//.0//1525bp//97%//Z29630
 55 C-OVARC1000275//DESMOPLAKIN I AND II (DPI AND DPII) (FRAGMENT).//9.90E-16//352aa//23%//P15924
 C-OVARC1000298
 C-OVARC1000410//Homo sapiens angiopoietin Y1 mRNA, complete cds./.2.10E-63//744bp//69%//AF107253
 C-OVARC1000439//HYPOTHETICAL 64.3 KD GTP-BINDING PROTEIN C02F5.3 IN CHROMOSOME III//1.40E-

EP 1 130 094 A2

33//143aa//53%//P34280
C-OVARC1000467
C-OVARC1000529//PROBABLE SERINE/THREONINE-PROTEIN KINASE YKL101W (EC 2.7.1.-).//1.40E-23//
165aa//39%//P34244
5 C-OVARC1000775
C-nnnnnnnnnnnn/ZINC FINGER PROTEIN 157.//1.00E-35//130aa//46%//P51786
C-OVARC1000811//PLASMINOGEN (EC 3.4.21.7) (FRAGMENT).//6.40E-13//115aa//34%//Q01177
C-OVARC1000853
C-OVARC1000916//H.sapiens PISSLRE mRNA.//7.30E-280//1117bp//95%//X78342
10 C-OVARC1000956//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//2.20E-09//250aa//
28%//P17437
C-OVARC1001030//Homo Sapiens mRNA for KIAA0886 protein, complete cds.//0//907bp//99%//AB020693
C-OVARC1001049//TRANSCRIPTION FACTOR HES- (C-HAIRY1).//7.50E-14//96aa//36%//O57337
C-OVARC1001086//Homo Sapiens cyclin T2a mRNA, complete cds.//0//1593bp//98%//AF048731
15 C-OVARC10011321//GC-RICH SEQUENCE DNA-BINDING FACTOR (GCF) (TRANSCRIPTION FACTOR 9)
(TCF-9).//2.30E-44//268aa//36%//P16383
C-OVARC1001163//HYPOTHETICAL 49.3 KD PROTEIN C30D11.06C IN CHROMOSOME I.//2.30E-20//152aa//
30//Q09906
C-OVARC1001222
20 C-OVARC1001338//AUTOPHAGY SERINE/THREONINE-PROTEIN KINASE APG1 (EC 2.7.1.-).//8.80E-30//
125aa//40%//P53104
C-OVARC1001569//PROBABLE SERINE/THREONINE-PROTEIN KINASE YKL101W (EC 2.7.1.-).//1.50E-22//
164aa//39%//P34244
C-OVARC1001596//Homo sapiens Arf-like 2 binding protein BART1 mRNA, complete cds.//0//1766bp//99%//
25 AF126062
C-OVARC1001725
C-OVARC1001727
C-OVARC1001807//Human TR3 orphan receptor mRNA, complete cds.//1.10E-243//1145bp//98%//L13740
C-OVARC1001991//VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID).//8.30E-06//114aa//
30 35//Q01956
C-OVARC1002058//Human 18S rRNA gene, complete.//1.50E-164//921bp//91%//M10098
C-OVARC1002178
C-PLACE1000033//VON WILLEBRAND FACTOR PRECURSOR.//3.80E-17//190aa//28%//Q28295
C-PLACE1000231//Rattus norvegicus WAP four-disulfide core domain protein (ps20) mRNA, complete cds.//
35 2.70E-101//947bp//74%//AF037272
C-PLACE1000258//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.70E-55//431aa//
35//Q05481
C-PLACE1000442//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//1.00E-88//213aa//67%//P16415
C-PLACE1000560
40 C-PLACE1000740//Mus musculus (Notch2) mRNA, complete cds.//5.60E-122//893bp//81%//M93661
C-PLACE1000912
C-PLACE1000914//Homo sapiens PB39 mRNA, complete cds.//7.50E-88//500bp//69%//AF045584
C-PLACE1000927//HYPOTHETICAL 20.9 KD PROTEIN B0563.3 IN CHROMOSOME X.//6.30E-21//123aa//
37%//Q11079
45 C-PLACE1001016//SODIUM CHANNEL PROTEIN PARA (PARALYTIC
PROTEIN).//6.80E-12//133aa//28%//P35500
C-nnnnnnnnnnnn//Homo sapiens T245 protein (T245) mRNA, complete cds.//0//1801bp//99%//AF043906
C-PLACE1001100
50 C-PLACE1001114//HYPOTHETICAL BHLF1 PROTEIN.//9.20E-06//389aa//31%//P03181
C-PLACE1001123
C-PLACE1001183
C-PLACE1001229
C-PLACE1001231//Rattus norvegicus sodium-dependent multi-vitamin transporter (SMVT) mRNA, complete
cds.//2.20E-137//918bp//80%//AF026554
55 C-nnnnnnnnnnnn//Human pregnancy-specific beta 1-glycoprotein 4 (PSG4) clone FL-64 mRNA, complete cds.//
7.60E-293//1631bp//90%//U18469
C-PLACE1001340//Homo sapiens mRNA for KIAA0719 protein, complete cds.//0//2868bp//99%//AB018262
C-PLACE1001401//HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT (FCER1) (IGE

EP 1 130 094 A2

FC RECEPTOR, BETA-SUBUNIT).//3.70E-18//148aa//39%//P13386
 C-PLACE1001407
 C-PLACE1001464//Human placental cDNA coding for 5'nucleotidase (EC 3.1.3.5).//0//2756bp//99%//X55740
 C-PLACE1001500//Homo sapiens RecQ5 mRNA for DNA helicase, complete cds.//2.30E-271//1230bp//99%//
 AB006533
 C-PLACE1001516//240 KD PROTEIN OF ROD PHOTORECEPTOR CNG-CHANNEL [CONTAINS: GLUTAMIC
 ACID-RICH PROTEIN (GARP); CYCLIC-NUCLEOTIDE-GATED CATION CHANNEL 4 (CNG CHANNEL 4) (CNG-
 4) (CYCLIC NUCLEOTIDE-GATED CATION CHANNEL MODULATORY SUBUNIT)].//2.30E-08//274aa//28%//
 Q28181
 C-PLACE1001536
 C-PLACE1001564//H.sapiens mRNA for HE6 Tm7 receptor.//5.10E-36//499bp//70%//X81892
 C-PLACE1001655//Homo sapiens Shab-related delayed-rectifier K+ channel alpha subunit (KCNS3) mRNA, com-
 plete cds.//0//1708bp//99%//AF043472
 C-nnnnnnnnnnnn//Homo sapiens calumein (Calu) mRNA, complete cds.//0//1776bp//99%//AF013759
 C-PLACE1001788
 C-PLACE1001795//HYPOTHETICAL 30.6 KD PROTEIN IN SCP160-SMC3 INTERGENIC REGION PRECUR-
 SOR.//3.40E-20//159aa//40%//P47032
 C-PLACE1001836//ENV POLYPROTEIN PRECURSOR (COAT POLYPROTEIN) [CONTAINS: OUTER MEM-
 BRANE PROTEIN GP70; TRANSMEMBRANE PROTEIN P2OE].//5.00E-27//134aa//47%//P10269
 C-PLACE1001918//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHE-
 ROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPO-
 NENT).//2.30E-53//339aa//33%//P32802
 C-PLACE1001949//PROBABLE CALCIUM-TRANSPORTING ATPASE 9 (EC 3.6.1.38).//3.00E-75//315aa//44%//
 Q12697
 C-PLACE1002080//Homo sapiens antigen NY-CO-9 (NY-CO-9) mRNA, partial cds.//0//1588bp//99%//AF039691
 C-PLACE1002095
 C-PLACE1002153//Homo sapiens TACC2 protein (TACC2) mRNA, partial cds.//0//1202bp//99%//AF095791
 C-PLACE1002329//EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8.//6.50E-105//
 213aa//45%//Q08509
 C-PLACE1002355//COMPLEMENT C4 PRECURSOR [CONTAINS: C4A ANAPHYLATOXIN].//4.20E-12//131aa//
 40%//P01029
 C-PLACE1002374//Human mRNA for pro-cathepsin L (major excreted protein MEP).//1.30E-313//1363bp//97%//
 X12451
 C-PLACE1002518
 C-PLACE1002547//Homo sapiens mRNA for KIAA0719 protein, complete cds.//0//2985bp//99%//AB018262
 C-PLACE1002726//Oryctolagus cuniculus mRNA for epithelial calcium channel (ECaC).//2.80E-202//926bp//
 82%//AJ133128
 C-PLACE1002905//ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DIAZEPAM
 BINDING INHIBITOR) (MA-DBI).//2.40E-37//188aa//40%//P07106
 C-PLACE1002911//POLIOVIRUS RECEPTOR HOMOLOG PRECURSOR.//4.50E-39//345aa//32%//P32507
 C-PLACE1002967//HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT (FCER1) (IGE
 FC RECEPTOR, BETA-SUBUNIT).//4.60E-08//156aa//30%//Q01362
 C-PLACE1003135//SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-).//1.30E-47//210aa//49%//P08458
 C-PLACE1003163//Homo sapiens DBI-related protein mRNA, complete cds.//1.00E-294//1344bp//99%//
 AF069301
 C-PLACE1003428//Homo sapiens mRNA for VNN1 protein.//1.80E-142//676bp//72%//AJ132099
 C-PLACE1003438
 C-PLACE1003460
 C-PLACE1003529//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAG-
 MENT).//1.30E-09//281aa//22%//P11414
 C-PLACE1003573//T-CELL SURFACE GLYCOPROTEIN YE1/48 (T LYMPHOCYTE ANTIGEN A1) (LY49-A AN-
 TIGEN).//3.70E-16//226aa//26%//P20937
 C-PLACE1003598//TRP-ASP REPEATS CONTAINING PROTEIN RBA-1.//1.80E-07//161aa//27%//P90917
 C-PLACE1003644
 C-PLACE1003737//TOLL PROTEIN PRECURSOR.//5.40E-07//203aa//27%//P08953
 C-PLACE1003772//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//
 2.40E-12//124aa//38%//P 13983
 C-PLACE1003839//Homo sapiens putative G protein-coupled receptor (RAIG1) mRNA, complete cds.//8.10E-18//

771bp//58%//AF095448
 C-PLACE1003845//PUTATIVE UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP-GALACTOSE 4-EPIMERASE).//3.40E-37//302aa//30%//Q57664
 C-PLACE1003852//Homo sapiens mRNA for KIAA0758 protein, partial cds.//0//1667bp//99%//AB018301
 5 C-PLACE1004028
 C-PLACE1004166//CREB-BINDING PROTEIN.//1.80E-12//147aa//35%//P45481
 C-PLACE1004168//Homo sapiens mRNA for KIAA1007 protein, partial cds.//0//2637bp//99%//AB023224
 C-PLACE1004199
 10 C-PLACE1004279//HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME III.//1.40E-08//166aa//30%//P30638
 C-PLACE1004282//MONO- AND DIACYLGLYCEROL LIPASE PRECURSOR (EC 3.1.1.-) (MDGL).//2.10E-11//189aa//30%//P25234
 C-PLACE1004305//RAS-RELATED PROTEIN RAC1.//9.60E-29//197aa//41%//P40792
 C-PLACE1004441//Human G protein-coupled receptor (GPR1) gene, complete cds.//0//1880bp//98%//AC007383
 15 C-PLACE1004450//AMINOPEPTIDASE N (EC 3.4.11.2) (MICROSOMAL AMINOPEPTIDASE) (LEUKEMIA ANTIGEN CD13).//1.30E-91//562aa//35%//P15541
 C-PLACE1004482//Rattus norvegicus hematopoietic lineage switch 2 related protein (Hls2-rp) mRNA, complete cds.//1.90E-246//1643bp//83%//AF097723
 C-PLACE1004519
 20 C-PLACE1004520//Human pregnancy-specific beta-glycoprotein d mRNA, complete cds.//9.10E-279//882bp//88%//M20881
 C-PLACE1004630
 C-PLACE1004637
 25 C-PLACE1004648//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//1.40E-18//395aa//25%//P08640
 C-nnnnnnnnnnnn//Homo sapiens tyrosylprotein sulfotransferase-2 mRNA, complete cds.//0//1825bp//99%//AF049891
 C-PLACE1004816//Homo sapiens mRNA for Hakata antigen, complete cds.//1.00E-166//856bp//94%//D88587
 C-PLACE1004887//GOLIATH PROTEIN (G1 PROTEIN).//4.80E-33//179aa//47%//Q06003
 30 C-PLACE1005003//PROSTASIN PRECURSOR (EC 3.4.21.-).//2.20E-52//269aa//41%//Q16651
 C-PLACE1005005//Homo sapiens ubiquitin conjugating enzyme G2 (UBE2G2) mRNA, complete cds.//4.10E-261//1209bp//98%//AF032456
 C-PLACE1005031//CHLORINE CHANNEL PROTEIN P64.//8.00E-92//205aa//87%//P35526
 C-PLACE1005239//Homo sapiens mRNA for HIRIP3 protein (clone pH4-31, pH4-17).//1.80E-235//1010bp//84%//
 35 AJ223351
 C-PLACE1005250//Homo sapiens D-type cyclin-interacting protein 1 (DIP1) mRNA, complete cds.//0//1046bp//96%//AF082569
 C-PLACE1005383//Homo sapiens UP50 mRNA, complete cds.//0//2019bp//99%//AF093118
 C-PLACE1005410//Canis familiaris sec61 homologue mRNA, complete cds.//2.40E-204//673bp//89%//M96629
 40 C-PLACE1005426//Human pregnancy-specific beta 1-glycoprotein 4 (PSG4) clone FL-64 mRNA, complete cds.//0//1629bp//95%//U18469
 C-PLACE1005519//Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds.//4.60E-108//1070bp//73%//AF024636
 C-PLACE1005544//Mus musculus junctional adhesion molecule (Jam) mRNA, complete cds.//2.00E-159//1237bp//76%//U89915
 45 C-PLACE1005660//HYPOTHETICAL 64.3 KD GTP-BINDING PROTEIN C02F5.3 IN CHROMOSOME III.//1.90E-33//143aa//53%//P34280
 C-PLACE1005669
 C-PLACE1005682//B-CELL LYMPHOMA 3-ENCODED PROTEIN (BCL-3 PROTEIN).//4.90E-09//183aa//33%//P20749
 50 C-PLACE1005725//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//7.60E-17//295aa//27%//Q11073
 C-PLACE1005736//Human mRNA for BAS-GRIP protein.//0//2378bp//99%//E16311
 C-PLACE1005768
 55 C-PLACE1005878//Bovine chlorine channel protein (p64) mRNA, complete cds.//5.90E-137//889bp//85%//L16547
 C-PLACE1006093
 C-PLACE1006208//Homo sapiens nGAP mRNA, complete cds.//3.30E-151//694bp//100%//AP047711
 C-PLACE1006219//PUTATIVE UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP-

EP 1 130 094 A2

GALACTOSE 4-EPIMERASE).//3.50E-37//302aa//30%//Q57664
 C-PLACE1006277//Homo sapiens mRNA for Z39lg protein.//0//1768bp//99%//AJ132502
 C-PLACE1006290//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//8.50E-75//301aa//39%//P43636
 C-PLACE1006443//Homo sapiens PB39 mRNA, complete cds.//4.30E-98//553bp//70%//AF045584
 C-PLACE1006515//Homo sapiens mRNA for KIAA0576 protein, partial cds.//0//2846bp//99%//AB011148
 C-PLACE1006716//30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN PRECURSOR (ACRP30) (ADIPOCYTE SPECIFIC PROTEIN ADIPOQ).//4.60E-25//181aa//35%//Q60994
 C-PLACE1006809//SLS1 PROTEIN PRECURSOR.//9.10E-10//273aa//27%//P08124
 C-PLACE1006959
 10 C-PLACE1007028
 C-PLACE1007040
 C-PLACE1007096//PUTATIVE SUGAR TRANSPORT PROTEIN GETA.//2.70E-17//174aa//27%//O34368
 C-nnnnnnnnnnnn//Homo sapiens mRNA for putative glucosyltransferase, partial cds.//0//1373bp//99%//AJ224875
 C-PLACE1007296//Human mRNA for a presumptive KDEL receptor.//1.10E-185//1038bp//91%//X55885
 C-PLACE1007591
 15 C-PLACE1007626//Homo sapiens unknown mRNA, complete cds.//3.00E-246//1122bp//99%//AF047439
 C-PLACE1007702//Mus musculus TRA1 mRNA, complete cds.//7.50E-41//662bp//64%//D78335
 C-PLACE1007845//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//4.80E-14//158aa//40%//P43636
 C-PLACE1007881//HYPOTHETICAL 69.4 KD PROTEIN F13H10.3 IN CHROMOSOME IV.//3.10E-99//504aa//
 20 42%//Q19425
 C-PLACE1008297//MYOSIN HEAVY CHAIN KINASE B (EC 2.7.1.129) (MHCK B).//1.30E-14//187aa//33%//
 P90648
 C-nnnnnnnnnnnn//Homo sapiens mRNA for putative glucosyltransferase, partial cds.//0//1616bp//99%//AJ224875
 C-PLACE1008469
 25 C-PLACE1008549//Homo sapiens Ets transcription factor ESE-2b mRNA, complete cds.//0//2274bp//99%//
 AF115403
 C-PLACE1008657//Bovine mRNA for adseverin, complete cds.//7.80E-227//1246bp//90%//D26549
 C-PLACE1008716//Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds.//0//
 1888bp//99%//U15128
 30 C-PLACE1008984
 C-PLACE1008985//Mus musculus synaptotagmin VIII mRNA, partial cds.//3.80E-140//650bp//81%//U20107
 C-PLACE1009067
 C-PLACE1009196
 35 C-PLACE1009279//cDNA encoding novel physiologically active protein which have serine protease activity.//
 6.60E-86//1414bp//64%//E12965
 C-PLACE1009527//Oryctolagus cuniculus mRNA for epithelial calcium channel (ECaC).//1.20E-87//585bp//83%//
 AJ133128
 C-PLACE1009546
 40 C-PLACE1009600//Mouse mRNA for tetracycline transporter-like protein, complete cds.//1.10E-264//924bp//
 88%//D88315
 C-PLACE1009735
 C-PLACE1009982//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.//5.20E-08//166aa//28%//P02840
 C-PLACE1010078//ORM1 PROTEIN.//3.70E-19//137aa//37%//P53224
 C-PLACE1010081//Homo sapiens serine/threonine kinase RICK (RICK) mRNA, complete cds.//0//2033bp//99%//
 45 AF027706
 C-PLACE1010251//FIBRILLIN 2 PRECURSOR.//1.70E-31//201aa//35%//Q61555
 C-PLACE1010784//Homo sapiens orphan G protein-coupled receptor (GPR34) gene, complete cds.//2.30E-252//
 1146bp//99%//AF008670
 C-PLACE1010827//COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).//1.90E-
 50 19//163aa//34%//P49020
 C-PLACE1010968//PROTEIN-TYROSINE PHOSPHATASE DLAR PRECURSOR (EC 3.1.3.48) (PROTEIN-TY-
 ROSINE-PHOSPHATE PHOSPHOHYDROLASE).//3.40E-30//690aa//26%//P16621
 C-PLACE1011045//Homo sapiens E1-like protein mRNA, complete cds.//0//2376bp//99%//AF094516
 C-PLACE1011116//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE)
 (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//3.30E-09//234aa//27%//P08640
 C-PLACE1011236//Mus musculus mRNA for RST, complete cds.//1.70E-90//1398bp//65%//AB005451
 C-PLACE1011407//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.80E-133//342aa//59%//Q99676
 C-PLACE1011516//HYPOTHETICAL 21.5 KD PROTEIN IN SEC15-SAP4 INTERGENIC REGION.//1.30E-13//
 55

139aa//34%//P53073
 C-PLACE1011708//Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds.//0//1840bp//98%//
 AF034611
 C-PLACE1011824//Human Ste20-like kinase (MST2) mRNA, complete cds.//6.40E-202//561bp//92%//U26424
 5 C-PLACE1011978//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.10E-194//547aa//
 57%//Q05481
 C-PLACE2000118//WISKOTT-ALDRICH SYNDROME PROTEIN HOMOLOG (WASP).//3.20E-27//205aa//43%//
 P70315
 C-PLACE2000219
 10 C-SKNMC100004
 C-THYRO1000036//Homo sapiens collagen alpha 3 type IX (COL9A3) mRNA, complete cds.//1.20E-258//
 1376bp//93%//L41162
 C-THYRO1000061
 C-THYRO1000099
 15 C-THYRO1000196//Homo sapiens Ksp-cadherin (CDH16) mRNA, complete cds.//0//1632bp//91%//AF016272
 C-THYRO1000400//Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 25795.//0//1893bp//99%//
 AL109665
 C-THYRO1000580//ZINC FINGER PROTEIN 184 (FRAGMENT).//9.90E-114//279aa//59%//Q99676
 C-THYRO1000584//Homo sapiens mRNA for KIAA0935 protein, partial cds.//0//1338bp//99%//AB023152
 20 C-THYRO1000678//Homo sapiens Cx30 gene.//0//1741bp//97%//AJ005585
 C-THYRO1000795//C.elegans mRNA for Oxoglutarate/malate carrier protein.//8.80E-42//821bp//63%//X76114
 C-THYRO1000846
 C-THYRO1000866//SHK1 KINASE-BINDING PROTEIN 1.//4.40E-91//449aa//44%//P78963
 C-THYRO1000956//Human G protein-coupled receptor APJ gene, complete cds.//0//1583bp//99%//U03642
 25 C-THYRO1000999
 C-THYRO1001063
 C-THYRO1001071//GAMMA-ADAPTIN (GOLGI ADAPTOR HA1/AP1 ADAPTIN GAMMA SUBUNIT) (CLATHRIN
 ASSEMBLY PROTEIN COMPLEX 1 GAMMA LARGE CHAIN).//8.20E-14//157aa//33%//P22892
 C-THYRO1001102
 30 C-THYRO1001113//Homo sapiens mRNA; cDNA DKFZp564E1616 (from clone DKFZp564E1616).//0//1361bp//
 99%//AL096713
 C-THYRO100128
 C-THYRO1001205
 C-THYRO1001237//PHYTOENE DEHYDROGENASE (EC 1.3.-.) (PHYTOENE DESATURASE) (ALBINO-1
 35 PROTEIN).//3.10E-13//346aa//22%//P21334
 C-THYRO1001266//Human sodium iodide symporter mRNA, complete cds.//7.20E-81//1466bp//62%//U66088
 C-THYRO1001327
 C-THYRO1001456//HYPOTHETICAL 56.2 KD PROTEIN CY31.25C.//9.40E-32//355aa//31%//Q10555
 C-THYRO1001457//H.sapiens mRNA for protein kinase C mu.//2.30E-218//1183bp//73%//X75756
 40 C-THYRO1001471
 C-THYRO1001478//CYTOCHROME B-245 HEAVY CHAIN (P22 PHAGOCYTE B-CYTOCHROME) (NEU-
 TROPHIL CYTOCHROME B, 91 KD POLYPEPTIDE) (CGD91-PHOX) (GP91-PHOX) (CYTOCHROME B(558)
 BETA CHAIN) (SUPEROXIDE-GENERATING NADPH OXIDASE HEAVY CHAIN SUBUNIT).//8.90E-50//296aa//
 35%//P04839
 45 C-THYRO1001495
 C-THYRO1001523//Homo sapiens mRNA for TM7XN1 protein.//0//3663bp//99%//AJ011001
 C-THYRO1001529//SERINE PALMITOYLTRANSFERASE 2 (EC 2.3.1.50) (LONG CHAIN BASE BIOSYNTHESIS
 PROTEIN 2) (SPT 2).//5.50E-25//115aa//53%//Q09925
 C-THYRO1001700//SERINE/THREONINE PROTEIN KINASE RIP (EC 2.7.1.-) (CELL DEATH PROTEIN RIP)
 50 (RECEPTOR INTERACTING PROTEIN).//9.70E-33//268aa//37%//Q60855
 C-THYRO1001702//Mus musculus mRNA for myeloid associated differentiation protein.//1.50E-128//1204bp//
 73%//AJ001616
 C-THYRO1001725
 C-THYRO1001803
 55 C-Y79AA1000127
 C-Y79AA1000207
 C-Y79AA1000226
 C-Y79AA1000270//Bos taurus vacuolar H⁺ ATPase subunit Ac45 mRNA, complete cds.//1.00E-271//1490bp//

83%//U10039
 C-Y79AA1000426//Mus musculus activin beta E subunit mRNA, complete cds //7.70E-200//1533bp//78%//U96386
 C-Y79AA1000521
 C-Y79AA1000776
 5 C-Y79AA1000777//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1 //8.10E-48//283aa//38%//Q00808
 C-nnnnnnnnnnnn//Homo sapiens intersectin long form mRNA, complete cds //0//1519bp//99%//AF064244
 C-Y79AA1000876//PROTEIN DISULFIDE ISOMERASE-RELATED PROTEIN PRECURSOR (ERP72) //1.60E-44//210aa//38%//P13667
 10 C-Y79AA1000959//Homo sapiens Hsp70 binding protein HspBP1 mRNA, complete cds //4.80E-283//1405bp//95%//AF093420
 C-Y79AA1000967//CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123) (CAM KINASE I) //1.00E-77//359aa//44%//Q14012
 C-Y79AA1001013
 15 C-Y79AA1001056
 C-Y79AA1001062//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN) //8.90E-12//132aa//38%//Q13829
 C-Y79AA1001090//NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT (DNA-BINDING FACTOR KBF1) (EBP-1) (NF-KAPPA-B1 P84/NF-KAPPA-B1 P98) [CONTAINS: NUCLEAR FACTOR NF-KAPPA-B P50 SUBUNIT] (FRAGMENT) //4.50E-09//144aa//31%//Q63369
 20 C-Y79AA1001264//HYPOTHETICAL 39.9 KD PROTEIN T15H9.1 IN CHROMOSOME II PRECURSOR //5.10E-106//351aa//58%//Q10005
 C-Y79AA1001272
 C-Y79AA1001328//Mus musculus mRNA for DII3 protein, complete cds //1.90E-263//1988bp//79%//ABO13440
 25 C-Y79AA1001430//Homo sapiens mRNA for KIAA0469 protein, complete cds //0//2943bp//99%//AB007938
 C-Y79AA1002022//POLIOVIRUS RECEPTOR HOMOLOG PECURSOR //2.20E-06//140aa//26%//P32507
 C-BNGH41000020//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 (EC 1.6.5.3) //9.80E-159//347aa//90%//P03891
 C-BNGH41000091//POTASSIUM CHANNEL PROTEIN EAG //1.20E-249//625aa//65%//Q02280
 30 C-HEMBA1000462//Human potential transcriptional repressor NOT4Hp (NOT4H) mRNA, complete cds //0//935bp//99%//U71267
 C-HEMBA1000477//HYPOTHETICAL 64.8 KD PROTEIN IN GDI1-COX15 INTERGENIC REGION //1.40E-38//344aa//34%//P40085
 C-HEMBA1000671//ZINC FINGER PROTEIN 184 (FRAGMENT) //3.90E-104//388aa//46%//Q99676
 35 C-HEMBA1000732//Homo sapiens mRNA for latent transforming growth factor-beta binding protein-4 //0//2153bp//94%//Y13622
 C-HEMBA1000835
 C-HEMBA1000875
 C-HEMBA1001184//SH3BGR PROTEIN (21-GLUTAMIC ACID-RICH PROTEIN) (21-GARP) //2.50E-32//100aa//60%//P55822
 40 C-HEMBA1001272//Homo sapiens mRNA for KIAA1171 protein, partial cds //0//1490bp//99%//AB032997
 C-HEMBA1001296
 C-HEMBA1002048//ODD-SKIPPED PROTEIN //1.60E-55//122aa//75%//P23803
 C-HEMBA1002985
 C-HEMBA1003120//ZINC FINGER PROTEIN 184 (FRAGMENT) //1.00E-193//547aa//54%//Q99676
 45 C-HEMBA1003497//ZINC FINGER PROTEIN 151 (POLYOMAVIRUS LATE INITIATOR PROMOTER BINDING PROTEIN) (LP-1) (ZINC FINGER PROTEIN Z13) //4.00E-28//358aa//29%//Q60821
 C-HEMBA1004007
 C-HEMBA1004085
 C-HEMBA1004785//MODIFIER 3 PROTEIN (M33) //1.40E-27//221aa//33%//P30658
 50 C-HEMBA1004952
 C-HEMBA1004971
 C-HEMBA1005230//ZINC FINGER PROTEIN 140 //2.00E-17//83aa//66%//P52738
 C-HEMBA1005246
 C-HEMBA1005267//ANKYRIN, BRAIN VARIANT 1 (ANKYRIN B) (ANKYRIN, NONERYTHROID) //8.40E-14//187aa//33%//Q01484
 55 C-HEMBA1006276//ZINC FINGER PROTEIN 90 (ZFP-90) (ZINC FINGER PROTEIN NK10) //1.70E-06//56aa//57%//Q61967
 C-HEMBA1006357//SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2 //3.70E-39//136aa//52%//

O15127
 C-HEMBA1006517
 C-HEMBA1006544
 C-HEMBA1006749//Homo sapiens mRNA for matrilin-4, partial./.1.40E-275//1942bp//83%//AJ007581
 5 C-HEMBA1006770//FLOWERING TIME CONTROL PROTEIN FCA./.1.20E-33//352aa//34%//O04425
 C-HEMBA1006912
 C-HEMBA1007063
 C-HEMBB1000106//CELLULAR NUCLEIC ACID BINDING PROTEIN (CNBP).//1.60E-10//139aa//30%//P53996
 C-HEMBB1000407
 10 C-HEMBB1000542//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds./.2.60E-232//
 1452bp//85%//AF084259
 C-HEMBB1001547//Homo sapiens CGI-02 protein mRNA, complete cds./.0//2311bp//99%//AF132937
 C-HEMBB1001959//CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN
 B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN SUBUNIT B).//7.30E-14//97aa//38%//P25210
 15 C-HEMBB1002039
 C-HEMBB1002041//Homo sapiens transmembrane protein TENB2 (TENB2) mRNA, complete cds./.0//1746bp//
 99%//AF179274
 C-HEMBB1002051//Homo sapiens Ets transcription factor ESE-2b mRNA, complete cds./.1.30E-95//454bp//99%//
 AF115403
 20 C-HEMBB1002120//UDP-N-ACETYLGLUCOSAMINE-PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE
 110 KD SUBUNIT (EC 2.4.1.-) (O-GLCNAC TRANSFERASE P110 SUBUNIT).//4.90E-22//337aa//27%//P56558
 C-HEMBB1002302
 C-HEMBB1002661//Homo sapiens cardiovascular helix-loop-helix factor 2 (CHF2) mRNA, complete cds./.0//
 2174bp//99%//AF179274
 25 C-MAMMA1000106
 C-MAMMA1000141
 C-MAMMA1000204//Homo sapiens dysferlin mRNA, complete cds./.0//2028bp//99%//AF075575
 C-MAMMA1000226
 30 C-MAMMA1000403//Homo sapiens CDK4-binding protein p34SEI1 (SEI1) mRNA, complete cds./.1.20E-255//
 1165bp//99%//AF117959
 C-MAMMA1000473//HYPOTHETICAL 35.6 KD PROTEIN IN SPC1-ILV3 INTERGENIC REGION./.5.10E-45//
 299aa//34%//P47088
 C-MAMMA1000496//MIC1 PROTEIN./.3.00E-25//202aa//33%//P53258
 C-MAMMA1000528
 35 C-MAMMA1000614//Homo sapiens pseudouridine synthase 1 (PUS1) mRNA, partial cds./.2.10E-302//1370bp//
 99%//AF116238
 C-MAMMA1000652
 C-MAMMA1000706
 C-MAMMA1000788//Bos taurus P14 (p14) mRNA, complete cds./.3.90E-85//502bp//89%//AF037349
 40 C-MAMMA1000810
 C-MAMMA1000814
 C-MAMMA1000881//Homo sapiens protein kinase (SGK3) mRNA, complete cds./.0//1292bp//100%//AF169035
 C-MAMMA1000986
 45 C-MAMMA1000994//Homo sapiens ISLR(immunoglobulin superfamily containing leucine-rich repeat) mRNA,
 complete cds, alternatively spliced transcript ISLR-2./.0//2211bp//99%//AB024536
 C-MAMMA1001141
 C-MAMMA1001150//PROTEIN KINASE C, MU TYPE (EC 2.7.1.-) (NPKC-MU).//7.50E-304//587aa//68%//Q15139
 C-MAMMA1001237//MONOCARBOXYLATE TRANSPORTER 2 (MCT 2).//7.70E-64//196aa//41%//P53988
 C-MAMMA1001284
 50 C-MAMMA1001310//HYPOTHETICAL 57.3 KD TRP-ASP REPEATS CONTAINING PROTEIN IN POM152-
 REC114 INTERGENIC REGION./.1.50E-67//441aa//37%//Q04225
 C-MAMMA1001344
 C-MAMMA1001418//HYPOTHETICAL PROTEIN H10519./.6.90E-27//181aa//38%//P44742
 C-MAMMA1001532//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//5.60E-126//319aa//56%//
 55 P51523
 C-MAMMA1001615//NEUROGENIC DIFFERENTIATION FACTOR 1./.3.80E-11//90aa//42%//Q13562
 C-MAMMA1001623//Homo sapiens mRNA; cDNA DKFZp434J1027 (from clone DKFZp434J1027); partial cds./.
 1.30E-269//1222bp//99%//AL133084

C-MAMMA1001634
 C-MAMMA1001957
 C-MAMMA1001978//Cimex lectularius apyrase (APY) mRNA, complete cds.//6.70E-19//988bp//56%//AF085499
 C-MAMMA1002070//PLASMINOGEN (EC 3.4.21.7) (FRAGMENT).//1.10E-07//103aa//33%//Q01177
 5 C-MAMMA1002080//RAS-RELATED PROTEIN RAB-13.//1.80E-29//208aa//37%//P51153
 C-MAMMA1002087
 C-MAMMA1002095//CALCIUM-TRANSPORTING ATPASE 1 (EC 3.6.1.38) (P-TYPE CALCIUM ATPASE).//
 3.70E-222//867aa//52%//O43108
 C-MAMMA1002128//ABC1 PROTEIN HOMOLOG PRECURSOR.//2.50E-97//464aa//45%//Q92338
 10 C-MAMMA1002142//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE- PRO-
 TEIN KINASE 1).//9.80E-17//146aa//35%//P18160
 C-MAMMA1002165//Homo sapiens connective tissue growth factor related protein WISP-2 (WISP2) mRNA, com-
 plete cds.//4.80E-60//382bp//89%//AF100780
 15 C-MAMMA1002205//Homo sapiens mRNA; cDNA DKFZp586C091 (from clone DKFZp586C091).//2.00E-81//
 308bp//81%//AL050119
 C-MAMMA1002234//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//0//627aa//96%//Q00004
 C-MAMMA1002586//Homo sapiens alpha 1,2-mannosidase mRNA, complete cds.//0//2228bp//99%//AF148509
 C-MAMMA1002633
 20 C-MAMMA1003126//Human Hpast (HPAST) mRNA, complete cds.//3.70E-162//1355bp//75%//AF001434
 C-NT2RM1000580//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//8.50E-75//301aa//39%//P43636
 C-NT2RM1000858//tricarboxylate carrier [rats, liver, mRNA Partial, 2986 nt].//2.10E-98//1035bp//70%//S70011
 C-NT2RM2000565//HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I.//9.40E-94//394aa//
 43%//Q09782
 25 C-NT2RM2000582//Homo sapiens mRNA for KIAA1053 protein, partial cds.//0//2666bp//99%//AB028976
 C-NT2RM2000589//Bos taurus myosin X, complete cds.//0//4376bp//84%//U55042
 C-NT2RM2000632//EXCISION REPAIR PROTEIN ERCC-6 (COCKAYNE SYNDROME PROTEIN CSB).//6.40E-
 62//183aa//47%//Q03468
 C-NT2RM2000773//Homo sapiens KNSL4 and MAZ genes for kinesin-like DNA binding protein and Myc-associ-
 ated zinc finger protein, complete cds.//3.00E-289//1092bp//99%//AB017335
 30 C-NT2RM2001558//Homo sapiens protein kinase A binding protein AKAP110 mRNA, complete cds.//0//2398bp//
 99%//AF093408
 C-NT2RM2001626//FLIGHTLESS-1 PROTEIN HOMOLOG.//4.30E-19//362aa//26%//P34268
 C-NT2RM2001643
 35 C-NT2RM2001738//SOF1 PROTEIN.//3.00E-110//325aa//47%//P33750
 C-NT2RM2001792//Homo sapiens angiopoietin-related protein-2 mRNA, complete cds.//7.10E-149//995bp//86%//
 AF125175
 C-NT2RM2001818//SIALIDASE (EC 3.2.1.18) (NEURAMINIDASE) (NA) (MAJOR SURFACE ANTIGEN).//4.30E-
 11//488aa//26%//P23253
 C-NT2RM4000100//Homo sapiens mRNA for KIAA0989 protein, partial cds.//0//2678bp//99%//AB023206
 40 C-NT2RM4000115//HYPOTHETICAL 68.8 KD PROTEIN B0464.6 IN CHROMOSOME III.//1.20E-16//204aa//
 30%//Q03564
 C-NT2RM4000417//SYNAPTOTAGMIN II.//2.70E-23//293aa//30%//P46097
 C-NT2RM4000593//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I.//3.90E-27//576aa//
 24%//Q10297
 45 C-NT2RM4000761//H.sapiens mitochondrial genome (consensus sequence).//0//1931bp//99%//X62996
 C-NT2RM4000965//PUTATIVE IMPORTIN BETA-4 SUBUNIT (KARYOPHERIN BETA-4 SUBUNIT).//9.00E-44//
 520aa//29%//O60100
 C-NT2RM4001377//Homo sapiens mRNA for KIAA0638 protein, partial cds.//0//1346bp//99%//AB014538
 C-NT2RM4001768//Homo sapiens CGI-82 protein mRNA, complete cds.//0//1925bp//99%//AF151840
 50 C-NT2RM4001843//BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE).//6.20E-33//263aa//38%//
 P48982
 C-NT2RP1000239
 C-NT2RP1000465//UBIQUITIN-LIKE PROTEIN SMT3.//5.10E-07//81aa//33%//P55857
 C-NT2RP1000468//CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN
 55 B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN SUBUNIT B).//2.00E-13//97aa//38%//P25210
 C-NT2RP1000679
 C-NT2RP1000740//Homo sapiens mRNA; cDNA DKFZp586F1918 (from clone DKFZp586F1918).//4.60E-97//
 456bp//99%//AL050091

EP 1 130 094 A2

C-NT2RP1001031//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1..//3.40E-42//285aa//35%//Q00808
 C-NT2RP2000178//MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.21.-)..
 778aa//48%//P93647
 C-NT2RP2000240
 5 C-NT2RP2000447//GOLGIN-95..
 C-NT2RP2000610//CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN
 B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN SUBUNIT B)..
 C-NT2RP2000616//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)..
 4.10E-12//323aa//30%//P13983
 10 C-NT2RP2000712//ZINC FINGER PROTEIN 135..
 C-NT2RP2000739//ZINC FINGER PROTEIN 83 (ZNCC FNNGER PROTENN HPF1)..
 P51522
 C-NT2RP2000818//Homo sapiens xenotropic and polytropic murine leukemia virus receptor (X3) mRNA, complete
 cds..
 15 C-NT2RP2001200//Homo sapiens mRNA for KIAA0676 protein, partial cds..
 C-NT2RP2001223//MYOTUBULARIN-RELATED PROTEIN 3 (FRAGMENT)..
 C-NT2RP2001276//NPDC-1 PROTEIN PRECURSOR..
 C-NT2RP2001388//TRNA-SPUCING ENDONUCLEASE SUBUNIT SEN2 (EC 3.1.27.9) (TRNA-INTRON ENDO-
 NUCLEASE)..
 20 C-NT2RP2001469//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1..
 C-NT2RP2001562//Homo Sapiens GLE1 (GLE1) mRNA, complete cds..
 C-NT2RP2001662//HOMEODOMAIN PROTEIN AKR (AVIAN KNOTTED-RELATED PROTEIN)..
 94aa//81%//Q90655
 C-NT2RP2001755//Rattus norvegicus f-spondin mRNA, complete cds..
 25 C-NT2RP2001817//Homo sapiens sirtuin type 1 (SIRT1) mRNA, complete cds..
 C-NT2RP2001948//HST2 PROTEIN (HOMOLOGOUS TO SIR2 PROTEIN 2)..
 C-NT2RP2002015
 C-NT2RP2003390//Homo sapiens mRNA for SEC63 protein..
 30 C-NT2RP2003664//Homo sapiens mRNA for leptin receptor gene-related protein..
 Y12670
 C-NT2RP2003940//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6)..
 C-NT2RP2004069//HYPOTHETICAL 26.4 KD PROTEIN EED8.8 IN CHROMOSOME II..
 52%//Q09297
 C-NT2RP2004108//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT)..
 35 C-nnnnnnnnnnnn//Homo sapiens calumein (Calu) mRNA, complete cds..
 C-NT2RP2005069//Rat vacuolar protein sorting homolog r-vps33b mRNA, complete cds..
 U35245
 C-NT2RP2005378//GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1.8 PRECURSOR (GRP 1.8)..
 28//183aa//47%//P10496
 40 C-NT2RP2005391//Homo sapiens partial mRNA for putative p621 protein which interacts with transcription factor
 Sp1..
 C-NT2RP2005597//Homo sapiens protein O-mannosyl-transferase 1 (POMT1) mRNA, complete cds..
 97%//AF095136
 C-NT2RP2005666
 45 C-NT2RP2006004//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN)..
 227aa//36%//Q06828
 C-NT2RP2006092//Homo sapiens mRNA for Fe65L2, complete cds..
 C-NT2RP2006134
 50 C-NT2RP300011//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1..
 C-NT2RP300022//Homo sapiens mRNA for KIAA0936 protein, complete cds..
 C-NT2RP3000171//Mus musculus partial mRNA for B-IND1 protein (B-ind1 gene)..
 Z97207
 C-NT2RP3000304//Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds..
 AF074264
 55 C-NT2RP3000378//PAIRED AMPHIPATHIC HELIX PROTEIN..
 C-NT2RP3000444
 C-NT2RP3000645
 C-NT2RP3000676//PUTATIVE MITOCHONDRIAL CARRIER YMR166C..
 2.10E-15//220aa//27%//Q03829

EP 1 130 094 A2

C-NT2RP3000677//DNA BINDING PROTEIN RFX2//3.60E-56//233aa//41%//P48378
C-NT2RP3000789//Homo sapiens IGF-II mRNA-binding protein 1 (IMP-1) mRNA, complete cds.//0//1458bp//
100%//AF117106
C-NT2RP3000818
5 C-NT2RP3000838//TRICHOHYALIN//9.80E-11//491aa//26%//Q07283
C-NT2RP3000921//TUMOR SUPPRESSOR PROTEIN DCC PRECURSOR (COLORECTAL CANCER SUP-
PRESSOR)//4.00E-21//316aa//29%//P43146
C-NT2RP3001159//Homo sapiens mRNA; cDNA DKFZp586C201 (from clone DKFZp586C201).//0//2558bp//
99%//AL050118
10 C-NT2RP3001271//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//
2.60E-09//334aa//22%//P52178
C-NT2RP3001542//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PRO-
TEIN).//4.70E-11//132aa//37%//Q13829
15 C-NT2RP3001685//PRPE PROTEIN.//1.00E-68//382aa//41%//P77495
C-NT2RP3001976//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//8.90E-143//379aa//55%//
P51523
C-NT2RP3002015//Homo sapiens CGI-71 protein mRNA, complete cds.//0//1991bp//99%//AF151829
C-NT2RP3002281//Homo sapiens mRNA for KIAA0765 protein, partial cds.//0//2286bp//99%//AB018308
20 C-NT2RP3002286//Homo sapiens candidate tumor suppressor protein DICE 1 mRNA, complete cds.//0//2719bp//
99%//AF097645
C-NT2RP3002324
C-NT2RP3002353
C-NT2RP3002571//Homo sapiens mRNA for KIAA1108 protein, partial cds.//4.40E-273//1311bp//97%//AB029031
C-NT2RP3002664
25 C-NT2RP3002737//Homo sapiens voltage-gated potassium channel KCNQ4 (KCNQ4) mRNA, complete cds.//0//
1552bp//99%//AF105202
C-NT2RP3002887
C-NT2RP3002900//Homo sapiens CGI-109 protein mRNA, complete cds.//8.70E-298//1321bp//92%//AF151867
C-NT2RP3002983
30 C-NT2RP3003473//Homo sapiens CGI-55 protein mRNA, complete cds.//5.50E-275//1309bp//98%//AF151813
C-NT2RP3003532//OX-2 MEMBRANE GLYCOPROTEIN PRECURSOR (FRAGMENT).//4.40E-139//263aa//
99%//P41217
C-NT2RP3004025
C-NT2RP3004067//Homo sapiens mRNA for NESCA, complete cds.//0//1962bp//99%//AB026894
35 C-NT2RP3004119//PEREGRIN (BE140 PROTEIN).//7.30E-39//227aa//43%//P55201
C-NT2RP3004294//Xenopus laevis ER1 mRNA, complete cds.//1.20E-71//335bp//79%//AF015454
C-NT2RP3004345//N2,N2-DIMETHYLGUANOSINE TRNA METHYLTRANSFERASE PRECURSOR (EC
2.1.1.32).//3.90E-18//279aa//27%//P15565
C-NT2RP4000634//Homo sapiens mitogen-activated protein kinase kinase kinase MEKK2 mRNA, complete cds.//
40 0//1501bp//98%//AF111105
C-NT2RP4001001//Homo sapiens clone 24856 mRNA sequence, complete cds.//3.90E-301//1374bp//99%//
AF131856
C-NT2RP4001877//Homo sapiens ribonucleoprotein RBM8 (RBM8) mRNA, complete cds.//0//2770bp//99%//
AF127761
45 C-NT2RP4001879
C-NT2RP4002187//Homo sapiens steroid dehydrogenase homolog mRNA, complete cds.//0//2373bp//99%//
AF078850
C-NT2RP4002451
C-NT2RP4002750//Mus musculus cationic amino acid transporter (CAT3) mRNA, complete cds.//1.00E-310//
2084bp//81%//U70859
C-OVARC1000003//Homo sapiens sodium dependent phosphate transporter isoform NaPi-3b mRNA, complete
cds.//4.30E-220//1158bp//94%//AF111856
C-OVARC1000313//Homo sapiens mRNA for KIAA0573 protein, partial cds.//0//1833bp//99%//AB011145
50 C-OVARC1000331//GMP REDUCTASE (EC 1.6.6.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCT-
ASE).//9.40E-44//106aa//59%//P36959
C-OVARC1000553//DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (THYMOCYTE-ACTIVATING MOLE-
CULE) (THAM).//1.30E-23//169aa//40%//P28843
C-OVARC1000873//Homo sapiens mRNA for KIAA1247 protein, partial cds.//0//2178bp//99%//AB033073

C-OVARC1000995
C-OVARC1001260
C-OVARC1001336//Homo sapiens sodium dependent phosphate transporter isoform NaPi-3b mRNA, complete cds./0//1435bp//99%//AF111856
5 C-OVARC1001570//Homo sapiens beta-site APP cleaving enzyme (BACE) mRNA, complete cds./0//1792bp//100%//AF190725
C-OVARC1001607//Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds./0//1836bp//96%//U15128
C-OVARC1001833//CIS-GOLGI MATRIX PROTEIN GM130./.6.60E-136//363aa//76%//Q62839
10 C-OVARC1001952//TRICHOHYALIN./.3.30E-16//487aa//27%//Q07283
C-PLACE1000986//Homo sapiens mRNA; cDNA DKFZp586C1817 (from clone DKFZp586C1817).//0//2055bp//99%//AL117450
C-PLACE1003407//Homo sapiens putative transmembrane protein (CLN5) mRNA, complete cds./0//1965bp//99%//AF068227
15 C-PLACE1004078//Bovine mRNA for adseverin, complete cds./0//2218bp//89%//D26549
C-PLACE1004492//VERPROLIN./.3.30E-07//149aa//29%//P37370
C-PLACE1005539//ACTIN POLYMERIZATION INHIBITOR (HEAT SHOCK 25 KD PROTEIN) (25-KD IAP).//3.10E-08//84aa//34%//Q00649
20 C-PLACE1005569//Homo sapiens mRNA for Z39Ig protein./.0//1768bp//99%//AJ132502
C-PLACE1005601
C-PLACE1005745//ORM1 PROTEIN./.2.40E-17//137aa//35%//P53224
C-PLACE1005815//COLORECTAL MUTANT CANCER PROTEIN (MCC PROTEIN).//1.50E-26//274aa//26%//P23508
25 C-PLACE1005927//HYPOTHETICAL 35.8 KD PROTEIN C12G12.12 IN CHROMOSOME 1./.1.60E-38//333aa//33%//Q09875
C-PLACE1006071//LAMININ BETA-1 CHAIN PRECURSOR (LAMININ B1 CHAIN).//6.00E-08//215aa//26%//P02469
C-PLACE1006073//Homo sapiens mRNA for glucuronyltransferase I, complete cds./.4.10E-316//1020bp//96%//AB009598
30 C-PLACE1006079//Homo sapiens distal-less homeobox protein (DLX3) gene, complete cds./0//1379bp//97%//AF028233
C-PLACE1006786
C-PLACE1007077//Homo sapiens mRNA for KIAA0977 protein, complete cds./0//2578bp//99%//AB023194
C-PLACE1007971
35 C-PLACE1008282//HEME-REGULATED EUKARYOTIC INITIATION FACTOR EIF-2-ALPHA KINASE (EC 2.7.1.-) (HRI).//7.10E-274//627aa//82%//P33279
C-PLACE1008359//BEM46 PROTEIN (FRAGMENT).//1.70E-50//289aa//42%//P54069
C-PLACE1008744//Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 248114./.0//1757bp//99%//AL079279
40 C-PLACE1010445
C-PLACE1010713//Homo sapiens steroid dehydrogenase homolog mRNA, complete cds./0//2374bp//99%//AF078850
C-nnnnnnnnnnnn//Homo sapiens angiopoietin-2 mRNA, complete cds./0//2227bp//99%//AF004327
C-PLACE1011181//MSP1 PROTEIN HOMOLOG./.9.40E-82//353aa//47%//P54815
45 C-PLACE1011364//MYOTONIN-PROTEIN KINASE (EC 2.7.1.-) (MYOTONIC DISTROPHY PROTEIN KINASE) (MDPK) (DM-KINASE) (DMK) (DMPK) (MT-PK).//2.20E-09//153aa//32%//Q09013
C-PLACE3000181//Human protocadherin 42 mRNA, complete cds for abbreviated PC42./0//2719bp//95%//L11370
C-SKNMC1000014
50 C-SKNMC1000082//BRITTLE-1 PROTEIN PRECURSOR./.3.70E-31//307aa//30%//P29518
C-THYRO1000964
C-THYRO1001242//Homo sapiens cleft lip and palate transmembrane protein 1 (CLPTM1) mRNA, complete cds./0//2468bp//99%//AF037339
C-THYRO1001608
55 C-THYRO1001641//Homo sapiens CGI-57 protein mRNA, complete cds./0//1668bp//99%//AF151815
C-THYRO1001770//PROBABLE SERINE/THREONINE-PROTEIN KINASE YNL020C (EC 2.7.1.-).//6.30E-20//1169aa//35%//P53974
C-Y79AA1000030//Homo sapiens mRNA for Fe65L2, complete cds./0//1828bp//100%//AB018247

EP 1 130 094 A2

C-Y79AA1001212//Homo sapiens SL15 protein mRNA, complete cds./.6.30E-306//1388bp//99%//AF038961
 C-Y79AA1001426//ANION EXCHANGE PROTEIN 3 (CARDIAC/BRAIN BAND 3-LIKE PROTEIN) (CAE3/BAE3).//
 6.20E-66//609aa//31%//P48751
 C-Y79AA1001427//Homo sapiens cytochrome b5 reductase 1 (B5R.1) mRNA, complete cds./0//1588bp//99%//
 AF169481
 C-Y79AA1001523//Homo sapiens transcriptional intermediary factor 1 alpha mRNA, complete cds./0//2263bp//
 99%//AF119042
 C-Y79AA1001530//Human beta-tubulin gene (5-beta) with ten Alu family members./0//1920bp//98%//X00734
 C-Y79AA1001592
 5 C-Y79AA1001727//CELL SURFACE A33 ANTIGEN PRECURSOR./1.10E-13//286aa//27%//Q99795
 C-Y79AA1001787//PROBABLE CALCIUM-TRANSPORTING ATPASE 9 (EC 3.6.1.38).//1.70E-133//544aa//37%//
 Q12697
 C-Y79AA1001793//Mus musculus mRNA for GSG1, complete cds./3.70E-126//532bp//78%//D87325
 C-Y79AA1001795//Homo sapiens mRNA for GaT4 protein./2.30E-250//1137bp//99%//Y15061
 C-Y79AA1001799//MITOCHONDRIAL RNA SPLICING PROTEIN MSR4./3.40E-54//182aa//39%//P23500
 C-Y79AA1001803//Homo sapiens secretogranin III mRNA, complete cds./0//1871bp//99%//AF078851
 C-Y79AA1001863
 C-Y79AA1002058//Mus musculus Gng31g mRNA, complete cds./4.10E-167//1145bp//83%//AF069954
 C-Y79AA1002121//HISTONE H1./4.90E-12//114aa//35%//P35060
 10 C-Y79AA1002213//HYPOTHETICAL 52.7 KD PROTEIN C38C10.2 IN CHROMOSOME III./1.20E-98//262aa//
 41%//Q03567
 C-Y79AA1002373//Mus musculus mRNA for GSG1, complete cds./7.20E-147//680bp//79%//D87325
 C-Y79AA1002376//Rattus norvegicus cytoplasmic dynein intermediate chain 2B mRNA, complete cds./1.50E-
 304//1667bp//90%//U39045
 15 C-Y79AA1002378//Homo sapiens zinc finger protein NY-REN-21 antigen mRNA, partial cds./0//963bp//99%//
 AF155100
 C-Y79AA1002381//Homo sapiens cell cycle related kinase mRNA, complete cds./0//1791bp//98%//AF035013
 C-BNGH41000087//Homo sapiens mRNA for KIAA1247 protein, partial cds./0//2294bp//99%//AB033073
 C-HEMBA1001886
 20 C-HEMBA1004067//Homo sapiens mRNA for KIAA0859 protein, complete cds./8.30E-309//623bp//99%//
 AB020666
 C-HEMBA1007226//Homo sapiens RPA-binding trans-activator (RBT1) mRNA, complete cds./7.30E-273//
 1242bp//99%//AF192529
 C-HEMBB1000309
 25 C-HEMBB1000567
 C-MAMMA100102//APOLIPOPROTEIN L PRECURSOR (APO-L).//1.40E-21//221aa//35%//O14791
 C-MAMMA1001066
 C-MAMMA1001094//Human potential transcriptional repressor NOT4Hp (NOT4H) mRNA, complete cds./0//
 1394bp//93%//U71267
 30 C-MAMMA1001609
 C-MAMMA1001901
 C-MAMMA1002091//Homo sapiens CD39L2 (CD39L2) mRNA, complete cds./0//2564bp//99%//AF039916
 C-NT2RM1000462
 35 C-NT2RM1000542//BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE).//1.40E-103//566aa//
 43%//P48982
 C-NT2RM1000789//Homo sapiens mRNA for hTCF-4./2.80E-221//757bp//99%//Y11306
 C-NT2RM1000855//Homo sapiens sec61 homolog mRNA, complete cds./0//3541bp//99%//AF084458
 C-NT2RM1000899//MITOCHONDRIAL RNA SPLICING PROTEIN MSR4./1.10E-54//182aa//39%//P23500
 40 C-NT2RP2000092//ZINC FINGER PROTEIN 136./1.90E-117//419aa//54%//P52737
 C-NT2RP2001538//Homo sapiens mRNA; cDNA DKFZp434K2235 (from clone DKFZp434K2235).//0//2139bp//
 99%//AL117513
 C-NT2RP2001921
 45 C-NT2RP2003138//5'-TG-3'INTERACTING FACTOR (HOMEobox PROTEIN TGIF).//2.10E-08//104aa//46%//
 P70284
 C-NT2RP2003302//Homo sapiens GIOT-4 mRNA for gonadotropin inducible transcription repressor-4, complete
 cds./0//2891bp//99%//AB021644
 50 C-NT2RP2003950//Homo sapiens clone 24778 unknown mRNA./0//1545bp//99%//AF070572
 C-NT2RP2005535//ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).//1.90E-172//489aa//
 55

EP 1 130 094 A2

62%//Q03923
 C-NT2RP2005774//Homo sapiens GIOT-4 mRNA for gonadotropin inducible transcription repressor-4, complete cds.//6.90E-224//1461bp//72%//AB021644
 C-NT2RP3000148//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//4.10E-106//350aa//47%//
 5 P51523
 C-NT2RP3000232//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.40E-130//693aa//41%//Q99676
 C-NT2RP3000427
 C-NT2RP3000652//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//1.90E-153//441aa//62%//P28160
 C-NT2RP3001650//BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (EC 3.4.24.-) (BMP-1).//2.20E-22//
 10 107aa//42%//P98063
 C-NT2RP3002409//Homo sapiens mRNA for KIAA0719 protein, complete cds.//0//2404bp//99%//AB018262
 C-NT2RP3002411//Homo sapiens steroid dehydrogenase homolog mRNA, complete cds.//0//2374bp//99%//
 AF078850
 15 C-NT2RP3003448
 C-NT2RP4002715
 C-OVARC1000307//HYPOTHETICAL 29.7 KD PROTEIN CY339.02.//3.00E-19//194aa//35%//Q50658
 C-PLACE1000907//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//1.30E-204//396aa//85%//
 P51522
 C-PLACE1007081
 20 C-PLACE1010011//Homo sapiens AAPT1-like protein mRNA, partial cds.//1.70E-237//1092bp//99%//AF047431
 C-PLACE3000213//COMPLEMENT RECEPTOR TYPE 2 PRECURSOR (CR2) (COMPLEMENT C3D RECEPTOR).//4.60E-68//317aa//34%//P19070
 C-PLACE4000354//COMPLEMENT RECEPTOR TYPE 1 PRECURSOR (C3B/C4B RECEPTOR) (CD35 ANTI-GEN).//1.00E-129//482aa//29%//P17927
 25 C-PLACE4000455
 C-THYRO1000776//PROBABLE SULFATE PERMEASE SPBC3H7.02.//1.30E-68//442aa//36%//O74377
 C-THYRO1001593//PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-).//3.10E-203//550aa//
 62%//P27448
 C-Y79AA1000750
 30 C-Y79AA1000888//TRNA PSEUDOURIDINE SYNTHASE A (EC 4.2.1.70) (PSEUDOURIDYLATE SYNTHASE I)
 (PSEUDOURIDINE SYNTHASE I) (URACIL HYDROLYASE).//1.50E-21//267aa//32%//P70973
 C-Y79AA1002129
 C-Y79AA1002334//GLUCOSE REPRESSION MEDIATOR PROTEIN.//1.70E-10//333aa//23%//P14922
 C-BNGH41000020//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 (EC 1.6.5.3).//9.80E-159//347aa//90%//
 35 P03891
 C-BNGH41000087//N-ACETYLGLUCOSAMINE-6-SULFATASE PRECURSOR (EC 3.1.6.14) (G6S) (GLUCOSAMINE-6-SULFATASE).//1.20E-17//83aa//40%//P50426
 C-BNGH41000091//POTASSIUM CHANNEL PROTEIN EAG.//1.20E-249//625aa//65%//Q02280
 C-HEMBA1000006//Homo sapiens mRNA for NESCA, complete cds.//0//1230bp//92%//AB026894
 40 C-HEMBA1000121//HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III.//4.80E-05//83aa//27%//
 P34679
 C-HEMBA1000128//PATHOGENESIS-RELATED PROTEIN 1 PRECURSOR (PR-1).//3.20E-07//89aa//34%//
 P33154
 C-HEMBA1000275
 45 C-HEMBA1000300
 C-HEMBA1000349//ATP-BINDING CASSETTE TRANSPORTER 1.//5.30E-65//352aa//39%//P41233
 C-HEMBA1000443//Homo sapiens CGI-96 protein mRNA, complete cds.//4.70E-129//686bp//91%//AF151854
 C-HEMBA1000462//Human potential transcriptional repressor NOT4Hp (NOT4H) mRNA, complete cds.//0//
 935bp//99%//U71267
 50 C-HEMBA1000477//HYPOTHETICAL 64.8 KD PROTEIN IN GDI1-COX15 INTERGENIC REGION.//1.40E-38//
 344aa//34%//P40085
 C-HEMBA1000590//Homo sapiens mRNA for matrilin-4, partial.//2.00E-273//1254bp//99%//AJ007581
 C-HEMBA1000634//Homo sapiens T-cell activation protein (PGR1) gene, complete cds.//0//994bp//99%//
 AF116272
 55 C-HEMBA1000671//ZINC FINGER PROTEIN 184 (FRAGMENT).//3.90E-104//388aa//46%//Q99676
 C-HEMBA1000713//Homo sapiens 10kD protein (BC10) mRNA, complete cds.//0//1254bp//99%//AF053470
 C-HEMBA1000732//Homo sapiens mRNA for latent transforming growth factor-beta binding protein-4.//0//
 2153bp//94%//Y13622

EP 1 130 094 A2

C-HEMBA1000745//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//2.00E-07//445aa//27%//P02454
 C-HEMBA1000835//FIBRILLIN 2 PRECURSOR.//1.30E-42//214aa//45%//P35556
 C-HEMBA1000875
 C-HEMBA1000907
 5 C-HEMBA1000940//GAP JUNCTION ALPHA-3 PROTEIN (CONNEXIN 44) (CX44).//2.90E-39//362aa//31%//
 P41987
 C-HEMBA1000962
 C-HEMBA1001184//SH3BGR PROTEIN (21-GLUTAMIC ACID-RICH PROTEIN) (21-GARP).//2.50E-32//100aa//
 10 60%//P55822
 C-HEMBA1001221//AGRIN PRECURSOR.//2.50E-25//294aa//29%//P31696
 C-HEMBA1001228//Human germline oligomeric matrix protein (COMP) mRNA, complete cds.//7.80E-286//
 1105bp//94%//L32137
 C-HEMBA1001272//Homo sapiens mRNA for KIAA1171 protein, partial cds.//0//1490bp//99%//AB032997
 C-HEMBA1001296
 15 C-HEMBA1001297//Homo sapiens putative transcription factor CA150 mRNA, complete cds.//4.60E-276//
 1081bp//99%//AF017789
 C-HEMBA1001390//Mus musculus polymerase I-transcript release factor mRNA, complete cds.//2.50E-57//
 464bp//82%//AF036249
 C-HEMBA1001563
 20 C-HEMBA1001621//PROBABLE G PROTEIN-COUPLED RECEPTOR APJ.//3.50E-123//259aa//89%//P35414
 C-HEMBA1001878//Homo sapiens U5 snRNP-specific 40 kDa protein mRNA, complete cds.//0//1488bp//99%//
 AF090988
 C-HEMBA1001886//ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).//1.40E-148//421aa//
 60%//Q03923
 25 C-HEMBA1002048//ODD-SKIPPED PROTEIN.//1.60E-55//122aa//75%//P23803
 C-HEMBA1002131//PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE 1//4.10E-10//140aa//
 30 30%//P24802
 C-HEMBA1002163//HYPOTHETICAL 40.7 KD PROTEIN IN DAK1-ORC1 INTERGENIC REGION.//9.40E-28//
 309aa//30%//Q04651
 C-HEMBA1002164
 C-HEMBA1002167//Rattus norvegicus neuroligin I mRNA, complete cds.//1.30E-305//1643bp//91%//U22952
 C-HEMBA1002178//PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE 1 PRECURSOR (EC
 1.14.11.4) (LYSYL HYDROXYLASE 1) (LH1).//3.70E-10//140aa//30%//P24802
 35 C-HEMBA1002195//VEGETATILE INCOMPATIBILITY PROTEIN HET-E-1.//8.80E-23//221aa//31%//Q00808
 C-HEMBA1002227//Homo sapiens mRNA for 80K-L protein, complete cds.//0//1324bp//98%//D10522
 C-HEMBA1002239
 C-HEMBA1002316//GTP-BINDING PROTEIN HFLX.//5.80E-12//196aa//29%//P25519
 C-HEMBA1002420
 40 C-HEMBA1002421//Human heparan sulfate proteoglycan (HSPG) core protein, 3' end.//0//2097bp//99%//J04621
 C-HEMBA1002524//Human MHC Class I region proline rich protein mRNA, complete cds.//0//1763bp//95%//
 U63336
 C-HEMBA1002551//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).//9.80E-08//110aa//
 37%//P49695
 45 C-HEMBA1002767//Homo sapiens chromosome 1p33-p34 beta-1,4-galactosyltransferase mRNA, complete cds.//
 0//1497bp//99%//AF038660
 C-HEMBA1002985
 C-HEMBA1002992//UBIQUITIN-LIKE PROTEIN DSK2.//2.00E-21//216aa//35%//P48510
 C-HEMBA1003047//Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds.//0//1768bp//
 99%//AF034611
 50 C-HEMBA1003072//Gallus gallus single-strand DNA-binding protein csdp mRNA, partial cds.//3.30E-93//927bp//
 73%//U68380
 C-HEMBA1003101//Homo sapiens tyrosylprotein sulfotransferase-2 mRNA, complete cds.//0//1854bp//99%//
 AF049891
 C-HEMBA1003120//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.00E-193//547aa//54%//Q99676
 55 C-HEMBA1003230//Homo sapiens fibulin-5.//5.60E-308//1398bp//99%//AJ133490
 C-HEMBA1003294
 C-HEMBA1003315//Mus musculus mRNA for DNA helicase, complete cds.//6.30E-250//1426bp//88%//AB013912
 C-HEMBA1003392//Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds.//0//1721bp//

100%//AF074264
C-HEMBA1003399//MVP1 PROTEIN//2.30E-15//279aa//23%//P40959
C-HEMBA1003487
C-HEMBA1003497//ZINC FINGER PROTEIN 151 (POLYOMAVIRUS LATE INITIATOR PROMOTER BINDING
5 PROTEIN) (LP-1) (ZINC FINGER PROTEIN Z13)//4.00E-28//358aa//29%//Q60821
C-HEMBA1003530//S.scrofa mRNA for BM88 antigen//1.20E-60//900bp//66%//X82027
C-HEMBA1003602//HYPOTHETICAL 29.7 KD PROTEIN CY339.02//2.80E-21//200aa//33%//Q50658
C-HEMBA1003732//SFT2 PROTEIN//1.50E-06//162aa//30%//P38166
C-HEMBA1003945//Homo sapiens hypothetical 43.2 Kd protein mRNA, complete cds//8.90E-287//757bp//97%//
10 AF077030
C-HEMBA1004007
C-HEMBA1004067//Homo sapiens mRNA for KIAA0859 protein, complete cds//0.00E+00//623bp//99%//
AB020666
C-HEMBA1004085
15 C-HEMBA1004110//Homo sapiens intersectin short form mRNA, complete cds//0//2033bp//99%//AF064243
C-HEMBA1004250//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN)//6.40E-51//
277aa//35%//P33450
C-HEMBA1004391//TUMOR SUPPRESSOR PROTEIN DCC PRECURSOR//5.60E-20//194aa//26%//F70211
C-HEMBA1004444//GLYCOPROTEIN 25L PRECURSOR (GP25L)//4.60E-41//148aa//52%//P27869
20 C-HEMBA1004454
C-HEMBA1004505//MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ISOFORM 1 (EC
3.2.1.113) (MAN(9)-ALPHA-MANNOSIDASE)//2.70E-45//239aa//43%//P53624
C-HEMBA1004785//MODIFIER 3 PROTEIN (M33)//1.40E-27//221aa//33%//P30658
C-HEMBA1004797
25 C-HEMBA1004952
C-HEMBA1004971
C-HEMBA1004982//TETRACYCLINE RESISTANCE PROTEIN, CLASS E (TETA(E))//6.30E-10//149aa//26%//
Q07282
C-HEMBA1005070//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)//1.10E-05//187aa//
30 29%//P17437
C-HEMBA1005084//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE- PRO-
TEIN KINASE 1)//1.20E-07//102aa//37%//P18160
C-HEMBA1005145
C-HEMBA1005230//ZINC FINGER PROTEIN 140//2.00E-17//83aa//66%//P52738
35 C-HEMBA1005246//HEPATOCYTE NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 4 (HFH-4)//2.10E-15//
230aa//28%//Q92949
C-HEMBA1005267//ANKYRIN, BRAIN VARIANT 1 (ANKYRIN B) (ANKYRIN, NONERYTHROID)//8.40E-14//
187aa//33%//Q01484
C-HEMBA1005430
40 C-HEMBA1005449//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)//
5.40E-10//224aa//24%//P13983
C-HEMBA1005489//Mus musculus semaphorin cytoplasmic domain-associated protein 3A (Semcap3) mRNA,
complete cds//8.40E-255//924bp//80%//AF127084
C-HEMBA1005522//COAGULATION FACTOR VII PRECURSOR (EC 3.4.21.21)//7.70E-15//78aa//51%//P98139
45 C-HEMBA1005545//MUSCARINIC ACETYLCHOLINE RECEPTOR M3//0//590aa//100%//P20309
C-HEMBA1005698//Homo sapiens vesicle trafficking protein (SEC22C) mRNA, complete cds//6.60E-163//
753bp//99%//AF039568
C-HEMBA1005913
C-HEMBA1005929//H.sapiens mRNA for serine/threonine protein kinase EMK//6.50E-92//1092bp//69%//X97630
50 C-HEMBA1005945//BRITTLE-1 PROTEIN PRECURSOR//1.70E-29//220aa//35%//P29518
C-HEMBA1006016
C-HEMBA1006171
C-HEMBA1006276//ZINC FINGER PROTEIN 90 (ZFP-90) (ZINC FINGER PROTEIN NK10)//1.70E-06//56aa//
57%//Q61967
55 C-HEMBA1006299
C-HEMBA1006311
C-HEMBA1006335
C-HEMBA1006357//SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2//3.70E-39//136aa//52%//

O15127
 C-HEMBA1006430//Human putative transmembrane protein precursor (B5) mRNA, complete cds././/2.40E-70//
 1108bp//65%//L38961
 C-HEMBA1006482//Homo sapiens h-sco1 (SCO1) mRNA, nuclear gene encoding mitochondrial protein, complete
 5 cds././/1101bp//98%//AF026852
 C-HEMBA1006517
 C-HEMBA1006544
 C-HEMBA1006572//ODD-SKIPPED PROTEIN././/2.60E-39//85aa//83%//P23803
 C-HEMBA1006658//Homo sapiens mRNA for NIK, partial cds././/1500bp//98%//AB013385
 10 C-HEMBA1006707//Homo sapiens mRNA for matrilin-4, partial././/2003bp//99%//AJ007581
 C-HEMBA1006724
 C-HEMBA1006749//Homo sapiens mRNA for matrilin-4, partial././/1.40E-275//1942bp//83%//AJ007581
 C-HEMBA1006770//FLOWERING TIME CONTROL PROTEIN FCA//1.20E-33//352aa//34%//O04425
 15 C-HEMBA1006902//Homo sapiens mRNA for matrilin-4, partial././/4.80E-275//1799bp//85%//AJ007581
 C-HEMBA1006912
 C-HEMBA1006916//Homo sapiens Grb14 mRNA, complete cds././/3.00E-277//1010bp//95%//L76687
 C-HEMBA1006960
 C-HEMBA1007013//Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds././/1.10E-14//412bp//63%//
 20 AF068749
 C-HEMBA1007057
 C-HEMBA1007063
 C-HEMBA1007226//Homo sapiens RPA-binding trans-activator (RBT1) mRNA, complete cds././/7.30E-273//
 1242bp//99%//AF192529
 C-HEMBA1007241//HYPOTHETICAL 24.5 KD PROTEIN IN SAP185-BCK1 INTERGENIC REGION././/2.70E-14//
 25 106aa//42%//P40857
 C-HEMBA1007291
 C-HEMBA1007332//Homo sapiens mRNA for unr-interacting protein././/6.40E-83//266bp//98%//AJ010025
 C-HEMBB1000106//CELLULAR NUCLEIC ACID BINDING PROTEIN (CNBP).//1.60E-10//139aa//30%//P53996
 30 C-HEMBB1000276
 C-HEMBB1000309
 C-HEMBB1000407
 C-HEMBB1000447//Homo sapiens JWA protein mRNA, complete cds././/2059bp//99%//AF070523
 C-HEMBB1000542//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds././/2.60E-232//
 35 1452bp//85%//AF084259
 C-HEMBB1000567
 C-HEMBB1000642
 C-HEMBB1000668//Homo sapiens mRNA for KIAA0893 protein, complete cds././/2375bp//99%//AB020700
 C-HEMBB1000679//C.familiaris mRNA for TRAM-protein././/4.10E-210//1149bp//80%//X63678
 C-HEMBB1000881//Danio rerio mRNA for MINDIN2, complete cds././/1.70E-67//948bp//66%//AB006085
 40 C-HEMBB1000905//TRANSCRIPTIONAL REPRESSOR RCO-1././/1.00E-11//311aa//27%//P78706
 C-HEMBB1001026//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHE-
 ROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPO-
 NENT).//5.30E-11//142aa//30%//P32802
 C-HEMBB1001048//SARCALUMENIN PRECURSOR././/6.50E-18//154aa//33%//P13666
 45 C-HEMBB1001200
 C-HEMBB1001407
 C-HEMBB1001530//SLS1 PROTEIN PRECURSOR././/9.80E-10//273aa//27%//Q99158
 C-HEMBB1001547//Homo sapiens CGI-02 protein mRNA, complete cds././/2311bp//99%//AF132937
 C-HEMBB1001573
 50 C-HEMBB1001847//NEUROGENIC PROTEIN BIG BRAIN././/4.70E-06//258aa//24%//P23645
 C-HEMBB1001959//CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN
 B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN SUBUNIT B).//7.30E-14//97aa//38%//P25210
 C-HEMBB1001978
 C-HEMBB1002039
 55 C-HEMBB1002041//Homo sapiens transmembrane protein TENB2 (TENB2) mRNA, complete cds././/1746bp//
 99%//AF179274
 C-HEMBB1002051//Homo sapiens Ets transcription factor ESE-2b mRNA, complete cds././/1.30E-95//454bp//99%//
 AF115403

EP 1 130 094 A2

C-HEMBB1002120//UDP-N-ACETYLGLUCOSAMINE--PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE
110 KD SUBUNIT (EC 2.4.1.-) (O-GLCNAC TRANSFERASE P110 SUBUNIT).//4.90E-22//337aa//27%//P56558
C-HEMBB1002162//Homo sapiens genethonin 1 mRNA, complete cds.//8.30E-67//328bp//99%//AF062534
C-HEMBB1002228
5 C-HEMBB 1002245//PROSTAGLANDIN F2-ALPHA RECEPTOR REGULATORY PROTEIN PRECURSOR
(PROSTAGLANDIN F2-ALPHA RECEPTOR ASSOCIATED PROTEIN).//0//879aa//89%//Q62786
C-HEMBB1002302
C-HEMBB1002427//FUCOSYLGlycoprotein ALPHA-N-ACETYLGLACTOSAMINYLTRANSFERASE (EC
10 2.4.1.40) (HISTO-BLOOD GROUP A TRANSFERASE) (A TRANSFERASE) / FUCOSYLGlycoprotein 3-AL-
PHA-GALACTOSYLTRANSFERASE (EC 2.4.1.37) (HISTO-BLOOD GROUP B TRANSFERASE) (B TRANS-
FERASE) (NAGAT).//1.80E-70//221aa//50%//P16442
C-HEMBB1002465//ACYL-COA DEHYDROGENASE (EC 1.3.99.-).//2.30E-53//249aa//48%//P45857
C-HEMBB1002661//Homo sapiens cardiovascular helix-loop-helix factor 2 (CHF2) mRNA, complete cds.//0//
15 2174bp//99%//AF176422
C-HEMBB1002663
C-HEMBB1002693
C-MAMMA1000046
C-MAMMA1000102//APOLIPOPROTEIN L PRECURSOR (APO-L).//1.40E-21//221aa//35%//O14791
C-MAMMA1000106
20 C-MAMMA1000118
C-MAMMA1000141
C-MAMMA1000204//Homo sapiens dysferlin mRNA, complete cds.//0//2028bp//99%//AF075575
C-MAMMA1000226
C-MAMMA1000403//Homo sapiens CDK4-binding protein p34SEI1 (SEI1) mRNA, complete cds.//1.20E-255//
25 1165bp//99%//AF117959
C-MAMMA1000449
C-MAMMA1000457//Human NADH-cytochrome b5 reductase mRNA, 3' end.//9.50E-79//829bp//71%//M16462
C-MAMMA1000473//HYPOTHETICAL 35.6 KD PROTEIN IN SPC1-ILV3 INTERGENIC REGION.//5.10E-45//
299aa//34%//P47088
30 C-MAMMA1000496//MIC1 PROTEIN.//3.00E-25//202aa//33%//P53258
C-MAMMA1000528
C-MAMMA1000591//POLYPEPTIDE N-ACETYLGLACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN-
35 UDP ACETYLGLACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYLGLACTOS-
AMINYLTRANSFERASE) (GALNAC-T1).//1.20E-115//515aa//49%//Q07537
C-MAMMA10006141//Homo sapiens pseudouridine synthase I (PUS1) mRNA, partial cds.//2.10E-302//1370bp//
99%//AF116238
C-MAMMA1000652
C-MAMMA1000681//PROBABLE G PROTEIN-COUPLED RECEPTOR EDG-1.//9.40E-82//311aa//52%//O08530
C-MAMMA1000706
40 C-MAMMA1000788//Bos taurus P14 (p14) mRNA, complete cds.//3.90E-85//502bp//89%//AF037349
C-MAMMA1000810
C-MAMMA1000814
C-MAMMA1000881//Homo sapiens protein kinase (SGK3) mRNA, complete cds.//0//1292bp//100%//AF169035
C-MAMMA1000986
45 C-MAMMA1000994//Homo sapiens ISLR(immunoglobulin superfamily containing leucine-rich repeat) mRNA,
complete cds, alternatively spliced transcript ISLR-2.//0//2211bp//99%//AB024536
C-MAMMA1001043//MRC OX-45 SURFACE ANTIGEN PRECURSOR (BCM1 SURFACE ANTIGEN) (BLAST-1)
(CD48).//2.90E-12//239aa//28%//P10252
C-MAMMA1001066
50 C-MAMMA1001094//Human potential transcriptional repressor NOT4Hp (NOT4H) mRNA, complete cds.//0//
1394bp//93%//U71267
C-MAMMA1001141
C-MAMMA1001150//PROTEIN KINASE C, MU TYPE (EC 2.7.1.-) (NPKC-MU).//7.50E-304//587aa//68%//Q15139
C-MAMMA1001237//MONOCARBOXYLATE TRANSPORTER 2 (MCT 2).//7.70E-64//196aa//41%//P53988
55 C-MAMMA1001284
C-MAMMA1001310//HYPOTHETICAL 57.3 KD TRP-ASP REPEATS CONTAINING PROTEIN IN POM152-
REC114 INTERGENIC REGION.//1.50E-67//441aa//37%//Q04225
C-MAMMA1001344

EP 1 130 094 A2

C-MAMMA1001418//HYPOTHETICAL PROTEIN HI0519..//6.90E-27//181aa//38%//P44742
C-MAMMA1001532//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)..//5.60E-126//319aa//56%//
P51523
5 C-MAMMA1001609//MYOSIN II HEAVY CHAIN, NON MUSCLE..//1.50E-26//204aa//38%//P05659
C-MAMMA1001615//NEUROGENIC DIFFERENTIATION FACTOR 1 ..//3.80E-11//90aa//42%//Q13562
C-MAMMA1001623
C-MAMMA1001634
C-MAMMA1001893
C-MAMMA1001901
10 C-MAMMA1001957
C-MAMMA1001978//Cimex lectularius apyrase (APY) mRNA, complete cds..//6.70E-19//988bp//56%//AF085499
C-MAMMA1002070//PLASMINOGEN (EC 3.4.21.7) (FRAGMENT)..//1.10E-07//103aa//33%//Q01177
C-MAMMA1002080//RAS-RELATED PROTEIN RAB-13..//1.80E-29//208aa//37%//P51153
C-MAMMA1002087
15 C-MAMMA1002091//Homo sapiens CD39L2 (CD39L2) mRNA, complete cds..//0//2564bp//99%//AF039916
C-MAMMA1002095//CALCIUM-TRANSPORTING ATPASE 1 (EC 3.6.1.38) (P-TYPE CALCIUM ATPASE)..//
3.70E-222//867aa//52%//O43108
C-MAMMA1002128//ABC1 PROTEIN HOMOLOG PRECURSOR..//2.50E-97//464aa//45%//Q92338
C-MAMMA1002142//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE-
20 PROTEIN KINASE 1)..//9.80E-17//146aa//35%//P18160
C-MAMMA1002165//Homo sapiens connective tissue growth factor related protein WISP-2 (WISP2) mRNA, com-
plete cds..//4.80E-60//382bp//89%//AF100780
C-MAMMA1002205//Homo sapiens mRNA; cDNA DKFZp586C091 (from clone DKFZp586C091)..//2.00E-81//
30 308bp//81%//AL050119
C-MAMMA1002224
C-MAMMA1002234//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68)..//0//627aa//96%//Q00004
C-MAMMA1002586//Homo sapiens alpha 1,2-mannosidase mRNA, complete cds..//0//2228bp//99%//AF148509
C-MAMMA1002633
35 C-MAMMA1003126//SARCALUMENIN PRECURSOR..//1.10E-51//388aa//32%//P13666
C-NT2RM1000462//ATRIAL GLAND-SPECIFIC ANTIGEN PRECURSOR (AGSA)..//8.60E-14//104aa//40%//
P15287
C-NT2RM1000542//BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE)..//1.40E-103//566aa//
43%//P48982
C-NT2RM1000580//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-)..//8.50E-75//301aa//39%//P43636
35 C-NT2RM1000789//Homo sapiens mRNA for hTCF-4..//2.80E-221//757bp//99%//Y11306
C-NT2RM1000855//Homo sapiens sec61 homolog mRNA, complete cds..//0//3541bp//99%//AF084458
C-NT2RM1000858//tricarboxylate carrier [rats, liver, mRNA Partial, 2986 nt]..//2.10E-98//1035bp//70%//S70011
C-NT2RM1000899//MITOCHONDRIAL RNA SPLICING PROTEIN MSR4..//1.10E-54//182aa//39%//P23500
C-NT2RM2000241
40 C-NT2RM2000306//PUTATIVE GTP-BINDING PROTEIN W08E3.3..//4.50E-130//362aa//68%//P91917
C-NT2RM2000410
C-NT2RM2000423//BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE)..//1.80E-38//308aa//35%//
P48982
C-NT2RM2000497//CHL1 PROTEIN..//9.90E-24//296aa//29%//P22516
45 C-NT2RM2000514//Homo sapiens F-box protein Fbx21 (FBX21) mRNA, complete cds..//4.40E-304//1374bp//
99%//AF174601
C-NT2RM2000565//HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME 1..//4.40E-304//394aa//
43%//Q09782
C-NT2RM2000582//Homo sapiens mRNA for KIAA1053 protein, partial cds..//0//2666bp//99%//AB028976
50 C-NT2RM2000589//Bos taurus myosin X, complete cds..//0//4376bp//84%//U55042
C-NT2RM2000622//Mus musculus F-box protein FBL10 mRNA, partial cds..//3.00E-203//915bp//91%//AF176524
C-NT2RM2000632//EXCISION REPAIR PROTEIN ERCC-6 (COCKAYNE SYNDROME PROTEIN CSB)..//6.40E-
62//183aa//47%//Q03468
C-NT2RM2000773//Homo sapiens KNSL4 and MAZ genes for kinesin-like DNA binding protein and Myc-associ-
55 ated zinc finger protein, complete cds..//3.00E-289//1092bp//99%//AB017335
C-NT2RM2001126//Homo sapiens mRNA for multi PDZ domain protein..//0//1600bp//99%//AJ001319
C-NT2RM2001558//Homo sapiens protein kinase A binding protein AKAP110 mRNA, complete cds..//0//2398bp//
99%//AF093408

EP 1 130 094 A2

C-NT2RM2001626//FLIGHTLESS-I PROTEIN HOMOLOG././/4.30E-19//362aa//26%//P34268
 C-NT2RM2001643
 C-NT2RM2001738//SOF1 PROTEIN././/3.00E-110//325aa//47%//P33750
 C-NT2RM2001792//Homo sapiens angiopoietin-related protein-2 mRNA, complete cds././/7.10E-149//995bp//86%//
 5 AF125175
 C-NT2RM2001818//SIALIDASE (EC 3.2.1.18) (NEURAMINIDASE) (NA) (MAJOR SURFACE ANTIGEN).//4.30E-11//488aa//26%//P23253
 C-NT2RM2001902//Homo sapiens mRNA for PAK4 protein././/5.40E-216//988bp//99%//AJ011855
 C-NT2RM2001939//Human G protein-coupled receptor GPR-NGA gene, complete cds././/0//1559bp//98%//U55312
 10 C-NT2RM2001941//MUSCARINIC ACETYLCHOLINE RECEPTOR M1././/7.40E-38//193aa//34%//P08482
 C-NT2RM4000100//Homo sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds././/0//2678bp//99%//
 AF175966
 C-NT2RM4000115
 C-NT2RM4000198//BUTYROPHILIN PRECURSOR (BT).//5.10E-12//162aa//33%//Q13410
 15 C-NT2RM4000284//Human IgG Fc receptor hFcRn mRNA, complete cds././/1.30E-257//603bp//96%//U12255
 C-NT2RM4000295
 C-NT2RM4000326//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//9.00E-100//434aa//43%//
 P51523
 C-NT2RM4000417//SYNAPTOTAGMIN II././/2.70E-23//293aa//30%//P46097
 20 C-NT2RM4000444//ANTIGEN PEPTIDE TRANSPORTER 1 (APT1).//1.70E-112//493aa//44%//P36370
 C-NT2RM4000587
 C-NT2RM4000593//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I././/3.90E-27//576aa//
 24%//Q10297
 C-NT2RM4000648//K-GLYCAN PRECURSOR././/4.00E-193//531aa//66%//P51655
 25 C-NT2RM4000761//CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1).//2.50E-245//306aa//91%//
 P00395
 C-NT2RM4000965//PUTATIVE IMPORTIN BETA-4 SUBUNIT (KARYOPHERIN BETA-4 SUBUNIT).//9.00E-44//
 520aa//29%//O60100
 C-NT2RM4000997//MONO- AND DIACYLGLYCEROL LIPASE PRECURSOR (EC 3.1.1.-) (MDGL).//1.80E-10//
 30 189aa//30%//P25234
 C-NT2RM4001321
 C-NT2RM4001325//CHONDROITIN 6-SULFOTRANSFERASE (EC 2.8.2.17) (C6ST).//2.90E-48//343aa//34%//
 Q92179
 C-NT2RM4001377//R.norvegicus LL5 mRNA././/8.50E-236//990bp//87%//X74226
 35 C-NT2RM4001735
 C-NT2RM4001768//Homo sapiens CGI-82 protein mRNA, complete cds././/1925bp//99%//AF151840
 C-NT2RM4001843//BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE).//6.20E-33//263aa//38%//
 P48982
 C-NT2RM4002352//Homo sapiens hLRp105 mRNA for LDL receptor related protein 105, complete cds././/0//
 40 2184bp//99%//AB009462
 C-NT2RP1000002
 C-NT2RP1000050
 C-NT2RP1000181//Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds././/3.30E-121//1394bp//69%//
 AF126799
 45 C-NT2RP1000239
 C-NT2RP1000261//ORM1 PROTEIN././/2.40E-17//137aa//35%//P53224
 C-NT2RP1000271//ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).//4.70E-199//547aa//
 66%//Q03923
 C-NT2RP1000300//Human transporter protein (g17) mRNA, complete cds././/3.80E-26//758bp//62%//U49082
 50 C-NT2RP1000325//H.sapiens gene for phosphate carrier././/0//439bp//98%//X77337
 C-NT2RP1000448
 C-NT2RP1000465//UBIQUITIN-LIKE PROTEIN SMT3././/5.10E-07//81aa//33%//P55857
 C-NT2RP1000468//CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN
 B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN SUBUNIT B).//2.00E-13//97aa//38%//P25210
 55 C-NT2RP1000551//Homo sapiens putative interferon-related protein (SM15) mRNA, partial cds././/0//1761bp//
 99%//U09585
 C-NT2RP1000579//Human succinate dehydrogenase flavoprotein subunit (SDH) mRNA, complete cds././/0//
 1951bp//94%//L21936

C-NT2RP1000613//CARBONIC ANHYDRASE VI (EC 4.2.1.1) (SALIVARY) (CARBONATE DEHYDRATASE VI).//
 3.40E-52//304aa//40%//P08060
 C-NT2RP1000679
 C-NT2RP1000740
 C-NT2RP1000903
 C-NT2RP1000981//CELL SURFACE A33 ANTIGEN PRECURSOR.//3.60E-14//286aa//27%//Q99795
 C-NT2RP1001004//F-SPONDIN PRECURSOR.//9.20E-43//322aa//35%//P35446
 C-NT2RP1001020//SERINE/THREONINE-PROTEIN KINASE PAK-BETA (EC 2.7.1.-) (BETA-PAK) (P21-ACTIVATED KINASE 3) (CDC42/RAC EFFECTOR KINASE PAK-B) //9.70E-22//227aa//31%//Q61036
 C-NT2RP1001031//VEGETATILE INCOMPATIBILITY PROTEIN HET-E-1.//3.40E-42//285aa//35%//Q00808
 C-NT2RP1001563//TESTIS-SPECIFIC PROTEIN TPX-1 PRECURSOR (AUTOANTIGEN 1) (25 KD ACROSOMAL AUTOANTIGEN) (AA1).//9.70E-19//201aa//31%//Q60477
 C-NT2RP2000092//ZINC FINGER PROTEIN 136.//1.90E-117//419aa//54%//P52737
 C-NT2RP2000178//MITOCHONDRIAL ION PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.21.-).//2.40E-192//
 15 778aa//48%//P93647
 C-NT2RP2000240
 C-NT2RP2000394//Gallus gallus p52 pro-apoptotic protein mRNA, complete cds.//1.60E-90//956bp//70%//AF029071
 C-NT2RP2000447//GOLGIN-95.//2.80E-33//99aa//66%//Q08379
 C-NT2RP2000479
 C-NT2RP2000514//Homo sapiens roundabout 2 (robo2) mRNA, partial cds.//3.00E-185//855bp//99%//AF040991
 C-NT2RP2000533//Homo sapiens cornichon protein mRNA, complete cds.//1.30E-290//1324bp//99%//AF070654
 C-NT2RP2000610//CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN SUBUNIT B).//1.50E-13//97aa//38%//P25210
 20 C-NT2RP2000616//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//4.10E-12//323aa//30%//P13983
 C-NT2RP2000649//Homo sapiens mRNA for Hs Ste24p, complete cds.//0//2847bp//99%//AB016068
 C-NT2RP2000663
 C-NT2RP2000694//Homo sapiens 5T4 oncofetal trophoblast glycoprotein gene.//0//2278bp//99%//AJ012159
 25 C-NT2RP2000712//ZINC FINGER PROTEIN 135.//3.70E-87//296aa//53%//P52742
 C-NT2RP2000739//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//7.50E-73//387aa//37%//P51522
 C-NT2RP2000818//Homo sapiens xenotropic and polytropic murine leukemia virus receptor (X3) mRNA, complete cds.//0//2724bp//99%//AF089744
 30 C-NT2RP2000903//Homo sapiens 5T4 oncofetal trophoblast glycoprotein gene.//0//2276bp//100%//AJ012159
 C-NT2RP2001200//Homo sapiens mRNA for KIAA0676 protein, partial cds.//0//1539bp//100%//AB014576
 C-NT2RP2001223//MYOTUBULARIN-RELATED PROTEIN 3 (FRAGMENT).//3.30E-05//76aa//39%//Q13615
 C-NT2RP2001276//NPDC-1 PROTEIN PRECURSOR.//3.00E-133//331aa//77%//Q64322
 35 C-NT2RP2001388//TRNA-SPlicing ENDONUCLEASE SUBUNIT SEN2 (EC 3.1.27.9) (TRNA-INTRON ENDO-NUCLEASE).//5.90E-13//157aa//33%//P16658
 C-NT2RP2001469//VEGETATILE INCOMPATIBILITY PROTEIN HET-E-1.//1.30E-14//242aa//24%//Q00808
 C-NT2RP2001480//Homo sapiens thrombospondin 3 (THBS3) gene, complete cds.//0//2547bp//99%//L38969
 C-NT2RP2001495//Human transporter protein (g17) mRNA, complete cds.//2.20E-65//641bp//65%//U49082
 40 C-NT2RP2001514//PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38).//1.20E-133//429aa//41%//P39986
 C-NT2RP2001529//Homo sapiens mRNA for ZIP-kinase, complete cds.//0//2079bp//99%//AB007144
 C-NT2RP2001538//Mus musculus mSin3A (sin3A) mRNA, complete cds.//7.60E-272//1480bp//84%//U22394
 C-NT2RP2001562//Homo sapiens GLE1 (GLE1) mRNA, complete cds.//0//1899bp//98%//AF058922
 45 C-NT2RP2001662//HOMEODOMAIN PROTEIN AKR (AVIAN KNOTTED-RELATED PROTEIN).//1.80E-49//94aa//81%//Q90655
 C-NT2RP2001755//Rattus norvegicus f-spondin mRNA, complete cds.//0//2974bp//86%//M88469
 C-NT2RP2001769//SERINE/THREONINE-PROTEIN KINASE ORB6 (EC 2.7.1.-).//9.10E-47//185aa//44%//O13310
 C-NT2RP2001817//Homo sapiens sirtuin type 1 (SIRT1) mRNA, complete cds.//0//3092bp//99%//AF083106
 50 C-NT2RP2001878
 C-NT2RP2001903//CALPAIN, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM- ACTIVATED NEUTRAL PROTEINASE) (CANP) (MU/M-TYPE).//3.80E-58//475aa//34%//P00789
 C-NT2RP2001915

C-NT2RP2001921
 C-NT2RP2001948//HST2 PROTEIN (HOMOLOGOUS TO SIR2 PROTEIN 2).//1.40E-08//191aa//27%//P53686
 C-NT2RP2001956//ORM1 PROTEIN./.3.90E-19//137aa//37%//P53224
 C-NT2RP2002015
 5 C-NT2RP2002063//GNS1 PROTEIN./.3.60E-18//231aa//33%//P25358
 C-NT2RP2002188//Rattus norvegicus neuregulin 3 mRNA, complete cds./.2.50E-226//1284bp//89%//U41663
 C-NT2RP2002232//HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I./.1.90E-93//420aa//
 10 43%//Q09782
 C-NT2RP2002304//Homo sapiens histone acetyltransferase MORF mRNA, complete cds./.0//2737bp//99%//
 AF113514
 C-NT2RP2002409
 C-NT2RP2002510
 C-NT2RP2002527//CYTOCHROME B5./.1.30E-11//92aa//38%//P40312
 C-NT2RP2002533//Homo sapiens alpha 2 delta calcium channel subunit isoform I mRNA, complete cds./.0//
 15 2365bp//99%//AF042792
 C-NT2RP2002564//Human zinc-finger protein C2H2-150 mRNA, complete cds./.0//2237bp//99%//U38864
 C-NT2RP2002674//SOLUBLE EPOXIDE HYDROLASE (SEH) (EC 3.3.2.3) (EPOXIDE HYDRATASE) (CY-
 TOSOLIC EPOXIDE HYDROLASE) (CEH).//5.50E-38//201aa//39%//P34913
 C-NT2RP2002721//REGULATORY PROTEIN UHPC./.1.60E-23//153aa//30%//P27669
 20 C-NT2RP2002824//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHE-
 ROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPO-
 NENT).//3.50E-63//404aa//33%//P32802
 C-NT2RP2002942//Homo sapiens mRNA for KIAA0806 protein, complete cds./.0//2090bp//99%//AB018349
 C-NT2RP2002974//HOMEobox PROTEIN SIXS (DM LOCUS-ASSOCIATED HOMEODOMAIN PROTEIN HO-
 25 MOLOG) (FRAGMENT).//8.20E-241//555aa//84%//P70178
 C-NT2RP2002976//HYPOTHETICAL 149.7 KD PROTEIN IN IRE1-KSP1 INTERGENIC REGION./.1.30E-20//
 99aa//47%//P38800
 C-NT2RP2003042//PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR (EC 2.3.1.43)
 30 (LECITHIN-CHOLESTEROL ACYLTRANSFERASE) (PHOSPHOLIPID-CHOLESTEROL ACYLTRANSFERASE)
 (FRAGMENT).//2.10E-109//385aa//52%//P53760
 C-NT2RP2003138//5'-TG-3' INTERACTING FACTOR (HOMEobox PROTEIN TGIF).//2.10E-08//104aa//46%//
 P70284
 C-NT2RP2003179//PUTATIVE SERINE/THREONINE-PROTEIN KINASE EMK (EC 2.7.1.-).//2.60E-67//256aa//
 35 49%//Q05512
 C-NT2RP2003210//Homo sapiens fatty acid transport protein (FATP) mRNA, complete cds./.9.80E-272//1265bp//
 98%//AF055899
 C-NT2RP2003302//Homo sapiens GIOT-4 mRNA for gonadotropin inducible transcription repressor-4, complete
 40 cds./.0//2891bp//99%//AB021644
 C-NT2RP2003369//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//5.90E-20//204aa//
 34%//Q15404
 C-NT2RP2003383//Homo sapiens mRNA for KIAA0458 protein, complete cds./.0//2565bp//99%//AB007927
 C-NT2RP2003390//Homo sapiens mRNA for SEC63 protein./.0//2629bp//99%//AJ011779
 C-NT2RP2003469//GALACTOSE-PROTON SYMPORT (GALACTOSE TRANSPORTER).//1.10E-45//324aa//
 45 29%//P37021
 C-NT2RP2003545//Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds./.5.40E-48//578bp//71%//
 AF024636
 C-NT2RP2003593
 C-NT2RP2003599
 C-NT2RP2003655//HYPOTHETICAL 26.3 KD PROTEIN IN OYE2-GND1 INTERGENIC//4.80E-15//93aa//47%//
 50 P38869
 C-NT2RP2003664//Homo sapiens mRNA for leptin receptor gene-related protein./.1.90E-237//1081bp//99%//
 Y12670
 C-NT2RP2003931
 C-NT2RP2003940//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//7.00E-111//401aa//43%//P28160
 55 C-NT2RP2003950//Homo sapiens clone 24778 unknown mRNA./.0//1545bp//99%//AF070572
 C-NT2RP2004069
 C-NT2RP2004108//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//3.30E-171//474aa//62%//P16415
 C-NT2RP2004141

5 C-NT2RP2004179
 C-NT2RP2004205//BUTYROPHILIN PRECURSOR (BT).//1.60E-21//276aa//32%//Q62556
 C-NT2RP2004447
 C-NT2RP2004495//Human transporter protein (g17) mRNA, complete cds.//9.80E-64//642bp//64%//L149082
 C-NT2RP2004524
 C-NT2RP2004556
 C-NT2RP2004606//Human fibroblast collagenase inhibitor mRNA, complete cds.//2.10E-166//768bp//99%//
 M12670
 C-NT2RP2004648//Mouse beta-galactosidase (BGAL) gene, complete cds.//1.20E-33//1136bp//59%//M57734
 10 C-NT2RP2004670//Rattus norvegicus vesicula-associate calmodulin-binding protein mRNA, complete cds.//0//
 1250bp//86%//L22557
 C-NT2RP2004794//HYPOTHETICAL 24.5 KD PROTEIN IN SAP185-BCK1 INTERGENIC REGION.//2.70E-09//
 203aa//26%//P40857
 C-NT2RP2004837
 15 C-NT2RP2004847//ZINC FINGER PROTEIN 135.//8.00E-35//193aa//40%//P52742
 C-NT2RP2005027//GLUCOSE TRANSPORTER TYPE 3, BRAIN.//6.20E-67//130aa//100%//P11169
 C-NT2RP2005069//Rat vacuolar protein sorting homolog r-vps33b mRNA, complete cds.//0//1792bp//87%//
 U35245
 20 C-NT2RP2005163
 C-NT2RP2005181//Mus musculus cationic amino acid transporter (CAT3) mRNA, complete cds.//5.30E-315//
 2126bp//81%//U70859
 C-NT2RP2005247//ZINC-FINGER PROTEIN RFP (RET FINGER PROTEIN).//5.00E-53//296aa//37%//Q62158
 C-NT2RP2005378//GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1.8 PRECURSOR (GRP 1.8).//6.30E-
 25 28//183aa//47%//P10496
 C-NT2RP2005391//Homo sapiens partial mRNA for putative p621 protein which interacts with transcription factor
 Sp1.//0//1544bp//99%//AJ242978
 C-NT2RP2005425//Homo sapiens mRNA for AKAP450 protein.//0//4341bp//99%//AJ131693
 C-NT2RP2005463//PROTEIN PTM1 PRECURSOR.//7.40E-15//284aa//28%//P32857
 C-NT2RP2005514
 30 C-NT2RP2005535//ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).//1.90E-172//489aa//
 62%//Q03923
 C-NT2RP2005541//N-ACETYLGLUCOSAMINE-6-SULFATASE PRECURSOR (EC 3.1.6.14) (G6S) (GLU-
 COSAMINE-6-SULFATASE).//4.70E-24//78aa//51%//P15586
 35 C-NT2RP2005597//Homo sapiens protein O-mannosyl-transferase 1 (POMT1) mRNA, complete cds.//0//1821bp//
 97%//AF095136
 C-NT2RP2005632
 C-NT2RP2005666
 C-NT2RP2005774//Homo sapiens Giot-4 mRNA for gonadotropin inducible transcription repressor-4, complete
 40 cds.//6.90E-224//1461bp//72%//AB021644
 C-NT2RP2005878//PUTATIVE STEROID DEHYDROGENASE KIK-I (EC 1.1.1.-).//3.60E-55//238aa//50%//
 O57314
 C-NT2RP2005883//DOPAMINE-BETA-MONOXYGENASE PRECURSOR (EC 1.14.17.1) (DOPAMINE BETA-
 HYDROXYLASE) (DBH).//6.70E-72//512aa//34%//P15101
 C-NT2RP2005887
 45 C-NT2RP2005941//Human paired box gene (PAX6) homologue, complete cds.//1.40E-308//1396bp//99%//
 M93650
 C-NT2RP2005994//HYPOTHETICAL 51.5 KD PROTEIN D2024.3 IN CHROMOSOME IV.//3.50E-35//144aa//
 47%//P49191
 C-NT2RP2006004//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN).//3.00E-26//
 50 227aa//36%//Q06828
 C-NT2RP2006042//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSI-
 DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//9.40E-15//501aa//25%//P08640
 C-NT2RP2006092//Homo sapiens mRNA for Fe65L2, complete cds.//0//1156bp//99%//AB018247
 C-NT2RP2006099
 55 C-NT2RP2006134
 C-NT2RP2006269//DOLICHYL-PHOSPHATE-MANNOSE--PROTEIN MANNOSYLTRANSFERASE 2 (EC
 2.4.1.109).//2.30E-78//679aa//32%//P31382
 C-NT2RP2006512//GNS1 PROTEIN.//2.00E-21//290aa//29%//P25358

EP 1 130 094 A2

5 C-NT2RP2006580//Homo sapiens transitional epithelia response protein (TERE1) mRNA, complete cds./0//
1483bp//99%//AF117064
C-NT2RP3000011//VEGETABLE INCOMPATIBILITY PROTEIN HET-E-1//4.00E-14//320aa//24%//Q00808
C-NT2RP3000022//Rat heart mRNA serine/threonine protein kinase, complete cds./4.80E-203//1496bp//78%//
D26178
10 C-NT2RP3000059//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID) (FRAGMENT).//
3.70E-12//133aa//32%//Q01485
C-NT2RP3000063//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).//
5.00E-29//596aa//30%//P19246
15 C-NT2RP3000125//RETINOBLASTOMA BINDING PROTEIN 2 (RBBP-2).//6.30E-08//70aa//41%//P29375
C-NT2RP3000148//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//4.10E-106//350aa//47%//
P51523
C-NT2RP3000169//Homo sapiens MRS1 mRNA, complete cds./0//1519bp//97%//AF093239
15 C-NT2RP3000171//Mus musculus partial mRNA for B-IND1 protein (B-ind1 gene).//4.40E-99//571bp//89%//
Z97207
C-NT2RP3000172//CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123) (CAM KI-
NASE I).//1.30E-80//359aa//44%//Q14012
C-NT2RP3000201//Homo sapiens HPK/GCK-like kinase HGK mRNA, complete cds./1.30E-270//1231bp//99%//
AF096300
20 C-NT2RP3000232//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.40E-130//693aa//41%//Q99676
C-NT2RP3000304//Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds./0//2895bp//99%//
AF074264
C-NT2RP3000378//PAIRED AMPHIPATHIC HELIX PROTEIN.//4.20E-39//186aa//36%//P22579
C-NT2RP3000427
25 C-NT2RP3000436//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//6.20E-27//
90aa//42%//P38660
C-NT2RP3000444
C-NT2RP3000460//Canis familiaris sec61 homologue mRNA, complete cds./1.80E-198//643bp//89%//M96629
30 C-NT2RP3000481//Homo sapiens RanBP7/importin 7 mRNA, complete cds./0//2623bp//100%//AF098799
C-NT2RP3000616//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN).//5.20E-26//
227aa//36%//Q06828
C-NT2RP3000645
C-NT2RP3000652//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//1.90E-153//441aa//62%//P28160
35 C-NT2RP3000676//PUTATIVE MITOCHONDRIAL CARRIER YMR166C.//2.10E-15//220aa//27%//Q03829
C-NT2RP3000677//DNA BINDING PROTEIN RFX2.//3.60E-56//233aa//41%//P48378
C-NT2RP3000721//HYPOTHETICAL 149.7 KD PROTEIN IN IRE1-KSP1 INTERGENIC REGION.//1.10E-22//
171aa//36%//P38800
C-NT2RP3000789//Homo sapiens IGF-II mRNA-binding protein 1 (IMP-1) mRNA, complete cds./0//1458bp//
40 100%//AF117106
C-NT2RP3000818
C-NT2RP3000820//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).//1.90E-30//269aa//
33%//P49695
C-NT2RP3000838//TRICHOHYALIN.//9.80E-11//491aa//26%//Q07283
C-NT2RP3000871
45 C-NT2RP3000907//PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38).//2.20E-134//296aa//
42%//P39986
C-NT2RP3000921//TUMOR SUPPRESSOR PROTEIN DCC PRECURSOR (COLORECTAL CANCER SUP-
PRESSOR).//4.00E-21//316aa//29%//P43146
C-NT2RP3001012//Homo sapiens mRNA for KIAA0829 protein, partial cds./0//2906bp//98%//AB020636
50 C-NT2RP3001044
C-NT2RP3001061//Homo sapiens mRNA for KIAA0853 protein, partial cds./0//3591bp//99%//AB020660
C-NT2RP3001159//Homo sapiens mRNA; cDNA DKFZp586C201 (from clone DKFZp586C201).//0//2558bp//
99%//AL050118
C-NT2RP3001170//Mus musculus activity-dependent neuroprotective protein (Adnp) mRNA, complete cds./
4.80E-240//850bp//88%//AF068198
55 C-NT2RP3001195//GALACTOSE-PROTON SYMPORT (GALACTOSE TRANSPORTER).//4.70E-48//339aa//
29%//P37021
C-NT2RP3001240//Canis familiaris sec61 homologue mRNA, complete cds./1.20E-301//1141bp//89%//M96629

C-NT2RP3001271//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//
 2.60E-09//34aa//22%//P52178
 C-NT2RP3001322//PROBABLE CALCIUM-TRANSPORTING ATPASE 3 (EC 3.6.1.38) (ENDOPLASMIC RETIC-
 ULUM CA2+-ATPASE).//1.70E-21//220aa//30%//P39524
 5 C-NT2RP3001388//SYNAPTOTAGMIN IV//2.00E-118//430aa//54%//P50232
 C-NT2RP3001542//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PRO-
 TEIN).//4.70E-11//132aa//37%//Q13829
 C-NT2RP3001560//Homo sapiens cleft lip and palate transmembrane protein 1 (CLPTM1) mRNA, complete cds.//
 10 0//2468bp//99%//AF037339
 C-NT2RP3001592//N2,N2-DIMETHYLGUANOSINE TRNA METHYLTRANSFERASE PRECURSOR (EC
 2.1.1.32).//1.30E-18//279aa//27%//P15565
 C-NT2RP3001650//BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (EC 3.4.24.-) (BMP-1).//2.20E-22//
 15 107aa//42%//P98063
 C-NT2RP3001685//PRPE PROTEIN.//1.00E-68//382aa//41%//P77495
 C-NT2RP3001738//CYTOCHROME B5.//1.30E-11//133aa//33%//P00169
 C-NT2RP3001754
 C-NT2RP3001858
 C-NT2RP3001976//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//8.90E-143//379aa//55%//
 20 P51523
 C-NT2RP3002015//Homo sapiens CGI-71 protein mRNA, complete cds.//0//1991bp//99%//AF151829
 C-NT2RP3002160//HISTO-BLOOD GROUP ABO SYSTEM TRANSFERASE (NAGAT) [INCLUDES: GLYCO-
 PROTEIN-FUCOSYLGALACTOSIDE ALPHA-N-ACETYLGLACOSAMINYLTRANSFERASE (EC 2.4.1.40)
 25 (FUCOSYLGlyCOPROTEIN ALPHA-N-ACETYLGLACOSAMINYLTRANSFERASE) (HISTO-BLOOD GROUP
 A TRANSFERASE) (A TRANSFERASE); GLYCOPROTEIN-FUCOSYLGALACTOSIDE ALPHA- GALACTOSYL-
 TRANSFERASE (EC 2.4.1.37) (FUCOSYLGlyCOPROTEIN 3-ALPHA- GALACTOSYLTRANSFERASE) (HISTO-
 BLOOD GROUP B TRANSFERASE) (B TRANSFERASE)].//3.50E-72//231aa//49%//P16442
 C-NT2RP3002281//Homo sapiens mRNA for KIAA0765 protein, partial cds.//0//2286bp//99%//AB018308
 C-NT2RP3002286//Homo sapiens candidate tumor suppressor protein DICE1 mRNA, complete cds.//0//2719bp//
 30 99%//AF097645
 C-NT2RP3002311//BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE).//9.80E-103//547aa//
 43%//P48982
 C-NT2RP3002324
 C-NT2RP3002342//Human transporter protein (g17) mRNA, complete cds.//1.70E-65//641bp//65%//U49082
 C-NT2RP3002353
 35 C-NT2RP3002409//Homo sapiens mRNA for KIAA0719 protein, complete cds.//0//2404bp//99%//AB018262
 C-NT2RP3002411//Homo sapiens steroid dehydrogenase homolog mRNA, complete cds.//0//2374bp//99%//
 AF078850
 C-NT2RP3002448
 C-NT2RP3002571//Bos taurus mRNA for lyncein.//7.30E-169//1115bp//84%//Y17923
 40 C-NT2RP3002664
 C-NT2RP3002721//CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7).//5.80E-249//466aa//
 98%//O75390
 C-NT2RP3002737//Homo sapiens voltage-gated potassium channel KCNQ4 (KCNQ4) mRNA, complete cds.//0//
 45 1552bp//99%//AF105202
 C-NT2RP3002738//Homo sapiens enhancer of filamentation (HEF1) mRNA, complete cds.//2.20E-47//763bp//
 65%//L43821
 C-NT2RP3002790
 C-NT2RP3002836//Homo sapiens mRNA for KIAA0463 protein, partial cds.//0//1617bp//99%//AB007932
 C-NT2RP3002887
 50 C-NT2RP3002900//Homo sapiens CGI-109 protein mRNA, complete cds.//8.70E-298//1321bp//92%//AF151867
 C-NT2RP3002958//TRANS-GOLGI NETWORK INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR.//
 8.00E-08//197aa//26%//P19814
 C-NT2RP3002983
 C-NT2RP3003000//Homo sapiens T-type calcium channel alpha-1 subunit mRNA, complete cds.//0//3160bp//
 55 96%//AF051946
 C-NT2RP3003076
 C-NT2RP3003354//SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 3.//5.10E-55//208aa//51%//
 O35609

C-NT2RP3003448
 C-NT2RP3003469
 C-NT2RP3003473//Homo sapiens CGI-55 protein mRNA, complete cds./.5.50E-275//1309bp//98%//AF151813
 C-NT2RP3003527//Homo sapiens mRNA for protein kinase Dyrk1B./0//2483bp//99%//Y17999
 5 C-NT2RP3003532//OX-2 MEMBRANE GLYCOPROTEIN PRECURSOR (FRAGMENT).//4.40E-139//263aa//
 99%//P41217
 C-NT2RP3003535//UDP-N-ACETYLGLUCOSAMINE--PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE
 110 KD SUBUNIT (EC 2.4.1.-) (O-GLCNAC TRANSFERASE P110 SUBUNIT).//8.80E-18//368aa//25%//P56558
 C-NT2RP3003559
 10 C-NT2RP3003614
 C-NT2RP3003729//HYPOTHETICAL 42.1 KD PROTEIN IN SNZ1-YPK2 INTERGENIC REGION./.5.80E-17//
 204aa//30%//Q03151
 C-NT2RP3003849//PROTEIN KINASE C, BRAIN ISOZYME (EC 2.7.1.-) (PKC) (DPKC53E(BR)). PKC1./.1.20E-
 13//126aa//34%//P05130
 15 C-NT2RP3003874//Homo sapiens incomplete cDNA for a mutated allele of a myosin class I, myh-1c./0//2160bp//
 98%//AJ001381
 C-NT2RP3003963
 C-NT2RP3004000
 C-NT2RP3004025
 20 C-NT2RP3004067//Homo sapiens mRNA for NESCA, complete cds./0//1962bp//99%//AB026894
 C-NT2RP3004075
 C-NT2RP3004083
 C-NT2RP3004090//GOLIATH PROTEIN (G1 PROTEIN).//9.00E-33//179aa//47%//Q06003
 C-NT2RP3004119//PEREGRNN (BR140 PROTEIN).//7.30E-39//227aa//43%//P55201
 25 C-NT2RP3004130//CELL SURFACE ANTIGEN 114/A10 PRECURSOR./.8.10E-06//71aa//42%//P19467
 C-NT2RP3004133//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//2.50E-48//198aa//37%//P43636
 C-NT2RP3004202
 C-NT2RP3004294//Xenopus laevis ER1 mRNA, complete cds./.1.20E-71//335bp//79%//AF015454
 C-NT2RP3004309//Homo sapiens mRNA; cDNA DKFZp586C201 (from clone DKFZp586C201).//0//2584bp//
 30 99%//AL050118
 C-NT2RP3004321
 C-NT2RP3004345//N2,N2-DIMETHYLGUANOSINE TRNA METHYLTRANSFERASE PRECURSOR (EC
 2.1.1.32).//3.90E-18//279aa//27%//P15565
 C-NT2RP3004355
 35 C-NT2RP3004374
 C-NT2RP3004406//HYPOTHETICAL 37.4 KD PROTEIN IN IRR1-TIM44 INTERGENIC REGION./.3.20E-15//
 165aa//33%//P40544
 C-NT2RP3004481//BUTYROPHILIN PRECURSOR (BT).//8.50E-22//276aa//32%//Q62556
 C-NT2RP3004552//COMPLEMENT RECEPTOR TYPE 1 PRECURSOR (C3B/C4B RECEPTOR) (CD35 ANTI-
 40 GEN).//8.50E-24//263aa//33%//P17927
 C-NT2RP3004557//Human Ki nuclear autoantigen mRNA, complete cds./0//2181bp//96%//U11292
 C-NT2RP3004625//Homo sapiens I-1 receptor candidate protein mRNA, complete cds./0//1339bp//99%//
 AF082516
 45 C-NT2RP3004640//Bos taurus tuftelin mRNA, complete cds./0//1204bp//88%//AF105228
 C-NT2RP3004647//PUTATIVE MITOCHONDRIAL CARRIER YMR166C./.2.00E-15//220aa//27%//Q03829
 C-NT2RP4000108//Human gene for neurofilament subunit NF-L./0//1998bp//99%//X05608
 C-NT2RP4000634//Homo sapiens mitogen-activated protein kinase kinase kinase MEKK2 mRNA, complete cds./0//1501bp//98%//AF111105
 50 C-NT2RP4000962//SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-).//2.60E-18//225aa//32%//P08458
 C-NT2RP4001001//Homo sapiens clone 24856 mRNA sequence, complete cds./.3.90E-301//1374bp//99%//
 AF131856
 C-NT2RP4001009//Homo sapiens mRNA for farnesylated-proteins converting enzyme 1./0//2965bp//99%//
 Y13834
 55 C-NT2RP4001467//Human placental cDNA coding for 5'nucleotidase (EC 3.1.3.5).//0//2140bp//99%//X55740
 C-NT2RP4001877//Homo sapiens ribonucleoprotein RBM8 (RBM8) mRNA, complete cds./0//2770bp//99%//
 AF127761
 C-NT2RP4001879
 C-NT2RP4002187//Homo sapiens steroid dehydrogenase homolog mRNA, complete cds./0//2373bp//99%//

AF078850
 C-NT2RP4002451
 C-NT2RP4002715
 C-NT2RP4002750//Mus musculus cationic amino acid transporter (CAT3) mRNA, complete cds//1.00E-310//
 5 2084bp//81%//U70859
 C-OVARC1000003//Homo sapiens sodium dependent phosphate transporter isoform NaPi-3b mRNA, complete
 cds//4.30E-220//1158bp//94%//AF111856
 C-OVARC1000090
 C-OVARC1000105//UBIQUITIN-CONJUGATING ENZYME E2-28.4 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN
 10 LIGASE) (UBIQUITIN CARRIER PROTEIN).//4.20E-47//171aa//56%//P33296
 C-OVARC1000137
 C-OVARC1000208//Human calcium-dependent group X phospholipase A2 mRNA, complete cds//1.50E-61//
 365bp//90%//U95301
 C-OVARC1000255//H.sapiens syk mRNA for protein-tyrosine kinase.//0//1525bp//97%//Z29630
 15 C-OVARC1000275//DESMOPLAKIN I AND II (DPI AND DPII) (FRAGMENT).//9.90E-16//352aa//23%//P15924
 C-OVARC1000298
 C-OVARC1000307//HYPOTHETICAL 29.7 KD PROTEIN CY339.02//3.00E-19//194aa//35%//Q50658
 C-OVARC1000313//PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1).//3.00E-24//353aa//
 20 27%//Q12730
 C-OVARC1000331//GMP REDUCTASE (EC 1.6.6.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCT-
 ASE).//9.40E-44//106aa//59%//P36959
 C-OVARC1000410//Homo sapiens angiopoietin Y1 mRNA, complete cds.//2.10E-63//744bp//69%//AF107253
 C-OVARC1000439//HYPOTHETICAL 64.3 KD GTP-BINDING PROTEIN C02F5.3 IN CHROMOSOME III.//1.40E-
 25 33//143aa//53%//P34280
 C-OVARC1000467
 C-OVARC1000529//PROBABLE SERINE/THREONINE-PROTEIN KINASE YKL101W (EC 2.7.1.-).//1.40E-23//
 165aa//39%//P34244
 C-OVARC1000553//DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (THYMOCYTE-ACTIVATING MOLE-
 30 CULE) (THAM).//1.30E-23//169aa//40%//P28843
 C-OVARC1000775
 C-OVARC1000811//PLASMINOGEN (EC 3.4.21.7) (FRAGMENT).//6.40E-13//115aa//34%//Q01177
 C-OVARC1000853
 C-OVARC1000873//N-ACETYLGLUCOSAMINE-6-SULFATASE PRECURSOR (EC 3.1.6.14) (G6S) (GLU-
 35 COSAMINE-6-SULFATASE).//1.00E-09//83aa//40%//P50426
 C-OVARC1000916//H.sapiens PISSLRE mRNA.//7.30E-280//1117bp//95%//X78342
 C-OVARC1000956//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG
 PROTEIN).//2.20E-09//250aa//28%//P17437
 C-OVARC1000995
 C-OVARC1001030//Homo sapiens mRNA for KIAA0886 protein, complete cds.//0//907bp//99%//AB020693
 40 C-OVARC1001049//TRANSCRIPTION FACTOR HES-1 (C-HAIRY1).//7.50E-14//96aa//36%//O57337
 C-OVARC1001086//Homo sapiens cyclin T2a mRNA, complete cds.//0//1593bp//98%//AF048731
 C-OVARC1001132//GC-RICH SEQUENCE DNA-BINDING FACTOR (GCF) (TRANSCRIPTION FACTOR 9)(TCF-
 9).//2.30E-44//268aa//36%//P16383
 C-OVARC1001163//HYPOTHETICAL 49.3 KD PROTEIN C30D11.06C IN CHROMOSOME I.//2.30E-20//152aa//
 45 30%//Q09906
 C-OVARC1001222
 C-OVARC1001260
 C-OVARC1001336//Homo sapiens sodium dependent phosphate transporter isoform NaPi-3b mRNA, complete
 cds.//0//1435bp//99%//AF111856
 C-OVARC1001338//AUTOPHAGY SERINE/THREONINE-PROTEIN KINASE APG1 (EC 2.7.1.-).//8.80E-30//
 50 125aa//40%//P53104
 C-OVARC1001569//PROBABLE SERINE/THREONINE-PROTEIN KINASE YKL101W (EC 2.7.1.-).//1.50E-22//
 164aa//39%//P34244
 C-OVARC1001570//Homo sapiens beta-site APP cleaving enzyme (BACE) mRNA, complete cds.//0//1792bp//
 55 100%//AF190725
 C-OVARC1001596//Homo sapiens Arf-like 2 binding protein BART1 mRNA, complete cds.//0//1766bp//99%//
 AF126062
 C-OVARC1001607//Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds.//0//

EP 1 130 094 A2

1836bp//96%//U15128
 C-OVARC1001725//Homo sapiens patched related protein TRC8 (TRC8) gene, exon 1 and partial cds./.0//
 1624bp//99%//AF064800
 C-OVARC1001727
 5 C-OVARC1001807//Human TR3 orphan receptor mRNA, complete cds./.1.10E-243//1145bp//98%//L13740
 C-OVARC1001833//CIS-GOLGI MATRIX PROTEIN GM130./.6.60E-136//363aa//76%//Q62839
 C-OVARC1001952//TRICHOHYALIN./.3.30E-16//487aa//27%//Q07283
 C-OVARC1001991//VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID).//8.30E-06//114aa//
 35%//Q01956
 10 C-OVARC1002058//Human 18S rRNA gene, complete./.1.50E-164//921bp//91%//M10098
 C-OVARC1002178
 C-PLACE1000033//VON WILLEBRAND FACTOR PRECURSOR./.3.80E-17//190aa//28%//Q28295
 C-PLACE1000231//Rattus norvegicus WAP four-disulfide core domain protein (ps20) mRNA, complete cds./.
 2.70E-101//947bp//74%//AF037272
 15 C-PLACE1000258//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.70E-55//431aa//
 35%//Q05481
 C-PLACE1000442//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//1.00E-88//213aa//67%//P16415
 C-PLACE1000560
 20 C-PLACE1000740//Mus musculus (Notch2) mRNA, complete cds./.5.60E-122//893bp//81%//M93661
 C-PLACE1000907//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//1.30E-204//396aa//85%//
 P51522
 C-PLACE1000912
 C-PLACE1000914//Homo sapiens PB39 mRNA, complete cds./.7.50E-88//500bp//69%//AF045584
 C-PLACE1000927//HYPOTHETICAL 20.9 KD PROTEIN B0563.3 IN CHROMOSOME X./.6.30E-21//123aa//
 25 37%//Q11079
 C-PLACE1000986//Homo sapiens mRNA; cDNA DKFZp586C1817 (from clone DKFZp586C1817).//0//2055bp//
 99%//AL117450
 C-PLACE1001016//SODIUM CHANNEL PROTEIN PARA (PARALYTIC PROTEIN).//6.80E-12//133aa//28%//
 P35500
 30 C-PLACE1001100//Homo sapiens nephrin (NPHS1) mRNA, complete cds./.3.10E-46//323bp//84%//AF035835
 C-PLACE1001114//HYPOTHETICAL BHLF1 PROTEIN./.9.20E-06//389aa//31%//P03181
 C-PLACE1001123//INTESTINAL MEMBRANE A4 PROTEIN (DIFFERENTIATION-DEPENDENT PROTEIN A4).//
 5.00E-08//95aa//31%//Q04941
 C-PLACE1001183
 35 C-PLACE1001229
 C-PLACE1001231//Rattus norvegicus sodium-dependent multi-vitamin transporter (SMVT) mRNA, complete
 cds./.2.20E-137//918bp//80%//AF026554
 C-PLACE1001340//MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (72 KD MITOCHONDRI-
 AL OUTER MEMBRANE PROTEIN) (MITOCHONDRIAL IMPORT RECEPTOR FOR THE ADP/ATP CARRIER)
 40 (TRANSLOCASE OF OUTER MEMBRANE TOM70).//1.20E-23//231aa//31%//P23231
 C-PLACE1001401//HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT (FCER1) (IGE
 FC RECEPTOR, BETA-SUBUNIT).//3.70E-18//148aa//39%//P13386
 C-PLACE1001407
 C-PLACE1001464//Human placental cDNA coding for 5'nucleotidase (EC 3.1.3.5).//0//2756bp//99%//X55740
 45 C-PLACE1001500//Homo sapiens RecQ5 mRNA for DNA helicase, complete cds./.2.30E-271//1230bp//99%//
 AB006533
 C-PLACE1001516//240 KD PROTEIN OF ROD PHOTORECEPTOR CNG-CHANNEL [CONTAINS: GLUTAMIC
 ACID-RICH PROTEIN (GARP); CYCLIC-NUCLEOTIDE-GATED CATION CHANNEL 4 (CNG CHANNEL 4) (CNG-
 50 4) (CYCLIC NUCLEOTIDE-GATED CATION CHANNEL MODULATORY SUBUNIT)].//2.30E-08//274aa//28%//
 Q28181
 C-PLACE1001536
 C-PLACE1001564//H.sapiens mRNA for HE6 Tm7 receptor./.5.10E-36//499bp//70%//X81892
 C-PLACE1001655//Homo sapiens Shab-related delayed-rectifier K+ channel alpha subunit (KCNS3) mRNA, com-
 plete cds./.0//1708bp//99%//AF043472
 55 C-PLACE1001788
 C-PLACE1001795//HYPOTHETICAL 30.6 KD PROTEIN IN SCP160-SMC3 INTERGENIC REGION PRECUR-
 SOR./.3.40E-20//159aa//40%//P47032
 C-PLACE1001836//ENV POLYPROTEIN PRECURSOR (COAT POLYPROTEIN) [CONTAINS: OUTER MEM-

BRANE PROTEIN GP70; TRANSMEMBRANE PROTEIN P20E]//5.00E-27//134aa/47%//P10269
 C-PLACE1001918//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT) //2.30E-53//339aa/33%//P32802

5 C-PLACE1001949//PROBABLE CALCIUM-TRANSPORTING ATPASE 9 (EC 3.6.1.38) //3.00E-75//315aa/44%//Q12697
 C-PLACE1002080//Homo sapiens antigen NY-CO-9 (NY-CO-9) mRNA, partial cds.//0//1588bp//99%//AF039691
 C-PLACE1002095
 10 C-PLACE1002153//Homo sapiens TACC2 protein (TACC2) mRNA, partial cds.//0//1202bp//99%//AF095791
 C-PLACE1002329//EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8//6.50E-105//213aa/45%//Q08509
 C-PLACE1002355//COMPLEMENT C4 PRECURSOR [CONTAINS: C4A ANAPHYLATOXIN] //4.20E-12//131aa/40%//P01029
 15 C-PLACE1002374//Human mRNA for pro-cathepsin L (major excreted protein MEP) //1.30E-313//1363bp//97%//X12451
 C-PLACE1002518//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds.//2.50E-14//396bp//64%//AF064801
 C-PLACE1002547//MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (72 KD MITOCHONDRIAL OUTER MEMBRANE PROTEIN) (MITOCHONDRIAL IMPORT RECEPTOR FOR THE ADP/ATP CARRIER) (TRANSLOCASE OF OUTER MEMBRANE TOM70) //2.30E-28//277aa/31%//P23231
 20 C-PLACE1002726//Oryctolagus cuniculus mRNA for epithelial calcium channel (ECaC) //2.80E-202//926bp//82%//AJ133128
 C-PLACE1002905//ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DIAZEPAM BINDING INHIBITOR) (MA-DBI) //2.40E-37//188aa/40%//P07106
 25 C-PLACE1002911//POLIOVIRUS RECEPTOR HOMOLOG PRECURSOR //4.50E-39//345aa/32%//P32507
 C-PLACE1002967//HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT (FCER1) (IGE FC RECEPTOR, BETA-SUBUNIT) //4.60E-08//156aa/30%//Q01362
 C-PLACE1003135//SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-) //1.30E-47//210aa/49%//P08458
 30 C-PLACE1003163//Homo sapiens DBI-related protein mRNA, complete cds.//1.00E-294//1344bp//99%//AF069301
 C-PLACE1003407//Homo sapiens putative transmembrane protein (CLN5) mRNA, complete cds.//0//1965bp//99%//AF068227
 C-PLACE1003428//Homo sapiens mRNA for VNN1 protein //1.80E-142//676bp//72%//AJ132099
 35 C-PLACE1003438
 C-PLACE1003460
 C-PLACE1003529//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT) //1.30E-09//281aa/22%//P11414
 C-PLACE1003573//T-CELL SURFACE GLYCOPROTEIN YE1/48 (T LYMPHOCYTE ANTIGEN A1) (LY49-A ANTIGEN) //3.70E-16//226aa/26%//P20937
 40 C-PLACE1003598//TRP-ASP REPEATS CONTAINING PROTEIN RBA-1 //1.80E-07//161aa/27%//P90917
 C-PLACE1003644
 C-PLACE1003737//TOLL PROTEIN PRECURSOR //5.40E-07//203aa/27%//P08953
 C-PLACE1003772//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN) //2.40E-12//124aa/38%//P13983
 45 C-PLACE1003839//Homo sapiens putative G protein-coupled receptor (RAIG1) mRNA, complete cds.//8.10E-18//771bp//58%//AF095448
 C-PLACE1003845//PUTATIVE UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP-GALACTOSE 4-EPIMERASE) //3.40E-37//302aa/30%//Q57664
 C-PLACE1003852//Homo sapiens mRNA for KIAA0758 protein, partial cds.//0//1667bp//99%//AB018301
 50 C-PLACE1004028
 C-PLACE1004078//Bovine mRNA for adseverin, complete cds.//0//2218bp//89%//D26549
 C-PLACE1004166//CREB-BINDING PROTEIN //1.80E-12//147aa/35%//P45481
 C-PLACE1004168//GENERAL NEGATIVE REGULATOR OF TRANSCRIPTION SUBUNIT 1 //9.10E-62//485aa/32%//P25655
 55 C-PLACE1004199
 C-PLACE1004279//HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME III //1.40E-08//166aa/30%//P30638
 C-PLACE1004282//MONO- AND DIACYLGLYCEROL LIPASE PRECURSOR (EC 3.1.1.-) (MDGL) //2.10E-11//

189aa//30%//P25234
 C-PLACE1004305//RAS-RELATED PROTEIN RAC1.//9.60E-29//197aa//41%//P40792
 C-PLACE1004441//Human G protein-coupled receptor (GPR1) gene, complete cds.//0//1880bp//98%//U13666
 C-PLACE1004450//AMINOPEPTIDASE N (EC 3.4.11.2) (MICROSOMAL AMINOPEPTIDASE) (LEUKEMIA AN-
 TIGEN CD13).//1.30E-91//562aa//35%//P15541
 C-PLACE1004482//Rattus norvegicus hematopoietic lineage switch 2 related protein (Hls2-rp) mRNA, complete
 cds.//1.90E-246//1643bp//83%//AF097723
 C-PLACE1004492//VERPROLIN//3.30E-07//149aa//29%//P37370
 C-PLACE1004519
 C-PLACE1004520//Human pregnancy-specific beta-glycoprotein d mRNA, complete cds.//9.10E-279//882bp//
 88%//M20881
 C-PLACE1004630//Homo sapiens ten integrin EGF-like repeat domains protein precursor (ITGBL1) mRNA, com-
 plete cds.//1.00E-138//643bp//99%//AF072752
 C-PLACE1004637
 C-PLACE1004648//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSI-
 DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//1.40E-18//395aa//25%//P08640
 C-PLACE1004816//Homo sapiens mRNA for Hakata antigen, complete cds.//1.00E-166//856bp//94%//D88587
 C-PLACE1004887//GOLIATH PROTEIN (G1 PROTENN).//4.80E-33//179aa//47%//Q06003
 C-PLACE1005003//PROSTASIN PRECURSOR (EC 3.4.21.-).//2.20E-52//269aa//41%//Q16651
 C-PLACE1005005//Homo sapiens ubiquitin conjugating enzyme G2 (UBE2G2) mRNA, complete cds.//4.10E-261//
 1209bp//98%//AF032456
 C-PLACE1005031//CHLORINE CHANNEL PROTEIN P64.//8.00E-92//205aa//87%//P35526
 C-PLACE1005239//Homo sapiens mRNA for HIRIP3 protein (clone pH4-31, PH4-17).//1.80E-235//1010bp//84%//
 AJ2233511
 C-PLACE1005250//Homo sapiens D-type cyclin-interacting protein 1 (DIP1) mRNA, complete cds.//0//1046bp//
 96%//AF082569
 C-PLACE1005383//Homo sapiens UP50 mRNA, complete cds.//0//2019bp//99%//AF093118
 C-PLACE1005410//Canis familiaris sec61 homologue mRNA, complete cds.//2.40E-204//673bp//89%//M96629
 C-PLACE1005426//Human pregnancy-specific beta 1-glycoprotein 4 (PSG4) clone FL-64 mRNA, complete cds.//
 0//1629bp//95%//U18469
 C-PLACE1005519//Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds.//4.60E-108//1070bp//73%//
 AF024636
 C-PLACE1005539//ACTIN POLYMERIZATION INHIBITOR (HEAT SHOCK 25 KD PROTEIN) (25-KD IAP).//
 3.10E-08//84aa//34%//Q00649
 C-PLACE1005544//Mus musculus junctional adhesion molecule (Jam) mRNA, complete cds.//2.00E-159//
 1237bp//76%//U89915
 C-PLACE1005569//Homo sapiens mRNA for Z39Ig protein.//0//1768bp//99%//AJ132502
 C-PLACE1005601
 C-PLACE1005660//HYPOTHETICAL 64.3 KD GTP-BINDING PROTEIN C02F5.3 IN CHROMOSOME III.//1.90E-
 33//143aa//53%//P34280
 C-PLACE1005669
 C-PLACE1005682//B-CELL LYMPHOMA 3-ENCODED PROTEIN (BCL-3 PROTEIN).//4.90E-09//183aa//33%//
 P20749
 C-PLACE1005725//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//7.60E-17//295aa//
 27%//Q11073
 C-PLACE1005736//Human mRNA for BAS-GRIP protein.//0//2378bp//99%//E16311 C-PLACE1005745//ORM1
 PROTEIN.//2.40E-17//137aa//35%//P53224
 C-PLACE1005768
 C-PLACE1005815//COLORECTAL MUTANT CANCER PROTEIN (MCC PROTEIN).//1.50E-26//274aa//26%//
 P23508
 C-PLACE1005878//Bovine chlorine channel protein (p64) mRNA, complete cds.//5.90E-137//889bp//85%//L16547
 C-PLACE1005927//HYPOTHETICAL 35.8 KD PROTEIN C12G12.12 IN CHROMOSOME I.//1.60E-38//333aa//
 33%//Q09875
 C-PLACE1006071//LAMININ BETA-1 CHAIN PRECURSOR (LAMININ B1 CHAIN).//6.00E-08//215aa//26%//
 P02469
 C-PLACE1006073//Homo sapiens mRNA for glucuronyltransferase I, complete cds.//4.10E-316//1020bp//96%//
 AB009598
 C-PLACE1006079//Homo sapiens distal-less homeobox protein (DLX3) gene, complete cds.//0//1379bp//97%//

AF028233
 C-PLACE1006093
 C-PLACE1006208//Homo sapiens nGAP mRNA, complete cds.//3.30E-151//694bp//100%//AF047711
 C-PLACE1006219//PUTATIVE UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP-GALACTOSE 4-EPIMERASE).//3.50E-37//302aa//30%//Q57664
 5 C-PLACE1006277//Homo sapiens mRNA for Z39lg protein.//0//1768bp//99%//AJ132502
 C-PLACE1006290//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//8.50E-75//301aa//39%//P43636
 C-PLACE1006443//Homo sapiens PB39 mRNA, complete cds.//4.30E-98//553bp//70%//AF045584
 10 C-PLACE1006515//Homo sapiens mRNA for KIAA0576 protein, partial cds.//0//2846bp//99%//AB011148
 C-PLACE1006716//30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN PRECURSOR (ACRP30) (ADIPOCYTE SPECIFIC PROTEIN ADIPOQ).//4.60E-25//181aa//35%//Q60994
 C-PLACE1006786
 C-PLACE1006809//SLS1 PROTEIN PRECURSOR.//9.10E-10//273aa//27%//P08124
 15 C-PLACE1006959
 C-PLACE1007028//Homo sapiens TDAG51/lp1 homologue 1 (TIH1) mRNA, complete cds.//1.40E-307//1423bp//99%//AF151100
 C-PLACE1007040
 C-PLACE1007077//Homo sapiens mRNA for KIAA0977 protein, complete cds.//0//2578bp//99%//AB023194
 20 C-PLACE1007081//COAGULATION FACTOR V PRECURSOR (ACTIVATED PROTEIN C COFACTOR).//5.00E-20//247aa//34%//Q28107
 C-PLACE1007096//PUTATIVE SUGAR TRANSPORT PROTEIN GUTA.//2.70E-17//174aa//27%//O34368
 C-PLACE1007296//Human mRNA for a presumptive KDEL receptor.//1.10E-185//1038bp//91%//X55885
 C-PLACE1007591
 25 C-PLACE1007626//Homo sapiens unknown mRNA, complete cds.//3.00E-246//1122bp//99%//AF047439
 C-PLACE1007702//Mus musculus TRA1 mRNA, complete cds.//7.50E-41//662bp//64%//D78335
 C-PLACE1007845//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//4.80E-14//158aa//40%//P43636
 C-PLACE1007881//HYPOTHETICAL 69.4 KD PROTEIN F13H10.3 IN CHROMOSOME IV.//3.10E-99//504aa//42%//Q19425
 C-PLACE1007971
 30 C-PLACE1008282//HEME-REGULATED EUKARYOTIC INITIATION FACTOR EIF-2-ALPHA KINASE (EC 2.7.1.-) (HRI).//7.10E-274//627aa//82%//P33279
 C-PLACE1008297//MYOSIN HEAVY CHAIN KINASE B (EC 2.7.1.129) (MHCK B).//1.30E-14//187aa//33%//P90648
 35 C-PLACE1008359//BEM46 PROTEIN (FRAGMENT).//1.70E-50//289aa//42%//P54069
 C-PLACE1008469
 C-PLACE1008549//Homo sapiens Ets transcription factor ESE-2b mRNA, complete cds.//0//2274bp//99%//AF115403
 C-PLACE1008657//Bovine mRNA for adseverin, complete cds.//7.80E-227//1246bp//90%//D26549
 40 C-PLACE1008716//Human beta-1,2-N-acetylglicosaminyltransferase II (MGAT2) gene, complete cds.//0//1888bp//99%//U15128
 C-PLACE1008744//P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (GMP-140) (PADGEM) (CD62P) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3).//4.80E-32//338aa//30%//Q01102
 C-PLACE1008984
 45 C-PLACE1008985//Mus musculus synaptotagmin VIII mRNA, partial cds.//3.80E-140//650bp//81%//U20107
 C-PLACE1009067
 C-PLACE1009196
 C-PLACE1009279//cDNA encoding novel physiologically active protein which have serine protease activity.//6.60E-86//1414bp//64%//E12965
 50 C-PLACE1009527//Oryctolagus cuniculus mRNA for epithelial calcium channel (ECaC).//1.20E-87//585bp//83%//AJ133128
 C-PLACE1009546
 C-PLACE1009600//Mouse mRNA for tetracycline transporter-like protein, complete cds.//1.10E-264//924bp//88%//D88315
 55 C-PLACE1009735
 C-PLACE1009982//SALIVARY GILUE PROTEIN SGS-3 PRECURSOR.//5.20E-08//166aa//28%//P02840
 C-PLACE1010011//Homo sapiens AAPT1-like protein mRNA, partial cds.//1.70E-237//1092bp//99%//AF047431
 C-PLACE1010078//ORM1 PROTEIN.//3.70E-19//137aa//37%//P53224

EP 1 130 094 A2

C-PLACE1010081//Homo sapiens serine/threonine kinase RICK (RICK) mRNA, complete cds./0//2033bp//99%//
AF027706
C-PLACE1010251//FIBRILLIN 2 PRECURSOR./1.70E-31//201aa//35%//Q61555
C-PLACE1010445
5 C-PLACE1010713//Homo sapiens steroid dehydrogenase homolog mRNA, complete cds./0//2374bp//99%//
AF078850
C-PLACE1010784//Homo sapiens orphan G protein-coupled receptor (GPR34) gene, complete cds./2.30E-252//
1146bp//99%//AF039686
C-PLACE1010827//COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).//1.90E-
10 19//163aa//34%//P49020
C-PLACE1010968//PROTEIN-TYROSINE PHOSPHATASE DLAR PRECURSOR (EC 3.1.3.48) (PROTEIN- TY-
ROSINE-PHOSPHATE PHOSPHOHYDROLASE).//3.40E-30//690aa//26%//P16621
C-PLACE1011045//Homo sapiens E1-like protein mRNA, complete cds./0//2376bp//99%//AF094516
C-PLACE1011116//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE)
15 (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//3.30E-09//234aa//27%//P08640
C-PLACE1011181//MSP1 PROTEIN HOMOLOG./9.40E-82//353aa//47%//P54815
C-PLACE1011236//Mus musculus mRNA for RST, complete cds./1.70E-90//1398bp//65%//AB005451
C-PLACE1011364//MYOTONIN-PROTEIN KINASE (EC 2.7.1.-) (MYOTONIC DISTROPHY PROTEIN KINASE)
(MDPK) (DM-KINASE) (DMK) (DMPK) (MT-PK).//2.20E-09//153aa//32%//Q09013
20 C-PLACE1011407//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.80E-133//342aa//59%//Q99676
C-PLACE1011516//HYPOTHETICAL 21.5 KD PROTEIN IN SEC15-SAP4 INTERGENIC REGION./1.30E-13//
139aa//34%//P53073
C-PLACE1011708//Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds./0//1840bp//98%//
AF034611
25 C-PLACE1011824//Human Ste20-like kinase (MST2) mRNA, complete cds./6.40E-202//561bp//92%//U26424
C-PLACE1011978//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.10E-194//547aa//
57%//Q05481
C-PLACE2000118//WISKOTT-ALDRICH SYNDROME PROTEIN HOMOLOG (WASP).//3.20E-27//205aa//43%//
P70315
30 C-PLACE2000219
C-PLACE3000181//Human protocadherin 42 mRNA, complete cds for abbreviated PC42 //0//2719bp//95%//
L11370
C-PLACE3000213//COMPLEMENT RECEPTOR TYPE 2 PRECURSOR (CR2) (COMPLEMENT C3D RECEP-
TOR).//4.60E-68//317aa//34%//P19070
35 C-PLACE4000354//COMPLEMENT RECEPTOR TYPE 1 PRECURSOR (C3B/C4B RECEPTOR) (CD35 ANTI-
GEN).//1.00E-129//482aa//29%//P17927
C-PLACE4000455
C-SKNMC1000004
C-SKNMC1000014
40 C-SKNMC1000082//BRITTLE-1 PROTEIN PRECURSOR./3.70E-31//307aa/130%//P29518
C-THYRO1000036//Homo sapiens collagen alpha 3 type IX (COL9A3) mRNA, complete cds./1.20E-258//
1376bp//93%//L41162
C-THYRO1000061//Mus musculus mRNA for UBE-1c1, UBE-1c2, UBE-1c3, complete cds./1.40E-117//1126bp//
74%//AB030505
45 C-THYRO1000099
C-THYRO1000196//Homo sapiens Ksp-cadherin (CDH16) mRNA, complete cds./0//1632bp//91%//AF016272
C-THYRO1000400//Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 25795./0//1893bp//99%//
AL109665
C-THYRO1000580//ZINC FINGER PROTEIN 184 (FRAGMENT).//9.90E-114//279aa//59%//Q99676
50 C-THYRO1000584//EPIDIDYMIS-SPECIFIC ALPHA-MANNOSIDASE (EC 3.2.1.24) (ALPHA-D-MANNOSIDE
MANNOHYDROLASE) (135 KD PROTEIN).//5.40E-127//335aa//71%//Q28949
C-THYRO1000678//Homo sapiens Cx30 gene./0//1741bp//97%//AJ005585
C-THYRO1000776//PROBABLE SULFATE PERMEASE SPBC3H7.02./1.30E-68//442aa//36%//O74377
C-THYRO1000795//C.elegans mRNA for Oxoglutarate/malate carrier protein./8.80E-42//821bp//63%//X76114
55 C-THYRO1000846
C-THYRO1000866//SHK1 KINASE-BINDING PROTEIN 1./4.40E-91//449aa//44%//P78963
C-THYRO1000956//Human G protein-coupled receptor APJ gene, complete cds./0//1583bp//99%//U03642
C-THYRO1000964//Drosophila melanogaster Pelle associated protein Pellino (Pli) mRNA, complete cds./1.10E-

34//759bp//63%//AF091624
 C-THYRO1000999
 C-THYRO1001063
 C-THYRO1001071//GAMMA-ADAPTIN (GOLGI ADAPTOR HA1/AP1 ADAPTIN GAMMA SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 1 GAMMA LARGE CHAIN).//8.20E-14//157aa//33%//P22892
 C-THYRO1001102
 C-THYRO1001113//Homo sapiens mRNA; cDNA DKFZp564E1616 (from clone DKFZp564E1616).//0//1361bp//99%//AL096713
 C-THYRO1001128//Homo sapiens mRNA for hypothetical protein (C9orf9 gene).//6.40E-155//648bp//99%//AJ011375
 C-THYRO1001205
 C-THYRO1001237//PHYTOENE DEHYDROGENASE (EC 1.3.-.-) (PHYTOENE DESATURASE) (ALBINO-1 PROTEIN).//3.10E-13//346aa//22%//P21334
 C-THYRO1001242//Homo sapiens cleft lip and palate transmembrane protein 1 (CLPTM1) mRNA, complete cds.//0//2468bp//99%//AF037339
 C-THYRO1001266//Human sodium iodide symporter mRNA, complete cds.//7.20E-81//1466bp//62%//U66088
 C-THYRO1001327
 C-THYRO1001456//HYPOTHÉTICAL 56.2 KD PROTEIN CY31.25C.//9.40E-32//355aa//31%//Q10555
 C-THYRO1001457//H.sapiens mRNA for protein kinase C mu.//2.30E-218//1183bp//73%//X75756
 C-THYRO1001471
 C-THYRO1001478//CYTOCHROME B-245 HEAVY CHAIN (P22 PHAGOCYTE B-CYTOCHROME) (NEUTROPHIL CYTOCHROME B, 91 KD POLYPEPTIDE) (CGD91-PHOX) (GP91-PHOX) (CYTOCHROME B(558) BETA CHAIN) (SUPEROXIDE-GENERATING NADPH OXIDASE HEAVY CHAIN SUBUNIT).//8.90E-50//296aa//35%//P04839
 C-THYRO1001495
 C-THYRO1001523//Homo sapiens mRNA for TM7XN1 protein.//0//3663bp//99%//AJ011001
 C-THYRO1001529//SERINE PALMITOYLTRANSFERASE 2 (EC 2.3.1.50) (LONG CHAIN BASE BIOSYNTHESIS PROTEIN 2) (SPT 2).//5.50E-25//115aa//53%//Q09925
 C-THYRO1001593//PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-).//3.10E-203//550aa//62%//P27448
 C-THYRO1001608
 C-THYRO1001641//Homo sapiens CGI-57 protein mRNA, complete cds.//0//1668bp//99%//AF151815
 C-THYRO1001700//SERINE/THREONINE PROTEIN KINASE RIP (EC 2.7.1.-) (CELL DEATH PROTEIN RIP) (RECEPTOR INTERACTING PROTEIN).//9.70E-33//268aa//37%//Q60855
 C-THYRO1001702//Mus musculus mRNA for myeloid associated differentiation protein.//1.50E-128//1204bp//73%//AJ001616
 C-THYRO1001725
 C-THYRO1001770//PROBABLE SERINE/THREONINE-PROTEIN KINASE YNL020C (EC 2.7.1.-).//6.30E-20//169aa//35%//P53974
 C-THYRO1001803
 C-Y79AA1000030//Homo sapiens mRNA for Fe65L2, complete cds.//0//1828bp//100%//AB018247
 C-Y79AA1000127
 C-Y79AA1000207
 C-Y79AA1000226
 C-Y79AA1000270//Bos taurus vacuolar H⁺ ATPase subunit Ac45 mRNA, complete cds.//1.00E-271//1490bp//83%//U10039
 C-Y79AA1000426//Mus musculus activin beta E subunit mRNA, complete cds.//7.70E-200//1533bp//78%//U96386
 C-Y79AA1000521
 C-Y79AA1000750
 C-Y79AA1000776//Mus musculus mRNA for GSG1, complete cds.//2.40E-161//820bp//85%//D87325
 C-Y79AA1000777//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//8.10E-48//283aa//38%//Q00808
 C-Y79AA1000876//PROTEIN DISULHDE ISOMERASE-RELATED PROTEIN PRECURSOR (ERP72).//1.60E-44//210aa//38%//P13667
 C-Y79AA1000888//TRNA PSEUDOURIDINE SYNTHASE A (EC 4.2.1.70) (PSEUDOURIDYLATE SYNTHASE I) (PSEUDOURIDINE SYNTHASE I) (URACIL HYDROLYASE).//1.50E-21//267aa//32%//P70973
 C-Y79AA1000959//Homo sapiens Hsp70 binding protein HspBP1 mRNA, complete cds.//4.80E-283//1405bp//95%//AF093420
 C-Y79AA1000967//CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123) (CAM KI-

NASE I).//1.00E-77//359aa//44%//Q14012
 C-Y79AA1001013
 C-Y79AA1001056//Homo sapiens MAID protein mRNA, complete cds.//0//1475bp//99%//AF113535
 C-Y79AA1001062//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PRO-
 5 TEIN).//8.90E-12//132aa//38%//Q13829
 C-Y79AA1001090//NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT (DNA-BINDING FACTOR KBF1) (EBP- 1)
 (NF-KAPPA-B1 P84/NF-KAPPA-B1 P98)[CONTAINS: NUCLEAR FACTOR NF-KAPPA-B P50 SUBUNIT] (FRAG-
 MENT).//4.50E-09//144aa//31%//Q63369
 C-Y79AA1001212//Homo sapiens SL15 protein mRNA, complete cds.//6.30E-306//1388bp//99%//AF038961
 10 C-Y79AA1001264//HYPOTHETICAL 39.9 KD PROTEIN T15H9.1 IN CHROMOSOME II PRECURSOR.//5.10E-
 106//351aa//58%//Q10005
 C-Y79AA1001272//Homo sapiens retinoic acid repressible protein (RARG-1) mRNA, complete cds.//1.50E-183//
 15 867bp//98%//AF172066
 C-Y79AA1001328//Mus musculus mRNA for DII3 protein, complete cds.//1.90E-263//1988bp//79%//AB013440
 C-Y79AA1001426//ANION EXCHANGE PROTEIN 3 (CARDIAC/BRAIN BAND 3-LIKE PROTEIN) (CAE3/BAE3).//
 20 6.20E-66//609aa//31%//P48751
 C-Y79AA1001427//Homo sapiens cytochrome b5 reductase 1 (B5R.1) mRNA, complete cds.//0//1588bp//99%//
 AF169481
 C-Y79AA1001430//Homo sapiens mRNA for KIAA0469 protein, complete cds.//0//2943bp//99%//AB007938
 25 C-Y79AA1001523//Homo sapiens transcriptional intermediary factor 1 alpha mRNA, complete cds.//0//2263bp//
 99%//AF119042
 C-Y79AA1001530//Human beta-tubulin gene (5-beta) with ten Alu family members.//0//1920bp//98%//X00734
 C-Y79AA1001592
 C-Y79AA1001727//CELL SURFACE A33 ANTIGEN PRECURSOR.//1.10E-13//286aa//27%//Q99795
 30 C-Y79AA1001787//PROBABLE CALCIUM-TRANSPORTING ATPASE 9 (EC 3.6.1.38).//1.70E-133//544aa//37%//
 Q12697
 C-Y79AA1001793//Mus musculus mRNA for GSG1, complete cds.//3.70E-126//532bp//78%//D87325
 C-Y79AA1001795//Homo sapiens mRNA for GaT4 protein.//2.30E-250//1137bp//99%//Y15061
 C-Y79AA1001799//MITOCHONDRIAL RNA SPLICING PROTEIN MSR4.//3.40E-54//182aa//39%//P23500
 35 C-Y79AA1001803//Homo sapiens secretogranin III mRNA, complete cds.//0//1871bp//99%//AF078851
 C-Y79AA1001863
 C-Y79AA1002022//POLIOVIRUS RECEPTOR HOMOLOG PRECURSOR.//2.20E-06//140aa//26%//P32507
 C-Y79AA1002058//Mus musculus Gng3lg mRNA, complete cds.//4.10E-167//1145bp//83%//AF069954
 C-Y79AA1002121//HISTONE H1.//4.90E-12//114aa//35%//P35060
 40 C-Y79AA1002129
 C-Y79AA1002213//HYPOTHETICAL 52.7 KD PROTEIN C38C10.2 IN CHROMOSOME III.//1.20E-98//262aa//
 41%//Q03567
 C-Y79AA1002334//GLUCOSE REPRESSION MEDIATOR PROTEIN.//1.70E-10//333aa//23%//P14922
 C-Y79AA1002373//Mus musculus mRNA for GSG1, complete cds.//7.20E-147//680bp//79%//D87325
 45 C-Y79AA1002376//Rattus norvegicus cytoplasmic dynein intermediate chain 2B mRNA, complete cds.//1.50E-
 304//1667bp//90%//U39045
 C-Y79AA1002378//Homo sapiens zinc finger protein NY-REN-21 antigen mRNA, partial cds.//0//963bp//99%//
 AF155100
 C-Y79AA1002381//Homo sapiens cell cycle related kinase mRNA, complete cds.//0//1791bp//98%//AF035013

Claims

- 50 1. Use of an oligonucleotide as a primer for synthesizing the polynucleotide comprising the nucleotide sequence set
 forth in any one of SEQ ID NOs: 1-829 and 2545, or the complementary strand thereof, wherein said oligonucleotide
 is complementary to said polynucleotide or the complementary strand thereof and comprises at least 15 nucle-
 otides.
- 55 2. A primer set for synthesizing polynucleotides, the primer set comprising an oligo-dT primer and an oligonucleotide
 complementary to the complementary strand of the polynucleotide comprising the nucleotide sequence set forth
 in any one of SEQ ID NOs: 1-829 and 2545, wherein said oligonucleotide comprises at least 15 nucleotides.
3. A primer set for synthesizing polynucleotides, the primer set comprising a combination of an oligonucleotide com-

prising a nucleotide sequence complementary to the complementary strand of the polynucleotide comprising a 5'-end nucleotide sequence and an oligonucleotide comprising a nucleotide sequence complementary to the polynucleotide comprising a 3'-end nucleotide sequence, wherein said oligonucleotides comprise at least 15 nucleotides and wherein said combination of 5'-end nucleotide sequence/3'-end nucleotide sequence is selected from the group consisting of:

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EP 1 130 094 A2

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EP 1 130 094 A2

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4. A polynucleotide which can be synthesized with the primer set of claim 2 or 3.

5. A polynucleotide comprising a coding region in the polynucleotide of claim 4.

40 6. A substantially pure protein encoded by polynucleotide of claim 4.

7. A partial peptide of the protein of claim 6.

45 8. An isolated polynucleotide selected from the group consisting of

(a) a polynucleotide comprising a coding region of the nucleotide sequence set forth in any one of the following SEQ ID NOS:

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(b) a polynucleotide comprising a nucleotide sequence encoding a protein comprising the amino acid sequence

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5 and SEQ ID NO:4179

- (c) a polynucleotide comprising a nucleotide sequence encoding a protein comprising an amino acid sequence selected from the amino acid sequences of (b), in which one or more amino acids are substituted, deleted, inserted, and/or added, wherein said protein is functionally equivalent to the protein comprising said amino acid sequence selected from the amino acid sequences of (b);
- 10 (d) a polynucleotide that hybridizes with a polynucleotide comprising a nucleotide sequence selected from the nucleotide sequences of (a), and that comprises a nucleotide sequence encoding a protein functionally equivalent to the protein encoded by the nucleotide sequence selected from the nucleotide sequences of (a);
- 15 (e) a polynucleotide comprising a nucleotide sequence encoding a partial amino acid sequence of a protein encoded by the polynucleotide of (a) to (d);
- (f) a polynucleotide comprising a nucleotide sequence with at least 70% identity to the nucleotide sequence of (a).

- 20 9. A substantially pure protein encoded by the polynucleotide of claim 8.
- 10 10. An antibody against the protein or peptide of any one of claims 6, 7, and 9.
- 11 11. A vector comprising the polynucleotide of claim 5 or 8.
- 25 12. A transformant carrying the polynucleotide of claim 5 or 8, or the vector of claim 11.
13. A transformant expressively carrying the polynucleotide of claim 5 or 8, or the vector of claim 11.
- 30 14. A method for producing the protein or peptide of any one of claims 6, 7, and 9, comprising culturing the transformant of claim 13 and recovering the expression product.
15. An oligonucleotide comprising the nucleotide sequence of claim 8 (a) or the nucleotide sequence complementary to the complementary strand thereof, wherein said oligonucleotide comprises 15 nucleotides or more.
- 35 16. Use of the oligonucleotide of claim 15 as a primer for synthesizing a polynucleotide.
17. Use of the oligonucleotide of claim 15 as a probe for detecting a gene.
18. An antisense polynucleotide against the polynucleotide of claim 8, or the portion thereof.
- 40 19. A method for synthesizing a polynucleotide, the method comprising:
 - a) synthesizing a complementary strand using a cDNA library as a template, and using the primer set of claim 2 or 3, or the primer of claim 16; and
 - 45 b) recovering the synthesized product.
20. The method of claim 19, wherein the cDNA library is obtainable by oligo-capping method.
21. The method of claim 19, wherein the complementary strand is obtainable by PCR.
- 50 22. A method for detecting the polynucleotide of claim 8, the method comprising:
 - a) incubating a target polynucleotide with the oligonucleotide of claim 15 under the conditions where hybridization occurs, and
 - 55 b) detecting the hybridization of the target polynucleotide with the oligonucleotide of claim 15.
23. A database of polynucleotides and/or proteins, the database comprising information on at least one sequence selected from the nucleotide sequences of claim 8 (a) and/or the amino acid sequences of claim 8 (b), or a medium

on which the database is stored.

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Figure 1

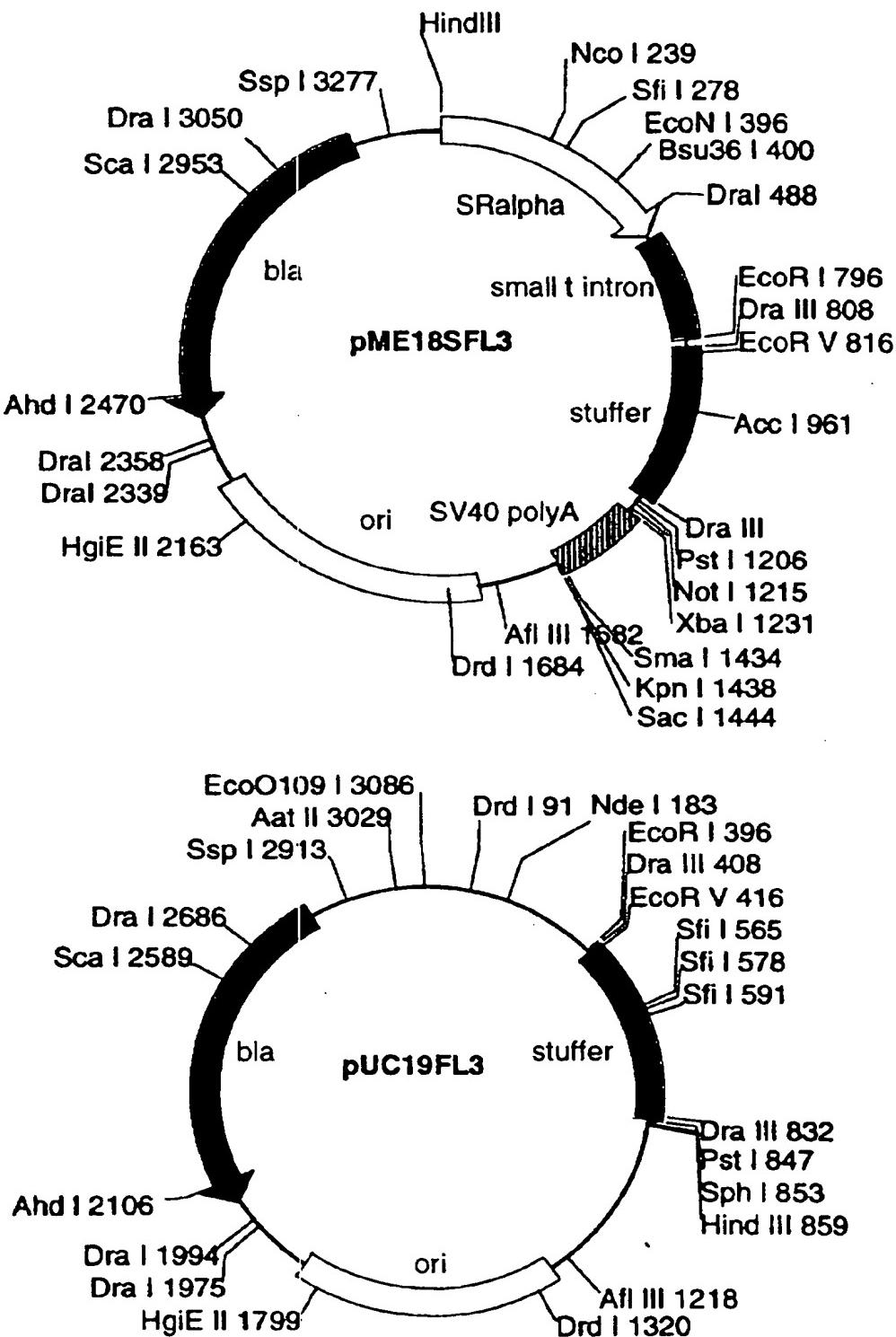


Figure 2

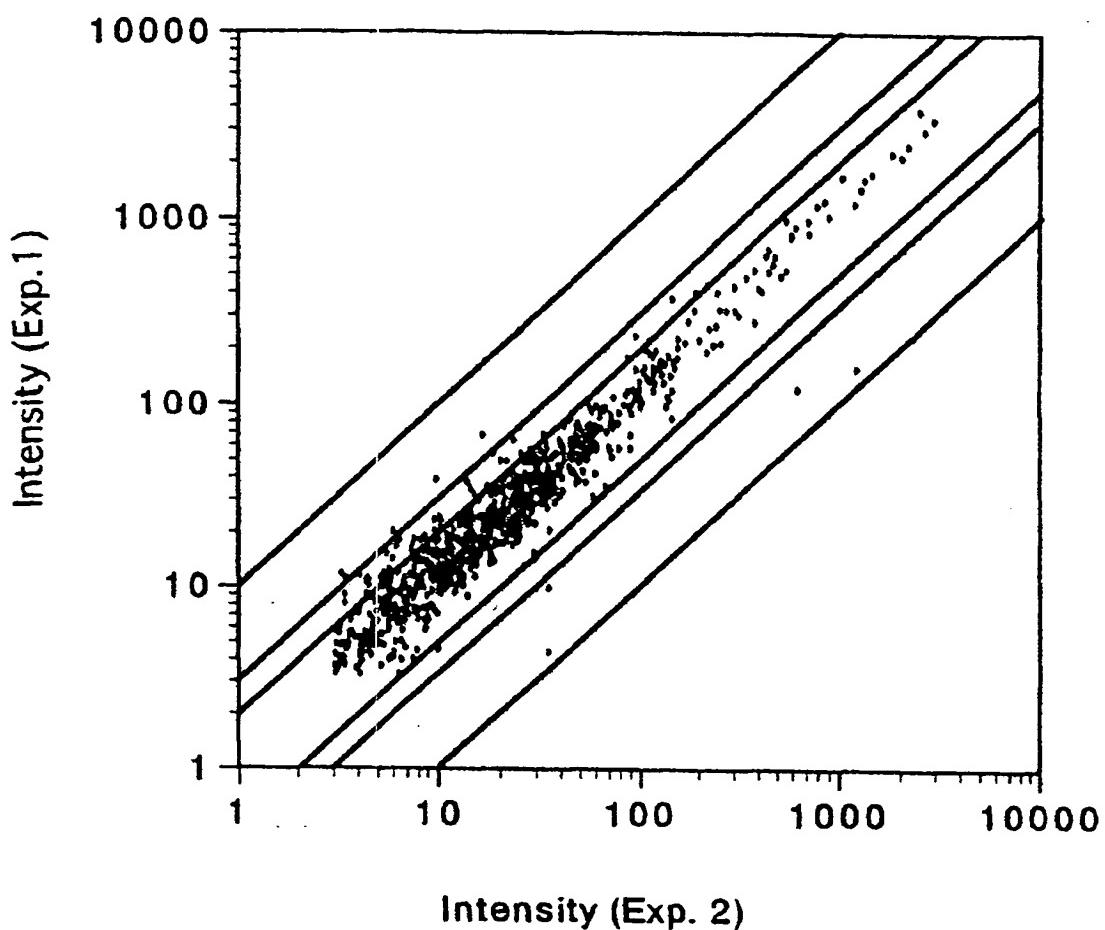
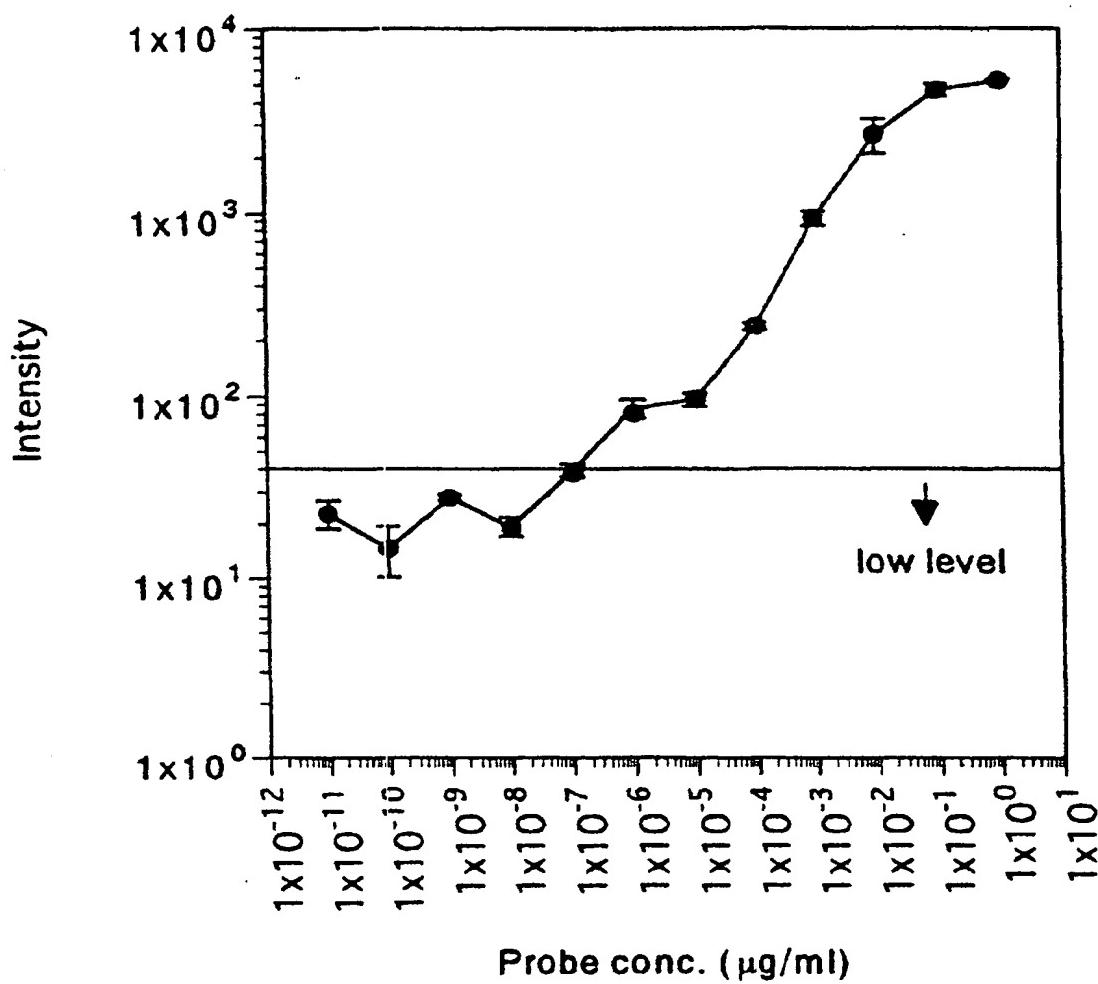


Figure 3



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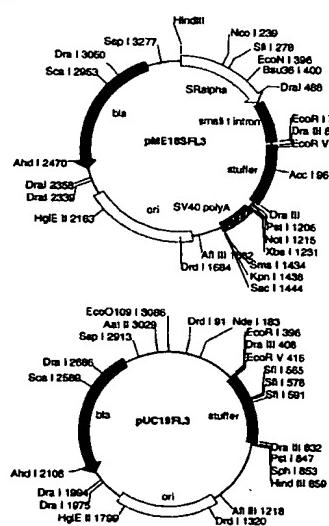
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(54) **Primers for synthesizing full length cDNA clones and their use**

(57) Primers for synthesizing full length cDNAs and their use are provided.

830 cDNA encoding a human protein has been isolated and nucleotide sequences of 5'-, and 3'-ends of the cDNA have been determined. Furthermore, primers for synthesizing the full length cDNA have been provided to clarify the function of the protein encoded by the cDNA. The full length cDNA of the present invention containing the translation start site provides information useful for analyzing the functions of the protein.

Figure





European Patent
Office

EUROPEAN SEARCH REPORT

Application Number
EP 00 11 4089

DOCUMENTS CONSIDERED TO BE RELEVANT			CLASSIFICATION OF THE APPLICATION (Int.Cl.7)						
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim							
X	DATABASE EMBL SEQUENCE DATABASE [Online] Hinxton, GB; 21 May 1992 (1992-05-21) S. MARZUKI: "H. sapiens mitochondrial genome" XP002170023 EMBL Accession no. X62996 * abstract *	8-22	C12N15/12 C12N15/11 C12N15/10 C12N15/70 C12N15/85 C12N5/10 C12N1/21 C07K14/47 C07K16/18 C12Q1/68						
X	DATABASE EMBL SEQUENCE DATABASE [Online] Hinxton, GB; 11 April 1996 (1996-04-11) U. ARNASON ET AL.: "Homo sapiens mitochondrial DNA" XP002170024 EMBL Accession no. X93334; * abstract *	8-22							
X	DATABASE EMBL SEQUENCE DATABASE [Online] Hinxton, GB; 27 April 1999 (1999-04-27) M.J. AGOSTINO ET AL.: "EST clone BG491" XP002170025 GCG GENESEQ D.V86857 * abstract * & WO 98 45435 A (GENETICS INST INC.) 15 October 1998 (1998-10-15) SEQ ID No. 684	8-22							
E	WO 00 44906 A (ELITRA PHARMACEUTICALS INC) 3 August 2000 (2000-08-03) SEQ ID No. 185 is 100% identical to SEQ ID No. 3595; * claims 8,9 *	8-22 -/-	C12N C07K C12Q						
<p>The present search report has been drawn up for all claims</p> <table border="1" style="width: 100%; border-collapse: collapse;"> <tr> <td style="width: 33%;">Place of search</td> <td style="width: 33%;">Date of completion of the search</td> <td style="width: 33%;">Examiner</td> </tr> <tr> <td>THE HAGUE</td> <td>19 June 2001</td> <td>HORNIG H.</td> </tr> </table> <p>CATEGORY OF CITED DOCUMENTS</p> <p>X : particularly relevant if taken alone Y : particularly relevant if combined with another document of the same category A : technological background O : non-written disclosure P : intermediate document</p> <p>T : theory or principle underlying the invention E : earlier patent document, but published on, or after the filing date D : document cited in the application L : document cited for other reasons</p> <p>& : member of the same patent family, corresponding document</p>				Place of search	Date of completion of the search	Examiner	THE HAGUE	19 June 2001	HORNIG H.
Place of search	Date of completion of the search	Examiner							
THE HAGUE	19 June 2001	HORNIG H.							



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Application Number

CLAIMS INCURRING FEES

The present European patent application comprised at the time of filing more than ten claims.

- Only part of the claims have been paid within the prescribed time limit. The present European search report has been drawn up for the first ten claims and for those claims for which claims fees have been paid, namely claim(s):

No claims fees have been paid within the prescribed time limit. The present European search report has been drawn up for the first ten claims.

LACK OF UNITY OF INVENTION

The Search Division considers that the present European patent application does not comply with the requirements of unity of invention and relates to several inventions or groups of inventions, namely:

see sheet B

- All further search fees have been paid within the fixed time limit. The present European search report has been drawn up for all claims.

As all searchable claims could be searched without effort justifying an additional fee, the Search Division did not invite payment of any additional fee.

Only part of the further search fees have been paid within the fixed time limit. The present European search report has been drawn up for those parts of the European patent application which relate to the inventions in respect of which search fees have been paid, namely claims:

None of the further search fees have been paid within the fixed time limit. The present European search report has been drawn up for those parts of the European patent application which relate to the invention first mentioned in the claims, namely claims:



European Patent
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EUROPEAN SEARCH REPORT

Application Number

EP 00 11 4089

DOCUMENTS CONSIDERED TO BE RELEVANT			
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (Int.Cl.)
A	ADAMS M D ET AL: "INITIAL ASSESSMENT OF HUMAN GENE DIVERSITY AND EXPRESSION PATTERNS BASED UPON 83 MILLION NUCLEOTIDES OF cDNA SEQUENCE" NATURE, GB, MACMILLAN JOURNALS LTD, LONDON, vol. 377, 28 September 1995 (1995-09-28), pages 3-17, XP002042918 ISSN: 0028-0836 * the whole document *		
D, A	NAKAI K ET AL: "KNOWLEDGE BASE FOR PREDICTING PROTEIN LOCALIZATION SITES IN EUKARYOTIC CELLS" GENOMICS, ACADEMIC PRESS, SAN DIEGO, US, vol. 14, no. 4, 1992, pages 897-911, XP000953039 ISSN: 0888-7543 * the whole document *		
A	MARUYAMA K ET AL: "OLIGO-CAPPING: A SIMPLE METHOD TO REPLACE THE CAP STRUCTURE OF EUKARYOTIC MRNAs WITH OLIGONUCLEOTIDES" GENE, NL, ELSEVIER BIOMEDICAL PRESS, AMSTERDAM, vol. 138, 1994, pages 171-174, XP002017391 ISSN: 0378-1119 * the whole document *		TECHNICAL FIELDS SEARCHED (Int.Cl.)
A	CARNINCI P ET AL: "High-efficiency full-length cDNA cloning by biotinylated CAP trapper" GENOMICS, ACADEMIC PRESS, SAN DIEGO, US, vol. 37, no. 3, 1 November 1996 (1996-11-01), pages 327-336, XP002081729 ISSN: 0888-7543 * the whole document *		
		-/-	
The present search report has been drawn up for all claims			
Place of search	Date of completion of the search	Examiner	
THE HAGUE	19 June 2001	HORNIG H.	
CATEGORY OF CITED DOCUMENTS		T : theory or principle underlying the invention E : earlier patent document, but published on, or after the filing date D : document cited in the application L : document cited for other reasons & : member of the same patent family, corresponding document	
X : particularly relevant if taken alone Y : particularly relevant if combined with another document of the same category A : technological background O : non-written disclosure P : intermediate document			



The Search Division considers that the present European patent application does not comply with the requirements of unity of invention and relates to several inventions or groups of inventions, namely:

1. Claims: (1,2,4-22)-partially

Use of an oligonucleotide as a primer for synthesizing the polynucleotide sequence of clone BNGH41000020 comprising the nucleotide sequence of SEQ ID No. 1, or the complementary strand thereof, wherein said oligonucleotide is complementary to said polynucleotide or the complementary strand thereof and comprises at least 15 nucleotides; a primer set for synthesizing polynucleotides, the primer set comprises an oligo-dT primer and an oligonucleotide complementary to the complementary strand of the polynucleotide sequence SEQ ID No. 1; a polynucleotide which can be synthesized with said primer set; a protein coding for said polynucleotide; a partial peptide of said protein; an isolated polynucleotide comprises (a) a coding region of SEQ ID No. 3595 or (b) a polynucleotide comprises a nucleotide sequence encoding a protein comprising the amino acid SEQ ID No. 3596; an antibody against said protein; a vector comprises said polynucleotide; a transformant expressing said vector; an antisense polynucleotide against said polynucleotide; a method of synthesizing said polynucleotide; a method for detecting said polynucleotide;

2. Claims: (1,2,4-22)-partially

Idem as subject 1 but limited to BNGH41000087; SEQ ID No. 2, SEQ ID Nos. 4078 and 4079;

3. Claims: (1,2,4-22)-partially

Idem as subject 1 but limited to BNGH41000091; SEQ ID No. 3, SEQ ID Nos. 3597 and 3598;

4. Claims: (1-22)-partially and as far as applicable

Idem as subject 1 but limited to HEMBA1000006, respectively SEQ ID nos. 2547 and 2548; a primer set for synthesizing polynucleotides, the primer set comprises a combination of an oligonucleotide comprises a nucleotide sequence complementary to the complementary strand of the polynucleotide comprising a 5'-end nucleotide sequence and an oligonucleotide comprising a nucleotide sequence complementary to the polynucleotide comprising a 3'-end nucleotide sequence, wherein said oligonucleotide comprises at least 15 nucleotides and wherein said combination of 5'-end nucleotide sequence 3'-end nucleotide sequence is selected from SEQ ID Nos. 4 and 830;

5.-830. Claims: (1-23)-partially

Idem as subject 4 but limited to HEMBA1000121 to

European Patent
OfficeLACK OF UNITY OF INVENTION
SHEET BApplication Number
EP 00 11 4089

The Search Division considers that the present European patent application does not comply with the requirements of unity of invention and relates to several inventions or groups of inventions, namely:

NT2RP2006580; (Invention 5 is limited to HEMBA1000121 respectively SEQ ID Nos. 5,831,2551 and 2552; Invention 6 is limited to HEMBA100128 respectively SEQ ID Nos. 6,832,2553 and 2554; Invention 830 is limited to NT2RP2006580 respectively SEQ ID Nos. 2545, 2546, 4178 and 4179).

831. Claim: 23-complete

A database of nucleotides and/or proteins, the database comprising information on at least one sequence selected from the nucleotides of clone BNHG41000020 (SEQ ID Nos. 1, 3595 and 3596) to NT2RP2006580 (SEQ ID Nos. 2545,2546,4178 and 4179).



European Patent
Office

EUROPEAN SEARCH REPORT

Application Number
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DOCUMENTS CONSIDERED TO BE RELEVANT			
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (Int.Cl.7)
A	<p>JACOBS K A ET AL: "A genetic selection for isolating cDNAs encoding secreted proteins" GENE: AN INTERNATIONAL JOURNAL ON GENES AND GENOMES, ELSEVIER SCIENCE PUBLISHERS, BARKING, GB, vol. 198, no. 1-2, 1 October 1997 (1997-10-01), pages 289-296, XP004116069 ISSN: 0378-1119 * the whole document *</p> <p>---</p>		
A	<p>TASHIRO K ET AL: "SIGNAL SEQUENCE TRAP: A CLONING STRATEGY FOR SECRETED PROTEINS AND TYPE I MEMBRANE PROTEINS" SCIENCE, US, AMERICAN ASSOCIATION FOR THE ADVANCEMENT OF SCIENCE, vol. 261, 30 July 1993 (1993-07-30), pages 600-603, XP000673204 ISSN: 0036-8075 * the whole document *</p> <p>---</p>		
A	<p>ALTSCHUL S F ET AL: "BASIC LOCAL ALIGNMENT SEARCH TOOL" JOURNAL OF MOLECULAR BIOLOGY, GB, LONDON, vol. 215, 1990, pages 403-410, XP000604562 ISSN: 0022-2836 * the whole document *</p> <p>---</p>		TECHNICAL FIELDS SEARCHED (Int.Cl.7)
A	<p>PEARSON W R ET AL: "IMPROVED TOOLS FOR BIOLOGICAL SEQUENCE COMPARISON" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA, NATIONAL ACADEMY OF SCIENCE, WASHINGTON, US, vol. 85, 1 April 1988 (1988-04-01), pages 2444-2448, XP002060460 ISSN: 0027-8424 * the whole document *</p> <p>-----</p>		
<p>The present search report has been drawn up for all claims</p>			
Place of search EPO FORM 1503 03.82 (P04C01)	Date of completion of the search 19 June 2001	Examiner HORNING H.	
<p>CATEGORY OF CITED DOCUMENTS</p> <p>X : particularly relevant if taken alone Y : particularly relevant if combined with another document of the same category A : technological background O : non-written disclosure P : intermediate document</p> <p>T : theory or principle underlying the invention E : earlier patent document, but published on, or after the filing date D : document cited in the application L : document cited for other reasons & : member of the same patent family, corresponding document</p>			

**ANNEX TO THE EUROPEAN SEARCH REPORT
ON EUROPEAN PATENT APPLICATION NO.**

EP 00 11 4089

This annex lists the patent family members relating to the patent documents cited in the above-mentioned European search report. The members are as contained in the European Patent Office EDP file on. The European Patent Office is in no way liable for these particulars which are merely given for the purpose of information.

19-06-2001

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WO 9845435 A	15-10-1998	AU EP	6956698 A 0973898 A	30-10-1998 26-01-2000
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For more details about this annex : see Official Journal of the European Patent Office, No. 12/82